

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:07:10 ; Search time 2114.72 Seconds
(without alignments)
11136.377 Million cell updates/sec

Title: US-10-048-046-1_COPY_1516_2013

Perfect score: 498
Sequence: 1 tgcctctgcaaggaagca.....gtcactggggccgctactgc 498

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1393428

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_dat:*
7: gb_db:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	3.2	20	6	CQ766678 Sequence
2	15	3.0	20	6	AR234610 Sequence
3	15	3.0	22	6	AR225071 Sequence
4	15	3.0	25	6	AR242539 Sequence
5	14	2.8	15	6	AR132365 Sequence
6	14	2.8	15	6	AR132365 Sequence
7	14	2.8	15	6	AR132367 Sequence
8	14	2.8	19	6	BD166119 Sequence
9	14	2.8	24	6	AB44252 Sequence
10	14	2.8	24	6	AB487528 Sequence
11	14	2.8	24	6	BD075290 Sequence
12	14	2.8	27	9	SA1367 T cell anti
13	14	2.8	30	6	EA9808 Mutation pr
14	14	2.8	30	6	AR214531 Sequence
15	14	2.6	17	6	CQ623099 Sequence
16	13	2.6	17	6	CQ623100 Sequence
17	13	2.6	17	6	CQ623101 Sequence
18	13	2.6	17	6	CQ623102 Sequence
19	13	2.6	17	6	CQ623103 Sequence

C 20	13	2.6	17	6	E34099
C 21	13	2.6	17	6	AR464162
C 22	13	2.6	17	6	AR464163
C 23	13	2.6	17	6	AR464164
C 24	13	2.6	17	6	AR464165
C 25	13	2.6	17	6	AR464166
C 26	13	2.6	17	6	AX762451
C 27	13	2.6	18	6	A26384
C 28	13	2.6	18	6	A87883
C 29	13	2.6	18	6	A89850
C 30	13	2.6	18	6	AR297846
C 31	13	2.6	18	6	AR300017
C 32	13	2.6	18	6	AX111589
C 33	13	2.6	18	6	AX111590
C 34	13	2.6	18	6	AX111597
C 35	13	2.6	18	6	AX111598
C 36	13	2.6	19	6	BD065396
C 37	13	2.6	19	6	CQ768769
C 38	13	2.6	19	6	AX395465
C 39	13	2.6	19	6	AX670675
C 40	13	2.6	20	6	AR004675
C 41	13	2.6	20	6	AR008161
C 42	13	2.6	20	6	AR136944
C 43	13	2.6	20	6	E12085
C 44	13	2.6	20	6	I76945
C 45	13	2.6	20	6	I80940
C 46	13	2.6	20	6	I81036
C 47	13	2.6	20	6	AR300298
C 48	13	2.6	20	6	AX613977
C 49	13	2.6	20	6	AX798039
C 50	13	2.6	20	6	BD105585
C 51	13	2.6	21	6	AX114695
C 52	13	2.6	21	6	AX114821
C 53	13	2.6	21	6	AX118750
C 54	13	2.6	21	6	AX128167
C 55	13	2.6	21	6	AX644766
C 56	13	2.6	21	6	AX815823
C 57	13	2.6	22	6	AR252249
C 58	13	2.6	22	6	AR489226
C 59	13	2.6	22	6	AX003054
C 60	13	2.6	22	6	AX224699
C 61	13	2.6	22	6	BD129696
C 62	13	2.6	23	6	BD234236
C 63	13	2.6	24	6	AR036150
C 64	13	2.6	24	6	AR084729
C 65	13	2.6	24	6	AR090647
C 66	13	2.6	24	6	BD183262
C 67	13	2.6	24	6	AR197682
C 68	13	2.6	24	6	AR259836
C 69	13	2.6	24	6	AX060739
C 70	13	2.6	24	6	AX060918
C 71	13	2.6	24	6	AX683912
C 72	13	2.6	25	6	BD141710
C 73	13	2.6	25	6	A22036
C 74	13	2.6	25	6	BD188936
C 75	13	2.6	25	6	CQ627991
C 76	13	2.6	25	6	CQ627992
C 77	13	2.6	25	6	CQ627993
C 78	13	2.6	25	6	CQ627994
C 79	13	2.6	25	6	CQ627995
C 80	13	2.6	25	6	CQ627996
C 81	13	2.6	25	6	CQ627997
C 82	13	2.6	25	6	CQ627998
C 83	13	2.6	25	6	CQ627999
C 84	13	2.6	25	6	CQ628000
C 85	13	2.6	25	6	CQ628001
C 86	13	2.6	25	6	CQ628002
C 87	13	2.6	25	6	CQ628003
C 88	13	2.6	25	6	AR282672
C 89	13	2.6	25	6	AR468054
C 90	13	2.6	25	6	AR469055
C 91	13	2.6	25	6	AR469056
C 92	13	2.6	25	6	AR469057

C 93	13	2.6	25	6	AR469058	Sequence
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C 96	13	2.6	25	6	AR469061	Sequence
C 97	13	2.6	25	6	AR469062	Sequence
C 98	13	2.6	25	6	AR469063	Sequence
C 99	13	2.6	25	6	AR469064	Sequence
C 100	13	2.6	25	6	AR469065	Sequence
C 101	13	2.6	25	6	AR469066	Sequence
C 102	13	2.6	25	6	AR469067	Sequence
C 103	13	2.6	25	6	AR469068	Sequence
C 104	13	2.6	25	6	AR469069	Sequence
C 105	13	2.6	27	6	AR469070	Sequence
C 106	13	2.6	27	6	AR469071	Sequence
C 107	13	2.6	27	6	AR469072	Sequence
C 108	13	2.6	27	6	AR469073	Sequence
C 109	13	2.6	27	6	AR469074	Sequence
C 110	13	2.6	27	6	AR469075	Sequence
C 111	13	2.6	28	6	AR469076	Sequence
C 112	13	2.6	28	6	AR469077	Sequence
C 113	13	2.6	29	6	AR469078	Sequence
C 114	13	2.6	29	6	AR469079	Sequence
C 115	13	2.6	30	6	AR469080	Sequence
C 116	13	2.6	30	6	AR469081	Sequence
C 117	13	2.6	30	6	AR469082	Sequence
C 118	13	2.6	30	6	AR469083	Sequence
C 119	13	2.6	30	6	AR469084	Sequence
C 120	13	2.6	30	6	AR469085	Sequence
C 121	13	2.6	30	6	AR469086	Sequence
C 122	13	2.6	30	6	AR469087	Sequence
C 123	13	2.6	30	6	AR469088	Sequence
C 124	13	2.6	30	6	AR469089	Sequence
C 125	13	2.6	30	6	AR469090	Sequence
C 126	13	2.6	30	6	AR469091	Sequence
C 127	13	2.6	30	6	AR469092	Sequence
C 128	13	2.6	30	6	AR469093	Sequence
C 129	13	2.6	30	6	AR469094	Sequence
C 130	13	2.6	30	6	AR469095	Sequence
C 131	13	2.6	30	6	AR469096	Sequence
C 132	13	2.6	30	6	AR469097	Sequence
C 133	13	2.6	30	6	AR469098	Sequence
C 134	13	2.6	30	6	AR469099	Sequence
C 135	13	2.6	30	6	AR469100	Sequence
C 136	13	2.6	30	6	AR469101	Sequence
C 137	13	2.6	30	6	AR469102	Sequence
C 138	13	2.6	30	6	AR469103	Sequence
C 139	13	2.6	30	6	AR469104	Sequence
C 140	13	2.6	30	6	AR469105	Sequence
C 141	13	2.6	30	6	AR469106	Sequence
C 142	13	2.6	30	6	AR469107	Sequence
C 143	13	2.6	30	6	AR469108	Sequence
C 144	13	2.6	30	6	AR469109	Sequence
C 145	13	2.6	30	6	AR469110	Sequence
C 146	13	2.6	30	6	AR469111	Sequence
C 147	13	2.6	30	6	AR469112	Sequence
C 148	13	2.6	30	6	AR469113	Sequence
C 149	13	2.6	30	6	AR469114	Sequence
C 150	13	2.6	30	6	AR469115	Sequence

ALIGNMENTS

RESULT 1
LOCUS CQ766678
DEFINITION Sequence 34 from Patent WO2004005541.
ACCESSION CQ766678
VERSION CQ766678.1 GI:44908908
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS van Broeckhoven, C., de Jonghe, P., Timmerman, V. and Verhoeven, K.
TITLE Diagnostic tests for the detection of peripheral neuropathy
JOURNAL Patent: WO 2004005541-A 34 15-JAN-2004;
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="reverse primer, exon 3, gene ABRN1"

ORIGIN

Query Match 3.2%; Score 16; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 CTGCGCTGACGCTTTC 126
Db 3 CTGCGCTGACGCTTTC 18

RESULT 2
LOCUS AR234610/c
DEFINITION Sequence 51 from patent US 6458591.
ACCESSION AR234610
VERSION AR234610.1 GI:27277317
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt, U.
TITLE Antisense modulation of phosphotyrase kinase Alpha 2 expression
JOURNAL Patent: US 6458591-A 51 01-OCT-2002;
FEATURES
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 3.0%; Score 15; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 CCTGTGACCTGCTG 38
Db 20 CCTGTGACCTGCTG 6

RESULT 3
LOCUS AR225071
DEFINITION Sequence 37 from patent US 6441156.
ACCESSION AR225071
VERSION AR225071.1 GI:23334206
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.

REFERENCE 1 (bases 1 to 22)
AUTHORS Ierman, M.I., Latiff, F., Wei, M.-H., Duh, F.-M., Minna, J.D., Sekido, Y. and Gao, B.
TITLE Calcium channel compositions and methods of use thereof
JOURNAL Patent: US 6441156-A 37 27-AUG-2002;
FEATURES
source
1..22
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 3.0%; Score 15; DB 6; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 GTTACTGCTGTGGCC 391
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6 GTTACTGCTGTGGCC 20

Db

RESULT 4
AR242539/c AR242539 25 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 12 from patent US 6472515.
ACCESSION AR242539
VERSION AR242539.1 GI:27288993
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Climent-Johansson,I., Dahlman-Wright,K., Lake,S. and Wasserman,W.
TITLE Response element
JOURNAL Patent: US 6472515-A 12 29-OCT-2002;
FEATURES
Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 AAAACATGTTGACCG 304
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21 AAAACATGTTGACCG 7

Db

RESULT 5
AR132365 AR132365 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 790 from patent US 6194150.
ACCESSION AR132365
VERSION AR132365.1 GI:14121270
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 790 27-FEB-2001;
FEATURES
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.8%; Score 14; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 AGAATTACTCTGGCA 270
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2 AGAATTACTCTGGCA 15

Db

RESULT 6
AR132366 AR132366 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 791 from patent US 6194150.
ACCESSION AR132366
VERSION AR132366.1 GI:14121271
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 791 27-FEB-2001;
FEATURES
Location/Qualifiers
1..15
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 AGAATTACTCTGGCA 270
|||||
2 AGAATTACTCTGGCA 15

Db

RESULT 7
AR132367 AR132367 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 792 from patent US 6194150.
ACCESSION AR132367
VERSION AR132367.1 GI:14121272
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 792 27-FEB-2001;
FEATURES
Location/Qualifiers
1..15
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/mol_type="unassigned DNA"

ORIGIN

Query Match 2.8%; Score 14; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 AGAATTACTCTGGCA 270
|||||
2 AGAATTACTCTGGCA 15

Db

RESULT 8
BD166119 BD166119 19 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method.
ACCESSION BD166119
VERSION BD166119.1 GI:27871931
KEYWORDS JP 2002191372-A/99.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaki,T.
TITLE Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method
JOURNAL NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence

PN JP 2002191372-A/99
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KUBANE, TAKAHIRO KANAGAWA, YOICHI KANAGATA, MASAKI PI
TORIMURA,
PI SHINYA KUDATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12M1/00, C12Q1/68, G01N33/56//G01N33/53, G01N33/566, PC
C12N15/00
CC The sequence hybridizes with the sequence of the above no.91.
FH Key
FT source
Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GAGAGCTCGTGGC 317
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Db 18 GAGAGCTCGTGGC 5

RESULT 9
LOCUS A84252
DEFINITION Sequence 19 from Patent WO9846645.
ACCESSION A84252
VERSION A84252.1 GI:6733294
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 24)
Kufner, P. and Raum, T.
TITLE NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND
USERS THEREOF
JOURNAL Patent: WO 9846645-A 19 22-OCT-1998;
KUPER PETER (DE); RAUM TOBIAS (DE)
FEATURES
source 1. .24
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 GTGAGCTCAACCTG 198
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Db 14 GTGAGCTCAACCTG 1

RESULT 10
LOCUS AX487528
DEFINITION Sequence 4828 from Patent WO02053728.
ACCESSION AX487528
VERSION AX487528.1 GI:22321676
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
AUTHORS Roemer, T., Jiang, B., Boone, C., Bussey, H. and Olsen, K.L.

TITLE
JOURNAL Gene disruption methodologies for drug target discovery
Patent: WO 02053728-A 4828 11-JUL-2002;
Eliara Pharmaceuticals, Inc. (US)
FEATURES
source 1. .24
Location/Qualifiers
/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

Query Match 2.8%; Score 14; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 TTTCCTGCTGCTGA 347
|||||
Db 11 TTTCCTGCTGCTGA 24

RESULT 11
LOCUS BD075290/c
DEFINITION Novel method for the production of anti-human antigen receptors and
uses thereof.
ACCESSION BD075290
VERSION BD075290.1 GI:22620893
KEYWORDS JP 2001519824-A/19.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE
AUTHORS 1 (bases 1 to 24)
Kufner, P. and Raum, T.
TITLE Novel method for the production of anti-human antigen receptors and
uses thereof
JOURNAL Patent: JP 2001519824-A 19 23-OCT-2001;
MICROMET AG
OS Artificial Sequence
COMMENT
PN JP 2001519824-A/19
PD 23-OCT-2001
PF 14-APR-1998 JP 1998543494
PR 14-APR-1997 EP 97106109.8
PI PETER KUFNER, TOBIAS RAUM
PC C07K16/00, C07K16/30, A61K39/395
CC Description of Artificial Sequence: primer
FH Key
FT source 1. .24
Location/Qualifiers
/organism="Artificial Sequence".
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 2.8%; Score 14; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 GTGAGCTCAACCTG 198
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Db 14 GTGAGCTCAACCTG 1

RESULT 12
LOCUS S81367/c
DEFINITION T cell antigen receptor-beta chain {rearranged DJ region} [human,
8-wk fetal thymus, sample 2, mRNA, 27 nt].
ACCESSION S81367
VERSION S81367.1 GI:245125
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REMARK
FEATURES
source

1 (bases 1 to 27)
George, J. F., Jr. and Schroeder, H. W., Jr.
Developmental regulation of D beta reading frame and junctional
diversity in T cell receptor-beta transcripts from human thymus
J. Immunol. 148 (4), 1230-1239 (1992)
92148146
1310710
Genbank staff at the National Library of Medicine created this
entry [NCBI gisdbq 81367] from the original journal article.
Location/Qualifiers
1..27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..27
/gene="T cell antigen receptor-beta chain"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 CGGCGCTGACCC 151
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21 CTGGGCTGACCC 8

Db

RESULT 13
E09808/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

E09808
Mutation primer for esterase.
E09808
E09808.1 GI:22026437
JP 1995213280-A/26.
unidentified
unclassified
1 (bases 1 to 30)
Matsuki, Y., Hori, S. and Yabusaki, Y.
THERMOSTABLE ESTERASE
Patent: JP 1995213280-A 26 15-AUG-1995;
SUMITOMO CHEM CO LTD
OS None
OC Artificial sequences.
PN JP 1995213280-A/26
PD 15-AUG-1995
PF 02-FEB-1994 JP 1994011014
PI MATSUKI YASUSHI, HORAI SHINTI, YABUSAKI YOSHITSUGU PC
C12N9/16, C12N1/21, C12N15/00, C12N9/16, C12R1/19, PC
C12R1/19;
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CC topology: Linear;
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FH Location/Qualifiers
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location/Qualifiers
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 CGGCGTCTGACA 229
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30 CGGCGTCTGACA 17

Db

RESULT 14
AR214531/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AR214531
Sequence 10 from patent US 6407284.
AR214531
AR214531.1 GI:23312359
Unknown.
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 30)
Kudo, J., Takashima, Y. and Mine, S.
Method of resolving 2-oxobicyclo [3.1.0] hexane-6-carboxylic acid
derivatives
Patent: US 6407284-A 10 18-JUN-2002;
Location/Qualifiers
1..30
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.8%; Score 14; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 CGGCGTCTGACA 229
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30 CGGCGTCTGACA 17

Db

RESULT 15
CQ623099/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

CQ623099
Sequence 7839 from Patent WO0192524.
CQ623099
CQ623099.1 GI:41673317
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Gu, Y., Ji, Y., Penn, S. G., Hanzel, D. K., Rank, D. R., Chen, W. and
Shannon, M. E.
Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 7839 06-DEC-2001;
Aeomica, Inc. (US)
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCTC 42
|||||
17 CACCTGCTGCTC 5

Db

RESULT 16
CQ623100/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

CQ623100
Sequence 7840 from Patent WO0192524.
CQ623100
CQ623100.1 GI:41673318
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Gu, Y., Ji, Y., Penn, S. G., Hanzel, D. K., Rank, D. R., Chen, W. and
Shannon, M. E.
Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 7839 06-DEC-2001;
Aeomica, Inc. (US)
Location/Qualifiers
1..17
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCTC 42
|||||
17 CACCTGCTGCTC 5

Db

REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 7840 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 CACCTGCTGCTTC 42
|||||
16 CACCTGCTGCTTC 4
|||||
RESULT 17
LOCUS C0623101 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 7841 from Patent WO0192524.
ACCESSION C0623101
VERSION C0623101.1 GI:41673319
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 7841 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 CACCTGCTGCTTC 42
|||||
15 CACCTGCTGCTTC 3
|||||
RESULT 18
LOCUS C0623102 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 7842 from Patent WO0192524.
ACCESSION C0623102
VERSION C0623102.1 GI:41673320
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 7842 06-DEC-2001;

FEATURES
source Aeomica, Inc. (US)
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 CACCTGCTGCTTC 42
|||||
14 CACCTGCTGCTTC 2
|||||
RESULT 19
LOCUS C0623103 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 7843 from Patent WO0192524.
ACCESSION C0623103
VERSION C0623103.1 GI:41673321
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 7843 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 CACCTGCTGCTTC 42
|||||
13 CACCTGCTGCTTC 1
|||||
RESULT 20
LOCUS E34099 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Protein participating in oxidation reaction of organosulfur compound and gene encoding the same.
ACCESSION E34099
VERSION E34099.1 GI:18624218
KEYWORDS JP 2000093180-A/17.
SOURCE JP 2000093180-A/17.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hayano, T., Hino, S. and Kajie, S.
TITLE Protein participating in oxidation reaction of organosulfur compound and gene encoding the same
JOURNAL Patent: JP 2000093180-A 17 04-APR-2000;
TOMEN CORP
OS Artificial sequence
PN JP 2000093180-A/17
PD 04-APR-2000
PF 28-SEP-1998 JP 1998272744
PI TOSHIBA HAYANO, SANAE HINO, SHINICHI KAJIE

PC C12N15/09, C12N1/21, C12N9/02//B09C1/10, C02F3/34, C10G32/00, PC
(C12N15/09, C12R1:38), (C12N1/21, C12R1:19), (C12N9/02, C12R1:19), PC
PC B09B3/00, (C12N15/00, C12R1:38)
CC
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
1..17
/organism="Artificial sequence".
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 GAGCGCGAGCAGG 79
|||||
17 GAGCGCGAGCAGG 5

Db

RESULT 21
AR464162/c 17 bp DNA linear PAT 20-FEB-2004
LOCUS
DEFINITION Sequence 7839 from patent US 6686188.
AR464162
ACCESSION
VERSION AR464162.1 GI:42699219
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
Patent: US 6686188-A 7839 03-FEB-2004;
JOURNAL Location/Qualifiers
FEATURES
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCTTC 42
|||||
17 CACCTGCTGCTTC 5

Db

RESULT 22
AR464163/c 17 bp DNA linear PAT 20-FEB-2004
LOCUS
DEFINITION Sequence 7840 from patent US 6686188.
AR464163
ACCESSION
VERSION AR464163.1 GI:42699220
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
Patent: US 6686188-A 7840 03-FEB-2004;
JOURNAL Location/Qualifiers
FEATURES
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCTTC 42
|||||
16 CACCTGCTGCTTC 4

Db

RESULT 23
AR464164/c 17 bp DNA linear PAT 20-FEB-2004
LOCUS
DEFINITION Sequence 7841 from patent US 6686188.
AR464164
ACCESSION
VERSION AR464164.1 GI:42699221
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
Patent: US 6686188-A 7841 03-FEB-2004;
JOURNAL Location/Qualifiers
FEATURES
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCTTC 42
|||||
15 CACCTGCTGCTTC 3

Db

RESULT 24
AR464165/c 17 bp DNA linear PAT 20-FEB-2004
LOCUS
DEFINITION Sequence 7842 from patent US 6686188.
AR464165
ACCESSION
VERSION AR464165.1 GI:42699222
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
Patent: US 6686188-A 7842 03-FEB-2004;
JOURNAL Location/Qualifiers
FEATURES
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCTTC 42
|||||
14 CACCTGCTGCTTC 2

Db

RESULT 25
AR464166/c
LOCUS AR464166 17 bp DNA
DEFINITION Sequence 7843 from patent US 6686188.
ACCESSION AR464166
VERSION AR464166.1 GI:42699223
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
Gu.Y., Ji.Y., Penn.S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7843 03-FEB-2004;
FEATURES
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCTTC 42
DB 13 CACCTGCTGCTTC 1

RESULT 26
AX762451/c
LOCUS AX762451 17 bp DNA
DEFINITION Sequence 5772 from patent WO03040369.
ACCESSION AX762451
VERSION AX762451.1 GI:32257067
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Tejerano,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5772 15-MAY-2003;
FEATURES
Molecular Engines Laboratories (FR)
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 TTCTGCTTACTG 383
DB 16 TTCTGCTTACTG 4

RESULT 27
A26384/c
LOCUS A26384 18 bp DNA
DEFINITION Probe no.2.
ACCESSION A26384
VERSION A26384.1 GI:904941

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE ANTIGEN PROCESSING
JOURNAL Patent: WO 9211289-A 10 09-JUL-1992;
FEATURES
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 CTGCTGCAGCCT 123
DB 13 CTGCTGCAGCCT 1

RESULT 28
A87883
LOCUS A87883 18 bp DNA
DEFINITION Sequence 31 from Patent WO9833904.
ACCESSION A87883
VERSION A87883.1 GI:6736453
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysck,W.D. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 31 06-AUG-1998;
FEATURES
BIOLOGISTIK GBS (DE); BRYSCCH WOLFGANG (DE)
Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 CTCTCCAGCGGG 329
DB 6 CTCTCCAGCGGG 18

RESULT 29
A89850
LOCUS A89850 18 bp DNA
DEFINITION Sequence 31 from Patent EP0856579.
ACCESSION A89850
VERSION A89850.1 GI:6738364
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysck,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 31 05-AUG-1998;
FEATURES
BIOLOGISTIK GBS (DE)
Location/Qualifiers
1..18
/organism="unidentified"

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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match      2.6%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      317 CTCCTCCAGCGGG 329
      |||||
      6 CTCCTCCAGCGGG 18

RESULT 30
AR297846/c      AR297846      18 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION      Sequence 9581 from patent US 6537751.
ACCESSION      AR297846
VERSION      AR297846.1 GI:31685130
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS      Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE      Biallelic markers for use in constructing a high density
JOURNAL      Patente: US 6537751-A 9581 25-MAR-2003;
FEATURES
source      1..18
/mol_type="genomic DNA"

ORIGIN
Query Match      2.6%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      332 TGTTCCTGCTGTC 344
      |||||
      16 TGTTCCTGCTGTC 4

RESULT 31
AR300017/c      AR300017      18 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION      Sequence 11752 from patent US 6537751.
ACCESSION      AR300017
VERSION      AR300017.1 GI:31687301
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 18)
AUTHORS      Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE      Biallelic markers for use in constructing a high density
JOURNAL      Patente: US 6537751-A 11752 25-MAR-2003;
FEATURES
source      1..18
/mol_type="genomic DNA"

ORIGIN
Query Match      2.6%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      412 ACCTATCAGATC 424
      |||||
      15 ACCTATCAGATC 3

RESULT 32
AX111589/c      AX111589      18 bp      DNA      linear      PAT 30-APR-2001
DEFINITION      Sequence 19 from Patent WO0123561.
ACCESSION      AX111589
VERSION      AX111589.1 GI:13927870
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
AUTHORS      Shimkets,R.A., Vernet,C., Tchernev,V.T., Boldog,F.L. and
Hermann,J.L.
TITLE      Novel polynucleotides encoding proteins containing thrombospondin
JOURNAL      type 1 repeats
Patent: WO 0123561-A 19 05-APR-2001;
Curagen Corporation (US)
FEATURES
source      1..18
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Chemically Synthesized"

ORIGIN
Query Match      2.6%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      207 GTGCTGGACGC 219
      |||||
      14 GTGCTGGACGC 2

RESULT 33
AX111590/c      AX111590      18 bp      DNA      linear      PAT 30-APR-2001
DEFINITION      Sequence 20 from Patent WO0123561.
ACCESSION      AX111590
VERSION      AX111590.1 GI:13927871
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
AUTHORS      Shimkets,R.A., Vernet,C., Tchernev,V.T., Boldog,F.L. and
Hermann,J.L.
TITLE      Novel polynucleotides encoding proteins containing thrombospondin
JOURNAL      type 1 repeats
Patent: WO 0123561-A 20 05-APR-2001;
Curagen Corporation (US)
FEATURES
source      1..18
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Chemically Synthesized"

ORIGIN
Query Match      2.6%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      207 GTGCTGGACGC 219
      |||||
      5 GTGCTGGACGC 17

RESULT 34
AX111597/c      AX111597      18 bp      DNA      linear      PAT 30-APR-2001
DEFINITION      Sequence 27 from Patent WO0123561.
ACCESSION      AX111597
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VERSION      AX11597.1 GI:13927878
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     synthetic construct
REFERENCE    1
AUTHORS      Shinkets,R.A., Vernet,C., Tchernev,V.T., Boldog,F.L. and
              Herrmann,J.L.
TITLE        Novel polynucleotides encoding proteins containing thrombospondin
              type 1 repeats
JOURNAL      Patent: WO 0123561-A 27 05-APR-2001;
              Cugen Corporation (US)
FEATURES     source
              1..18
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Chemically Synthesized"
ORIGIN
Query Match      2.6%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      207 GTGCTGACGCGC 219
      |||||
      14 GTGCTGACGCGC 2

RESULT 35
LOCUS      AX11598 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 28 from Patent WO0123561.
ACCESSION  AX11598
VERSION     AX11598.1 GI:13927879
KEYWORDS
SOURCE      synthetic construct
            artificial sequences.
REFERENCE    1
AUTHORS      Shinkets,R.A., Vernet,C., Tchernev,V.T., Boldog,F.L. and
              Herrmann,J.L.
TITLE        Novel polynucleotides encoding proteins containing thrombospondin
              type 1 repeats
JOURNAL      Patent: WO 0123561-A 28 05-APR-2001;
              Cugen Corporation (US)
FEATURES     source
              1..18
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Chemically Synthesized"
ORIGIN
Query Match      2.6%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      207 GTGCTGACGCGC 219
      |||||
      5 GTGCTGACGCGC 17

RESULT 36
LOCUS      BD065396 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD065396
VERSION     BD065396.1 GI:22610999
KEYWORDS
SOURCE      unidentified
            unidentified
            unclassified.
ORGANISM
KEYWORDS

```

```

REFERENCE    1 (bases 1 to 18)
AUTHORS      Schlingensiepen,K.H. and Brysch,W.
TITLE        An antisense oligonucleotide preparation method
JOURNAL      Patent: JP 200151000-A 31 07-AUG-2001;
              BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT      OS Unknown
            PN JP 2001511000-A/31
            PD 07-AUG-2001
            PF 30-JAN-1998 JP 1998532533
            PR 31-JAN-1997 EP 97101531.8
            PI KARL HERMANN SCHLINGENSIEPEN WOLFGANG BRYSCH
            PC C12N15/11,C07H21/04,A61K31/70
            CC An antisense oligonucleotide preparation method FH Key
            Location/Qualifiers
            FT source
            1..18
            /organism="Unknown".
            Location/Qualifiers
            1..18
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
ORIGIN
Query Match      2.6%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      317 CTCTCCAGCGGG 329
      |||||
      6 CTCTCCAGCGGG 18

RESULT 37
LOCUS      CQ768769/c 19 bp DNA linear PAT 04-MAR-2004
DEFINITION Sequence 17 from Patent WO2004007762.
ACCESSION  CQ768769
VERSION     CQ768769.1 GI:45112009
KEYWORDS
SOURCE      Rattus norvegicus (Norway rat)
            Rattus norvegicus
            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE    1
AUTHORS      Bilbe,G., Kinnunen,A. and Koenig,J.I.
TITLE        Genes associated with schizophrenia, adhd and bipolar disorders
JOURNAL      Patent: WO 2004007762-A 17 22-JAN-2004;
              Novartis AG (CH); Novartis Pharma GmbH (AT); University of Maryland
              (US)
FEATURES     source
              1..19
              /organism="Rattus norvegicus"
              /mol_type="unassigned DNA"
              /db_xref="taxon:10116"
ORIGIN
Query Match      2.6%; Score 13; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GCCCATGCCCGAC 57
      |||||
      19 GCCCATGCCCGAC 7

RESULT 38
LOCUS      AX395465 19 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 37 from Patent WO0208453.
ACCESSION  AX395465
VERSION     AX395465.1 GI:21066427
KEYWORDS

```


SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Tilton,G.B., Shockey,J.M. and Browne,J.A.
TITLE ACyl coenzyme A thioesterases
JOURNAL Patent: WO 0206433-A 37 31-JAN-2002;
Tilton, Gregory B. (US); Shockey, Jay M. (US); Browne, John A. (US)

FEATURES
source Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic"

ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 ATCCTGAAGATT 262
Db 2 ATCCTGAAGATT 14

RESULT 39
AX670675 19 bp DNA linear PAT 26-MAR-2003
LOCUS Sequence 2 from Patent WO0206685.
DEFINITION AX670675
ACCESSION AX670675
VERSION AX670675.1 GI:29292060
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Levett,L.J. and Liddle,S.
TITLE Diagnostic test for the detection of chromosomal abnormalities in a fetus
JOURNAL Patent: WO 0206685-A 2 06-SEP-2002;
FEATURES Cytogenetic DNA Services Ltd (GB)
source Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 CTTGGTGACAG 207
Db 7 CTTGGTGACAG 19

RESULT 40
AR004675/c 20 bp DNA linear PAT 04-DEC-1998
LOCUS AR004675
DEFINITION Sequence 4 from patent US 5747282.
ACCESSION AR004675
VERSION AR004675.1 GI:3965554
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Hershan,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.
and Futreal,P.Andrew.

TITLE 17Q-linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5747282-A 4 05-MAY-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCCTGCTCC 444
Db 16 CATTCCTGCTCC 4

RESULT 41
AR008161/c 20 bp DNA linear PAT 04-DEC-1998
LOCUS AR008161
DEFINITION Sequence 4 from patent US 5753441.
ACCESSION AR008161
VERSION AR008161.1 GI:3967270
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Hershan,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.
and Futreal,P.Andrew.
TITLE 17Q-linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5753441-A 4 19-MAY-1998;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCCTGCTCC 444
Db 16 CATTCCTGCTCC 4

RESULT 42
ARI36944/c 20 bp DNA linear PAT 16-JUN-2001
LOCUS ARI36944
DEFINITION Sequence 4 from patent US 6162897.
ACCESSION ARI36944
VERSION ARI36944.1 GI:14478194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Hershan,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.
and Futreal,P.Andrew.
TITLE 17q-linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 6162897-A 4 16-DEC-2000;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCCTGCTTC 444
Db 16 CATTCCTGCTTC 4

RESULT 43
E12085/c
LOCUS PCR primer for amplification of unspecific DNA sequence.
DEFINITION E12085
ACCESSION E12085
VERSION E12085.1 GI:22027752
KEYWORDS JP 1996242897-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Imai,H.
TITLE REPLICATION AND AMPLIFICATION OF GENE
JOURNAL Patent: JP 1996242897-A 1 24-SEP-1996;
NIPPON ZOKI PHARMACEUT CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1996242897-A/1
PD 24-SEP-1996
PF 07-MAR-1995 JP 1995074616
PI IMAI HIDEKI
PC C1201/68.C07H21/04.C12N15/09;
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
FH key Location/Qualifiers
FT source 1..20
location/Qualifiers
1..20
/organism="Artificial sequences"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 TGTGAGCTCAACC 196
Db 20 TGTGAGCTCAACC 8

RESULT 44
I76945/c
LOCUS 176945
DEFINITION Sequence 4 from patent US 5693473.
ACCESSION I76945
VERSION I76945.1 GI:3013099
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Shattuck-Eidens,D.M., Simard,J., Durocher,F., Emi,M. and Nakamura,Y.
TITLE Linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5693473-A 4 02-DEC-1997;
FEATURES location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCCTGCTTC 444
Db 16 CATTCCTGCTTC 4

RESULT 45
I80940/c
LOCUS Sequence 4 from patent US 5709999.
DEFINITION I80940
ACCESSION I80940
VERSION I80940.1 GI:3209230
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Shattuck-Eidens,D.M., Simard,J., Durocher,F., Emi,M. and Nakamura,Y.
TITLE Linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5709999-A 4 20-JAN-1998;
FEATURES location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCCTGCTTC 444
Db 16 CATTCCTGCTTC 4

RESULT 46
I81036/c
LOCUS 181036
DEFINITION Sequence 4 from patent US 5710001.
ACCESSION I81036
VERSION I81036.1 GI:3209326
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A., Hershman,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W. and Futreal,P.Andrew.
TITLE 17q-linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5710001-A 4 20-JAN-1998;
FEATURES location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCCTGCTTC 444
Db 16 CATTCCTGCTTC 4

RESULT 47
AR300298
LOCUS 20 bp
DEFINITION Sequence 100 from patent US 6537775.
PAT 12-JUN-2003

ACCESSION AR300298
VERSION AR300298.1 GI:31687717
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tourner-Lasserre, E., Joutel, A., Bousger, M.-G. and Bach, J.-F.
TITLE Gene involved in cadasil, method of diagnosis and therapeutic application
JOURNAL Patent: US 6537775-A 100 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TGGTTCCAGCCCA 49
|||||
8 TGGTTCCAGCCCA 20

RESULT 48
AX613977 20 bp DNA linear PAT 17-FEB-2003
LOCUS Sequence 5002 from Patent WO02072862.
DEFINITION AX613977
ACCESSION AX613977
VERSION AX613977.1 GI:28409406
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Cullen, P. and Seedorf, U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 5002 19-SEP-2002;
OCHAM GmbH (DE)
FEATURES Location/Qualifiers
source 1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 CCTGAGATTAC 264
|||||
4 CCTGAGATTAC 16

RESULT 49
AX798039 20 bp DNA linear PAT 08-OCT-2003
LOCUS Sequence 2 from Patent WO03054230.
DEFINITION AX798039
ACCESSION AX798039
VERSION AX798039.1 GI:37604329
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Hampson, G.N.
TITLE Detection of disease due to abnormal oestrogen levels
JOURNAL Patent: WO 03054230-A 2 03-JUL-2003;

KING'S COLLEGE LONDON (GB)
FEATURES Location/Qualifiers
source 1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 GTTCTGCTTACT 382
|||||
13 GTTCTGCTTACT 1

RESULT 50
BD105585/c 20 bp DNA linear PAT 27-AUG-2002
LOCUS Genes sensitive to 17q-chained breast cancer and ovarian cancer.
DEFINITION BD105585
ACCESSION BD105585
VERSION BD105585.1 GI:22651159
KEYWORDS JP 2001346593-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 20)
AUTHORS Skolnick, M.H., Goldgar, D.E., Miki, Y., Swenson, J., Kamb, A., and Harshman, K.D., Eidsens, D.M.S., Tavtigian, S.V., Wiseman, R.W. and Putrel, A.P.
TITLE Genes sensitive to 17q-chained breast cancer and ovarian cancer
JOURNAL Patent: JP 2001346593-A 3 18-DEC-2001;
MYRIAD GENETICS INC, UNIVERSITY OF UTAH RESEARCH FOUNDATION, THE UNITED STATES OF AMERICA
COMMENT OS Homo sapiens (human)
PN JP 2001346593-A/3
PD 18-DEC-2001
PF 18-APR-2001 JP 2001119644
PR 12-AUG-1994 US 08/289221, 02-SEP-1994 US 08/300266 PR
16-SEP-1994 US 08/308104, 29-NOV-1994 US 08/348824 PR
24-MAR-1995 US 08/409305, 07-JUN-1995 US 08/483554 PR
07-JUN-1995 US 08/487002
PI MARK H SKOLNICK, DAVID E GOLDFAR, YOSHIO MIKI, JEFF SWENSON, PI ALEXANDER KAMB,
PI KEITH D HARSHMAN, DONNA M SHATTUCK EIDENS, SEAN V TAVTIGIAN, PI ROGER W WISEMAN,
PI ANDREW P PUTREL,
PI C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/68, C12N15/00, C12N5/00
PC Strandedness: Single;
CC Topology: Linear;
CC Genes sensitive to 17q-chained breast cancer and ovarian CC
FH Key Location/Qualifiers
FT source 1..20
/organism="Homo sapiens (human)".
1..20
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCCTGCTTCC 444
|||||
16 CATTCCTGCTTCC 4

RESULT 51
AX114695/c
LOCUS AX114695 21 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 107 from Patent WO0128540.
ACCESSION AX114695
VERSION AX114695.1 GI:14031638
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Purvis, I.J. and Mccarthy, L.C.
TITLE Therapy of cephalic pain
JOURNAL Patent: WO 0128540-A 107 26-APR-2001;
GLAXO GROUP LIMITED (GB)
FEATURES
Source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"
ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 124 TTCTGCCACCTGT 136
DB 13 TTCTGCCACCTGT 1
RESULT 52
AX114821/c
LOCUS AX114821 21 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 107 from Patent WO0128539.
ACCESSION AX114821
VERSION AX114821.1 GI:14031763
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Purvis, I.J. and Mccarthy, L.C.
TITLE Agent for treating cephalic pain
JOURNAL Patent: WO 0128539-A 107 26-APR-2001;
GLAXO GROUP LIMITED (GB)
FEATURES
Source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"
ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 124 TTCTGCCACCTGT 136
DB 13 TTCTGCCACCTGT 1
RESULT 53
AX118750/c
LOCUS AX118750 21 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 106 from Patent WO0129255.
ACCESSION AX118750
VERSION AX118750.1 GI:14035701
KEYWORDS
SOURCE synthetic construct

ORGANISM
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Purvis, I.J. and Mccarthy, L.C.
TITLE Diagnostic test for cephalic pain
JOURNAL Patent: WO 0129255-A 106 26-APR-2001;
GLAXO GROUP LIMITED (GB)
FEATURES
Source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"
ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 124 TTCTGCCACCTGT 136
DB 13 TTCTGCCACCTGT 1
RESULT 54
AX128167/c
LOCUS AX128167 21 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 106 from Patent WO0129256.
ACCESSION AX128167
VERSION AX128167.1 GI:14134707
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Purvis, I.J. and Mccarthy, L.C.
TITLE Cephalic pain susceptibility marker
JOURNAL Patent: WO 0129256-A 106 26-APR-2001;
GLAXO GROUP LIMITED (GB)
FEATURES
Source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"
ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 124 TTCTGCCACCTGT 136
DB 13 TTCTGCCACCTGT 1
RESULT 55
AX644766/c
LOCUS AX644766 21 bp DNA linear PAT 27-FEB-2003
DEFINITION Sequence 104 from Patent WO0233121.
ACCESSION AX644766
VERSION AX644766.1 GI:28610774
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hosford, D. and Purvis, I.J.
TITLE Test for the diagnosis of diabetes and compounds for the treatment thereof
JOURNAL Patent: WO 0233121-A 104 25-APR-2002;
GLAXO GROUP LIMITED (GB)
FEATURES
Source Location/Qualifiers

source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 TTCTGCCACCTGT 136
|||||
13 TTCTGCCACCTGT 1

Db

RESULT 56
AX815823 21 bp DNA linear PAT 09-DEC-2003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE
AUTHORS
TITLE
JOURNAL
Herdge, T., Schellander, K. and Wimmers, K.
Genetic markers for the diagnosis of the expression of inverted
nipples in pigs, breeding animals and domestic cattle
Patent: WO 03066891-A 78 14-AUG-2003;
Foerderverein Biotechnologieforschung der deutschen
Schweineproduktion e.V. (DE)
Location/Qualifiers

FEATURES
source 1..21
/organism="Sus scrofa"
/mol_type="unassigned DNA"
/db_xref="taxon:9823"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 GAGCTGACCTATC 418
|||||
4 GAGCTGACCTATC 16

Db

RESULT 57
AR252249 22 bp DNA linear PAT 20-DEC-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 22)
Eagles, P.A.M. and Zheng, R.Q.
Inhibition of cytokine production
Patent: US 6476214-A 2 05-NOV-2002;
Location/Qualifiers

FEATURES
source 1..22
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TGCACCTGACT 139
|||||
7 TGCACCTGACT 19

Db

RESULT 58
AR489226 22 bp DNA linear PAT 15-MAY-2004
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 22)
Enerback, S. and Carlsson, P.
Animal model
Patent: US 6709860-A 5 23-MAR-2004;
Location/Qualifiers

FEATURES
source 1..22
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 CTGCAGCTTCT 127
|||||
9 CTGCAGCTTCT 21

Db

RESULT 59
AX003054 22 bp DNA linear PAT 24-AUG-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
Eagles, P.A. and Zheng, R.Q.
Inhibition of cytokine production
Patent: WO 9937760-A 2 25-JUL-1999;
EAGLES PETER ANTHONY WINTER (GB); ZHENG RICHARD QIHAO (GB)
Location/Qualifiers

FEATURES
source 1..22
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Human interleukin-4 promoter"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TGCACCTGACT 139
|||||
7 TGCACCTGACT 19

Db

RESULT 60
AX224699 22 bp DNA linear PAT 10-SEP-2001
LOCUS
DEFINITION
ACCESSION
AX224699 Sequence 46 from Patent WO0161021.
AX224699

VERSION AX224699.1 GI:15554816
KEYWORDS Cucumis melo (muskmelon)
SOURCE Cucumis melo
ORGANISM Cucurbitaceae; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE 1
AUTHORS Cohen, Y. and Kenigbuch, D.
TITLE Transgenic plants having resistance to a fungal disease
JOURNAL Patent: WO 0161021-A 46 23-AUG-2001;
Bar Ilan University (IL)
FEATURES
source 1. .22
/organism="Cucumis melo"
/mol_type="unassigned DNA"
/db_xref="taxon:3656"
/note="P1124111F"

ORIGIN
Query Match 2.6%; Score 13; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 GAACACACACAGC 237
DB 5 GAACACACACAGC 17

RESULT 61
LOCUS BD129696 22 bp DNA linear PAT 18-SEP-2002
DEFINITION Inhibition of cytokine production.
ACCESSION BD129696
VERSION BD129696.1 GI:23224641
KEYWORDS JP 2002500883-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 22)
AUTHORS Eagles, P.A.M. and Zheng, R.Q.
TITLE Inhibition of cytokine production
JOURNAL Patent: JP 2002500883-A 2 15-JAN-2002;
BRT INTERNATIONAL LTD
COMMENT OS Homo sapiens (human)
PN JP 2002500883-A/2
PD 15-JAN-2002
PF 20-JAN-1999 JP 2000528668
PR 22-JAN-1998 GB 9801391.5, 11-NOV-1998 GB 9824794.3 PI
PTER ANTHONY WINTER EAGLES, RICHARD QIHAO ZHENG PC
CI2N15/09, A61K9/127, A61K31/711, A61K35/76, A61K48/00, A61P11/06, PC
A61P19/02,
PC A61P29/00, A61P43/00//A61K38/00, CI2N15/00, A61K37/02 CC Human
Interleukin-4 promoter
FH Key Location/Qualifiers
FT source 1. .22
/organism="Homo sapiens (human)"

FEATURES
source 1. .22
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TGCCACCTGACT 139
DB 7 TGCCACCTGACT 19

RESULT 62
LOCUS BD234236/c 23 bp DNA linear PAT 17-JUL-2003
DEFINITION ATP-binding cassette genes and proteins for diagnosis and remedy of
lipid disorders and inflammatory diseases.
ACCESSION BD234236
VERSION BD234236.1 GI:33044006
KEYWORDS JP 2002525111-A/46.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 23)
AUTHORS Schmitz, G. and Klucken, J.
TITLE ATP-binding cassette genes and proteins for diagnosis and remedy of
lipid disorders and inflammatory diseases
JOURNAL Patent: JP 2002525111-A 46 13-AUG-2002;
BAYER AKTIEGESELLSCHAFT
COMMENT OS Homo sapiens (human)
PN JP 2002525111-A/46
PD 13-AUG-2002
PF 21-SEP-1999 JP 2000572359
PR 25-SEP-1998 US 60/101706
PI GERD SCHMITZ, JOCHEN KLUCKEN
PC CI2N15/09, A61K38/00, A61K45/00, A61K48/00, A61P3/06, A61P9/10, PC
A61P29/00,
PC C07K14/47, C07K16/18, CI2N1/15, CI2N1/19, CI2N1/21, CI2N5/10 PC
C12P21/02, C12Q1/68,
PC GOIN3/53, CI2N15/00, CI2N5/00, A61K37/02
CC Primer
FH Key Location/Qualifiers
FT source 1. .23
/organism="Homo sapiens (human)"

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source 1. .23
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 TGAGCTGACCTAT 417
DB 13 TGAGCTGACCTAT 1

RESULT 63
LOCUS AR036150/c 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5871992.
ACCESSION AR036150
VERSION AR036150.1 GI:5952818
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Teebor, G.W. and Hilbert, T.P.
TITLE Mammalian endonuclease III, and diagnostic and therapeutic uses
JOURNAL Patent: US 5871992-A 8 16-FEB-1999;
FEATURES
source 1. .24
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

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Best Local Similarity 100.0%; Pred. No. 1.6e+05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AGGAGCCAGCC 24
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18 AGGAGCCAGCC 6

Db 18 AGGAGCCAGCC 6

RESULT 64
LOCUS AR084729 24 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 53 from patent US 5981218.
ACCESSION AR084729
VERSION AR084729.1 GI:10011499
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Rlo,M.-C., Tomasetto,C., Basset,P. and Byrne,J.
TITLE Isolated nucleic acid molecules useful as leukemia markers and in breast cancer prognosis and encoded polypeptides
JOURNAL Patent: US 5981218-A 53 09-NOV-1999;
FEATURES
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 CTGGGCTGCACC 150
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18 CTGGGCTGCACC 6

Db 18 CTGGGCTGCACC 6

RESULT 65
LOCUS AR090647 24 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 767 from patent US 5994076.
ACCESSION AR090647
VERSION AR090647.1 GI:10017402
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 767 30-NOV-1999;
FEATURES
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AGCCAGCCCTGT 28
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6 AGCCAGCCCTGT 18

Db 6 AGCCAGCCCTGT 18

RESULT 66
LOCUS BD183262 24 bp DNA linear PAT 17-JUN-2003
DEFINITION Method for estimating genotype of fertility restoration gene site against rice BT type male sterile cytoplasm.
ACCESSION BD183262
VERSION BD183262.1 GI:31875462

KEYWORDS JP 2002345485-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Komori,T., Yamamoto,T., Nitta,N. and Takemori,N.
TITLE Method for estimating genotype of fertility restoration gene site against rice BT type male sterile cytoplasm
JOURNAL Patent: JP 2002345485-A 1 03-DEC-2002;
COMMENT JAPAN TOBACCO INC.,SYNGENTA LTD
OS Artificial Sequence
PN JP 2002345485-A/1
PD 03-DEC-2002
PF 17-AUG-2001 JP 2001247600
PI TOSHITUKI KOMORI,TOSHIO YAMAMOTO,NAOTO NITTA,NAOKI TAKEMORI PC
C12N15/09,A01H1/04,C12Q1/68,C12N15/00
CC Oligonucleotide primer for amplification of R1877 EcORI marker
CC
FH Key sequence.
FT source 1..24
Location/Qualifiers
FT Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"

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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATCTCTGCTTC 444
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1 CATCTCTGCTTC 13

Db 1 CATCTCTGCTTC 13

RESULT 67
LOCUS AR197682 24 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 767 from patent US 6352829.
ACCESSION AR197682
VERSION AR197682.1 GI:20247531
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 767 05-MAR-2002;
FEATURES
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AGCCAGCCCTGT 28
|||||
6 AGCCAGCCCTGT 18

Db 6 AGCCAGCCCTGT 18

RESULT 68
LOCUS AR259836 24 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 767 from patent US 6489455.
ACCESSION AR259836
VERSION AR259836.1 GI:27310347

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1 (bases 1 to 24)
AUTHORS Chenchik, A., Jekhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 767 03-DEC-2002;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.6%; Score 13; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AGCCACGCCCTGT 28
|||||
6 AGCCACGCCCTGT 18

RESULT 69
LOCUS AX060739 24 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 27 from Patent WO0078972.
ACCESSION AX060739
VERSION AX060739.1 GI:12406126
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lawn, R.M., Wade, D. and Garvin, M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: WO 0078972-A 27 28-DEC-2000;
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ABCl sequencing primer"

ORIGIN

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 TGAGCTGACCTAT 417
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6 TGAGCTGACCTAT 18

RESULT 70
LOCUS AX060918 24 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 27 from Patent WO0078971.
ACCESSION AX060918
VERSION AX060918.1 GI:12406293
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
TITLE Abp binding cassette transporter protein abcl polypeptides
JOURNAL Patent: WO 0078971-A 27 28-DEC-2000;
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 TGAGCTGACCTAT 417
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6 TGAGCTGACCTAT 18

RESULT 71
LOCUS AX683912/c 24 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 12 from Patent WO03008588.
ACCESSION AX683912
VERSION AX683912.1 GI:29370924
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Eichler, K., Beck, C. and Friedrich, T.
TITLE Method for producing 2-keto-1-gulonic acid and vitamin C
JOURNAL Patent: WO 03008588-A 12 30-JAN-2003;
FEATURES BASF AKTIENGESSELLSCHAFT (DE)
Location/Qualifiers
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CTTCCAGCCCATG 51
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23 CTTCCAGCCCATG 11

RESULT 72
LOCUS BD141710 24 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of estimating genotype of fertility recovery locus for rice
BT type male sterile cytoplasm.
ACCESSION BD141710
VERSION BD141710.1 GI:23236655
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Komori, T., Yamamoto, T., Nitta, N. and Takemori, N.
TITLE Method of estimating genotype of fertility recovery locus for rice
BT type male sterile cytoplasm
JOURNAL Patent: WO 0214506-A 1 21-FEB-2002;
JAPAN TOBACCO INC, SYNGENTA LTD, TOSHIYUKI KOMORI, TOSHIO YAMAMOTO,
NAOTO NITTA, NAOKI TAKEMORI
OS Artificial Sequence
PN WO 0214506-A/1
PD 21-FEB-2002
PF 16-AUG-2001 WO 2001JP007052
PI 17-AUG-2000 JP 00P 247204
CC C12N15/09, C12N1/68//A01H1/00
CC Oligonucleotide primer for amplification
of R187 EcoRI marker


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CC      sequence.
FH      Location/Qualifiers
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                  /mol_type='genomic DNA'
                  /db_xref='taxon:32630'
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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      432 CATTCTGCTTCC 444
      |||||
      1 CATTCTGCTTCC 13

RESULT 73
A22036 LOCUS          25 bp DNA linear PAT 04-OCT-1994
DEFINITION Oligonucleotide P4.
ACCESSION A22036
VERSION A22036.1 GI:641411
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Sonigo, P., Brechot, C. and Cournaud, V.
TITLE Oligonucleotide sequences for amplification of type HIV-2 and siv
retroviruses genomes and their application to in-vitro diagnostic
Patent: EP 0404625-A 12 27-DEC-1990;
INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE
MEDICALE (INSERM)
FEATURES
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                  /mol_type='unassigned DNA'
                  /db_xref='taxon:32630'
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Query Match          2.6%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      124 TTCTGCCACCTGT 136
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      3 TTCTGCCACCTGT 15

RESULT 74
BD188936 LOCUS          25 bp DNA linear PAT 17-JUL-2003
DEFINITION Protein capable of catalyzing dehydrogenation reaction, gene
encoding said protein and use thereof.
ACCESSION BD188936
VERSION BD188936.1 GI:32998675
KEYWORDS JP 2003024072-A/7.
SOURCE
ORGANISM
REFERENCE
AUTHORS Arata, Y., Nakajima, H. and Mukumoto, F.
TITLE Protein capable of catalyzing dehydrogenation reaction, gene
encoding said protein and use thereof
Patent: JP 2003024072-A 7 28-JAN-2003;
Sumitomo Chemical Co Ltd
OS Artificial Sequence
PN JP 2003024072-A/7

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PD      28-JAN-2003
FF      06-JUL-2001 JP 2001205993
FT      Yuto arata,hiroki nakajima,fujio mukumoto
CC      Designed oligonucleotide primer for PCR
FH      Key
FEATURES
  source          1..25 /organism='synthetic construct'
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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      281 TGACATGAAAAA 293
      |||||
      11 TGACATGAAAAA 23

RESULT 75
CO627991 LOCUS          25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 12731 from Patent WO0192524.
ACCESSION CO627991
VERSION CO627991.1 GI:41678209
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S. G., Hanzel, D. K., Rank, D. R., Chen, W. and
Shannon, M. E.
TITLE Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 12731 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
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                  /mol_type='unassigned DNA'
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      25 CACCTGCTGCTTC 13

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SUMMARIES

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C 4	14	10.6	17	6	AX579065 Sequence
C 5	14	10.6	17	6	AX727571 Sequence
C 6	14	10.6	26	6	AX300552 Sequence
C 7	14	10.6	30	10	S86452
C 8	13	9.8	17	6	AX578467 Sequence
C 9	13	9.8	20	6	AR064476 Sequence
C 10	13	9.8	20	6	AX356984 Sequence
C 11	13	9.8	20	6	AX938772 Sequence
C 12	13	9.8	20	6	BD016601 Sequence
C 13	13	9.8	23	6	C0831876 Sequence
C 14	13	9.8	24	6	I06916
C 15	13	9.8	24	6	I06927
C 16	13	9.8	25	6	I34981
C 17	13	9.8	28	6	BD076701 Sequence
C 18	13	9.8	28	6	BD134515 Method fo
C 19	13	9.8	29	6	I89953 Sequence 33

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C 21	13	9.8	29	6	BD138846
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C 23	12	9.1	17	6	C0617442 Sequence
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C 25	12	9.1	17	6	C0617444 Sequence
C 26	12	9.1	17	6	C0617445 Sequence
C 27	12	9.1	17	6	C0617446 Sequence
C 28	12	9.1	17	6	AR286071 Sequence
C 29	12	9.1	17	6	AR398061 Sequence
C 30	12	9.1	17	6	AR458504 Sequence
C 31	12	9.1	17	6	AR458505 Sequence
C 32	12	9.1	17	6	AR458506 Sequence
C 33	12	9.1	17	6	AR458507 Sequence
C 34	12	9.1	17	6	AR458508 Sequence
C 35	12	9.1	17	6	AR458509 Sequence
C 36	12	9.1	17	6	AX579068 Sequence
C 37	12	9.1	17	6	AX579465 Sequence
C 38	12	9.1	17	6	AX731734 Sequence
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C 49	12	9.1	20	6	AR314616
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C 52	12	9.1	21	6	C0802500 Sequence
C 53	12	9.1	21	6	AR487575 Sequence
C 54	12	9.1	21	6	AX057523 Sequence
C 55	12	9.1	21	6	AX179541
C 56	12	9.1	21	6	AX740333
C 57	12	9.1	22	6	C0802965 Sequence
C 58	12	9.1	22	6	AX553601
C 59	12	9.1	22	6	AX955623
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C 62	12	9.1	23	6	A33878
C 63	12	9.1	23	6	A38170
C 64	12	9.1	23	6	A51842
C 65	12	9.1	23	6	A51879
C 66	12	9.1	23	6	A51891
C 67	12	9.1	23	6	A87525
C 68	12	9.1	23	6	A87543
C 69	12	9.1	23	6	AR077607
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C 78	12	9.1	23	6	AR428830
C 79	12	9.1	23	6	AR438232
C 80	12	9.1	23	6	AR487574
C 81	12	9.1	23	6	AX357150
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C 83	12	9.1	23	6	AX795228
C 84	12	9.1	24	6	AX799233
C 85	12	9.1	24	6	A27073
C 86	12	9.1	24	6	E13463
C 87	12	9.1	24	6	E31858
C 88	12	9.1	24	6	AR202747
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C 91	12	9.1	24	6	AX472836
C 92	12	9.1	25	6	C0620370

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A51842 Sequence 6
A51879 Sequence 43
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C0846582 Sequence
E09118 Synthetic o
I27562 Sequence 76
AR265670 Sequence
AR301940 Sequence
AR428830 Sequence
AR438232 Sequence
AR487574 Sequence
AX357150 Sequence
AX376796 Sequence
AX795228 Sequence
AX799233 Sequence
A27073 oligonucleo
E13463 PCR primer
E31858 Novel cance
AR202747 Sequence
AX010356 Sequence
AX446591 Sequence
AX472836 Sequence
C0620370 Sequence

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c 93      12      9.1      25      6      C0620371 Sequence
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c 101     12      9.1      25      6      C0620379 Sequence
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c 106     12      9.1      25      6      AR461433 Sequence
c 107     12      9.1      25      6      AR461434 Sequence
c 108     12      9.1      25      6      AR461435 Sequence
c 109     12      9.1      25      6      AR461436 Sequence
c 110     12      9.1      25      6      AR461437 Sequence
c 111     12      9.1      25      6      AR461438 Sequence
c 112     12      9.1      25      6      AR461439 Sequence
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c 115     12      9.1      25      6      AR461442 Sequence
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c 117     12      9.1      25      6      AR461444 Sequence
c 118     12      9.1      25      6      AR461445 Sequence
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c 122     12      9.1      25      6      AR090238 Sequence
c 123     12      9.1      25      6      AR197273 Sequence
c 124     12      9.1      25      6      AR259427 Sequence
c 125     12      9.1      25      6      AR259427 Sequence
c 126     12      9.1      25      6      AR491190 Sequence
c 127     12      9.1      25      6      AX148207 Sequence
c 128     12      9.1      25      6      AX148267 Sequence
c 129     12      9.1      25      6      BD167846 Sequence
c 130     12      9.1      25      6      AX181024 Sequence
c 131     12      9.1      25      6      BD175158 Sequence
c 132     12      9.1      25      6      AR215278 Sequence
c 133     12      9.1      25      6      AR061345 Sequence
c 134     12      9.1      25      6      AR108244 Sequence
c 135     12      9.1      25      6      E28972 Sequence
c 136     12      9.1      25      6      E63132 Sequence
c 137     12      9.1      25      6      I16201 Sequence
c 138     12      9.1      25      6      I66687 Sequence
c 139     12      9.1      25      6      I84781 Sequence
c 140     12      9.1      25      6      AR263205 Sequence
c 141     12      9.1      25      6      AR348847 Sequence
c 142     12      9.1      25      6      C0828796 Sequence
c 143     12      9.1      25      6      A11466 Sequence
c 144     12      9.1      25      6      A09420 Sequence
c 145     12      9.1      25      6      A10623 Sequence
c 146     12      9.1      25      6      A35091 Sequence
c 147     12      9.1      25      6      AR142688 Sequence
c 148     12      9.1      25      6      AR142690 Sequence
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ALIGNMENTS

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RESULT 1
AX578466/c      17 bp      RNA
LOCUS           Sequence 304 from Patent WO0211674.
DEFINITION      AX578466
ACCESSION       AX578466
VERSION         AX578466.1 GI:27647668
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
1      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS
1      Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
      and Grube,A.
TITLE
      Method and reagent for the inhibition of calcium activated chloride
      channel-1 (clca-1)
JOURNAL
      Patent: WO 0211674-A 304 14-FEB-2002;
      RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
      Thompson, James (US)
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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Query Match      11.4%; Score 15; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

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QY      86      GCTGATGAGCGCT 100
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Db      17      GCTGATGAGCGCT 3

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RESULT 2
AX579066/c      17 bp      RNA
LOCUS           Sequence 904 from Patent WO0211674.
DEFINITION      AX579066
ACCESSION       AX579066
VERSION         AX579066.1 GI:27648268
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE
1      Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
      and Grube,A.
TITLE
      Method and reagent for the inhibition of calcium activated chloride
      channel-1 (clca-1)
JOURNAL
      Patent: WO 0211674-A 904 14-FEB-2002;
      RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
      Thompson, James (US)
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source
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

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QY      86      GCTGATGAGCGCT 100
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Db      16      GCTGATGAGCGCT 2

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RESULT 3
AX579067/c      17 bp      RNA
LOCUS           Sequence 905 from Patent WO0211674.
DEFINITION      AX579067
ACCESSION       AX579067
VERSION         AX579067.1 GI:27648269
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1      Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.

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JOURNAL Patent: WO 0211674-A 905 14-FEB-2002;
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES Location/Qualifiers
SOURCE 1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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Query Match 11.4%; Score 15; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86 GCTGATGAGCGCT 100
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Db 15 GCTGATGAGCGCT 1
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RESULT 4
AX579065/c 17 bp RNA linear PAT 10-JAN-2003
LOCUS Sequence 903 from Patent WO0211674.
DEFINITION AX579065
ACCESSION AX579065
VERSION AX579065.1 GI:27648267
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Thompson, J., Mcswigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grupe, A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 903 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES Location/Qualifiers
SOURCE 1. .17
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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Query Match 10.6%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 87 CTGATGAGCGCT 100
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Db 17 CTGATGAGCGCT 4
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RESULT 5
AX727571 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 5258 from Patent WO03025176.
DEFINITION AX727571
ACCESSION AX727571
VERSION AX727571.1 GI:30506914
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines

JOURNAL Patent: WO 03025176-A 5258 27-MAR-2003;
TITLE Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
SOURCE 1. .17
/organism="Mus musculus"
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/db_xref="taxon:10090"
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Query Match 10.6%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 113 CTACCTCCGCTGT 126
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Db 4 CTACCTCCGCTGT 17
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RESULT 6
AX300552/c 26 bp DNA linear PAT 30-NOV-2001
LOCUS Sequence 58 from Patent WO0185933.
DEFINITION AX300552
ACCESSION AX300552
VERSION AX300552.1 GI:17381903
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS van Roy, F., Bonne, S. and Vanlandschoot, A.
TITLE Plakoglobin interacting proteins
JOURNAL Patent: WO 0185933-A 58 15-NOV-2001;
Vlaams Internuiveritair Instituut voor Biotechnologie vzw. (BE)
FEATURES Location/Qualifiers
SOURCE 1. .26
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="splice acceptor no 3"
ORIGIN
Query Match 10.6%; Score 14; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TCATCTCCAGGAC 21
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Db 19 TCATCTCCAGGAC 6
|||||
RESULT 7
S86452 30 bp mRNA linear ROD 07-MAY-1993
LOCUS TCR V beta 16/J beta 2.7-T cell receptor beta chain variable (VDJ
DEFINITION junction) (trab, Lewis, spinal cord, mRNA partial, 30 nt).
S86452
ACCESSION S86452
VERSION S86452.1 GI:246984
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
AUTHORS 1 (bases 1 to 30)
Gold, D.P., Vainiene, M., Celnik, B., Wiley, S., Gibbs, C., Hashim, G.A.,
vandenbark, A.A. and Offner, H.
TITLE Characterization of the immune response to a secondary
encephalitogenic epitope of basic protein in Lewis rats. II. Biased
T cell receptor V beta expression predominates in spinal cord
infiltrating T cells
JOURNAL J. Immunol. 148 (6), 1712-1717 (1992)
MEDLINE 92176627

1371786
REMARK GenBank staff at the National Library of Medicine created this entry (NCBI gisdbseq 86452) from the original journal article.
FEATURES
source
1..30
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="taxon:10118"
1..30 "TCR V<beta>16/J<beta>2.7"
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/note="T cell receptor beta chain variable"
1..30
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/codon_start=1
/product="T cell receptor beta chain variable"
/protein_id="AAB21736.1"
/db_xref="GI:246985"
/translation="CASSAHRDEQ"
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Query Match 10.6%; Score 14; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 GCTGCTCCTCTGT 111
DB 28 GCTGCTCCTCTGT 15
RESULT 8
AX578467/c 17 bp RNA linear PAT 10-JAN-2003
LOCUS AX578467
DEFINITION Sequence 305 from Patent WO0211674.
ACCESSION AX578467
VERSION AX578467.1 GI:27647669
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E. and Grube,A.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (Clca-1)
JOURNAL Patent: WO 0211674-A 305 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US); Thompson, James (US)
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 5.6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86 GCTGATGAGCG 98
DB 13 GCTGATGAGCG 1
RESULT 9
AR064476 20 bp DNA linear PAT 29-SEP-1999
LOCUS AR064476
DEFINITION Sequence 49 from patent US 5847096.
ACCESSION AR064476
VERSION AR064476.1 GI:5993784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 20)
AUTHORS Schubert,M., Harmison,G.G., II, Chen,C.-J. and Banerjee,A.
TITLE DNA constructs encoding CD4 fusion proteins
JOURNAL Patent: US 5847096-A 49 08-DEC-1998;
FEATURES
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/organism="unknown"
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Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 GCCCTGCATGCAC 60
DB 2 GCCCTGCATGCAC 14
RESULT 10
AX356984 20 bp DNA linear PAT 13-FEB-2002
LOCUS AX356984
DEFINITION Sequence 26 from Patent WO0206523.
ACCESSION AX356984
VERSION AX356984.1 GI:18674180
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Acuna,G., Foerzler,D. and Jeong,D.U.
TITLE Method for detecting pre-disposition to hepatotoxicity
JOURNAL Patent: WO 0206523-A 26 24-JAN-2002;
F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
source
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 CCTGTGTCTTAC 116
DB 17 CCTGTGTCTTAC 5
RESULT 11
AX938772 20 bp DNA linear PAT 07-JAN-2004
LOCUS AX938772
DEFINITION Sequence 217 from Patent EP1365034.
ACCESSION AX938772
VERSION AX938772.1 GI:40733152
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Wirtz,R., Munnes,M. and Kallabis,H.
TITLE Methods and compositions for the prediction, diagnosis, prognosis, prevention and treatment of malignant neoplasia
JOURNAL Patent: EP 1365034-A 217 26-NOV-2003;
Bayer Healthcare AG (DE)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN /note="LOC51242 for"

Query Match 9.8%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GTCCCTGTCCT 114
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DB 4 GTCCCTGTCCT 16

RESULT 12
BD016601/c
LOCUS

DEFINITION BD016601 20 bp DNA linear PAT 27-AUG-2002
Genes and proteins participating in the upstream of degradation
passage of aromatic polycyclic compound.

ACCESSION BD016601
BD016601.1 GI:22557777
VERSION JP 2001245662-A/89
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 20)
Saito, A., Tamatsubo, K. and Adachi, K.
AUTHORS Genes and proteins participating in the upstream of degradation
TITLE passage of aromatic polycyclic compound
JOURNAL Patent: JP 2001245662-A 89 11-SEP-2001;
MARINE BIOTECHNOLOGY INST CO LTD

COMMENT OS Artificial Sequence
PN JP 2001245662-A/89
PD 11-SEP-2001
PF 03-MAR-2000 JP 2000059523
PT ATSUISHI SAITO, KAZUAKI TAMATSUBO, KYOKO ADACHI
PC C12N15/09, C12N9/02, C12N15/00
CC Description of Artificial Sequence: Synthetic primer KP234. FH

FEATURES
source location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

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Query Match 9.8%; Score 13; DB 6; Length 20;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 CTGATGAGCGC 99
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DB 19 CTGATGAGCGC 7

RESULT 13
CO831876 23 bp DNA linear PAT 29-JUL-2004
LOCUS
DEFINITION Sequence 11 from Patent WO2004056996.
CO831876
CO831876.1 GI:50831751
VERSION
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
Romeo, T., Weillbacher, T., Suzuki, K. and Wang, X.
AUTHORS The escherichia coli carc gene and uses thereof for biofilm
TITLE modulation
JOURNAL Patent: WO 2004056996-A 11 08-JUL-2004;
UNIVERSITY OF NORTH TEXAS HEALTH SCIENCE CENTER AT FORT WORTH (US)
LOCATION/Qualifiers

FEATURES
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/mol_type="unassigned DNA"

ORIGIN /db_xref="taxon:32630"
/note="primer"

Query Match 9.8%; Score 13; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 CTGCGTAGTTTG 45
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DB 2 CTGCGTAGTTTG 14

RESULT 14
I06916/c
LOCUS

DEFINITION I06916 24 bp DNA linear PAT 02-DEC-1994
Sequence 6 from Patent EP 0340948.

ACCESSION I06916
I06916.1 GI:589835
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
Wilcox, E., Edwards, D. L., Schwab, G. E., Thompson, M. and Culver, P.
AUTHORS Novel hybrid pesticidal toxins
TITLE Patent: EP 0340948-A1 6 08-NOV-1989;
JOURNAL location/Qualifiers

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/mol_type="unassigned DNA"

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Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 CTGCGATGCAC 62
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DB 14 CTGCGATGCAC 2

RESULT 15
I06927/c 24 bp DNA linear PAT 02-DEC-1994
LOCUS
DEFINITION Sequence 17 from Patent EP 0340948.
I06927
I06927.1 GI:589843
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
Wilcox, E., Edwards, D. L., Schwab, G. E., Thompson, M. and Culver, P.
AUTHORS Novel hybrid pesticidal toxins
TITLE Patent: EP 0340948-A1 17 08-NOV-1989;
JOURNAL location/Qualifiers

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/mol_type="unassigned DNA"

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Query Match 9.8%; Score 13; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
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QY 50 CTGCGATGCAC 62
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DB 14 CTGCGATGCAC 2

RESULT 16
I34981

LOCUS 134981 25 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 67 from patent US 559704.
ACCESSION 134981 GI:2087949
VERSION 134981.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Thompson,J.D. and Draper,K.G.
TITLE ExB2/new targeted ribozymes
JOURNAL Patent: US 559704-A 67 04-FEB-1997;
FEATURES location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 9.8%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACCTGCTG 27
DB 2 CCAGGACCTGCTG 14

RESULT 17
LOCUS BD076701 28 bp DNA linear PAT 27-AUG-2002
DEFINITION Lentivirus vector.
ACCESSION BD076701 GI:22622304
VERSION BD076701.1
KEYWORDS JP 2001510053-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 28)
AUTHORS Chen,X.T., Gasmil,M., Yi,J.K. and Jolly,D.J.
TITLE Lentivirus vector
JOURNAL Patent: JP 2001510053-A 10 31-JUL-2001;
COMMENT CHIRON CORP
OS Artificial Sequence
PN JP 2001510053-A/10
PD 31-JUL-2001
PF 20-JUL-1998 JP 2000503232
PR 18-JUL-1997 US 60/053066
PI XIN TAI CHEN,MEHDI GASMIL,JIN KUANG YI,DOUGLAS J JOLLY PC
CI2N15/09,A61K48/00,CI2N5/10,CI2N7/00//A61K35/76,A61K38/00, PC
A61K38/43,
PC CI2N15/00,CI2N5/00,A61K37/02,A61K37/465
CC Description of Artificial Sequence: Synthesized CC
Oligonucleotide
FH source location/Qualifiers
FT 1..28
/organism='Artificial Sequence'.
FEATURES source 1..28
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 9.8%; Score 13; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 GCCCTGCATGCAC 60
DB 14 GCCCTGCATGCAC 26

RESULT 18

BD134515
LOCUS BD134515 28 bp DNA linear PAT 18-SEP-2002
DEFINITION Method for assaying an enzyme participating in conjugation with
glucuronic acid in human beings, and probe and kit therefor.
ACCESSION BD134515
VERSION BD134515.1 GI:23229460
KEYWORDS JP 2002085066-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 28)
AUTHORS Nishimura,M., Yaguchi,H., Naito,S. and Hiraoka,I.
TITLE Method for assaying an enzyme participating in conjugation with
glucuronic acid in human beings, and probe and kit therefor
JOURNAL Patent: JP 2002085066-A 1 26-MAR-2002;
OS Human UGT1 gene
COMMENT OTSUKA PHARMACEUTICAL FACTORY INC
PN JP 2002085066-A/1
PD 26-MAR-2002
PF 07-SEP-2000 JP 2000272228
PI MASUHIRO NISHIMURA,HIROSHI YAGUCHI,SHINSAKU NAITO,ISAO HIRAKA
PC CI2N15/09,CI2Q1/25,CI2Q1/68,G01N21/78,G01N33/50,G01N33/566, PC
CI2N15/00
CC Method for assaying an enzyme participating in conjugation CC
with glucuronic acid in human beings, and probe and kit therefor FH Key
FT source location/Qualifiers
FT 1..28
/organism='Human UGT1 gene'.
FEATURES source 1..28
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 9.8%; Score 13; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 CCTGTGTCTCTAC 116
DB 2 CCTGTGTCTCTAC 14

RESULT 19
LOCUS I89953/c 29 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 33 from patent US 5723315.
ACCESSION I89953
VERSION I89953.1 GI:3409893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 29)
AUTHORS Jacobs,K., McCoy,J.M., LaValle,E.R., Racie,L.A., Merberg,D.,
Tresacy,M. and Spaulding,V.
TITLE Secreted proteins and polynucleotides encoding them
JOURNAL Patent: US 5723315-A 33 03-MAR-1998;
FEATURES location/Qualifiers
source 1..29
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 9.8%; Score 13; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CAGCCCTGCATGC 58
DB 25 CAGCCCTGCATGC 13

RESULT 20
BD005393/c 29 bp DNA linear PAT 31-JAN-2002
LOCUS Secreted proteins and polynucleotides encoding them.
DEFINITION BD005393
ACCESSION BD005393.1 GI:18633764
VERSION JP 2001501460-A/24.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Merberg,D., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Treacy,M., Spaulding,V. and Jacobs,K.
TITLE Secreted proteins and polynucleotides encoding them
JOURNAL Patent: JP 2001501460-A 24 06-FEB-2001;
GENETICS INSTITUTE INC
COMMENT OS Unidentified
PN JP 2001501460-A/24
PD 06-FEB-2001
PF 22-AUG-1997 JP 1998511030
PR 23-AUG-1996 US 08/702344
PI DAVID MERBERG,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI MAURICE TREACY,
PI VIKKI SPAULDING,KENNETH JACOBS
PC C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC
Strandedness: Single;
CC Topology: linear;
FH Key Location/Qualifiers
FT source 1..29 /organism='Unidentified'.
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source 1..29 /organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
ORIGIN
Query Match 9.8%; Score 13; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 46 CAGCCCTGCATGC 58
DB 25 CAGCCCTGCATGC 13
RESULT 21
BD138846/c 29 bp DNA linear PAT 18-SEP-2002
LOCUS Secreted proteins and polynucleotides encoding them.
DEFINITION BD138846
ACCESSION BD138846.1 GI:2323791
VERSION JP 2002504306-A/18.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 29)
AUTHORS Jacoby,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A.C., Evans,C., Merberg,D., Treacy,M. and Spaulding,V.
TITLE Secreted proteins and polynucleotides encoding them
JOURNAL Patent: JP 2002504306-A 18 12-FEB-2002;
GENETICS INSTITUTE INC
COMMENT OS Artificial Sequence
PN JP 2002504306-A/18
PD 12-FEB-2002
PF 20-NOV-1998 JP 2000522129
PR 21-NOV-1997 US 08/576112,19-NOV-1998 US 09/196027 PI
KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A COLLINS PI RACIE,
PI CHERYL EVANS,DAVID MERBERG,MAURICE TREACY,VIKKI SPAULDING PC C12N15/09,C07K14/47,C12N5/10,C12P21/02,C12N15/00,C12N5/00 CC

oligonucleotide
CC: biotinylated phosphoramidite residue
FH Key Location/Qualifiers
FT misc_feature (2).
LOCATION/Qualifiers
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/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Query Match 9.8%; Score 13; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 46 CAGCCCTGCATGC 58
DB 25 CAGCCCTGCATGC 13
RESULT 22
CO617441/c 17 bp DNA linear PAT 02-FEB-2004
LOCUS CO617441
DEFINITION Sequence 2181 from Patent WO0192524.
ACCESSION CO617441
VERSION CO617441.1 GI:41667659
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2181 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1..17 /organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CCAGGACCTGCT 26
DB 17 CCAGGACCTGCT 6
RESULT 23
CO617442/c 17 bp DNA linear PAT 02-FEB-2004
LOCUS CO617442
DEFINITION Sequence 2182 from Patent WO0192524.
ACCESSION CO617442
VERSION CO617442.1 GI:41667660
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2182 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1..17 /organism='Homo sapiens'

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ORIGIN /mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 9.1%; Score 12; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 CCAGAGCTGCT 26
|||||
16 CCAGAGCTGCT 5

RESULT 24
CO617443/c 17 bp DNA linear PAT 02-FEB-2004
LOCUS Sequence 2183 from Patent WO0192524.
DEFINITION CO617443
ACCESSION CO617443
VERSION GI:4167661
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2183 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN /mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 9.1%; Score 12; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 CCAGAGCTGCT 26
|||||
15 CCAGAGCTGCT 4

RESULT 25
CO617444/c 17 bp DNA linear PAT 02-FEB-2004
LOCUS Sequence 2184 from Patent WO0192524.
DEFINITION CO617444
ACCESSION CO617444
VERSION GI:4167662
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2184 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN /mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 9.1%; Score 12; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 CCAGAGCTGCT 26
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12 CCAGAGCTGCT 1

RESULT 28
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ORIGIN /mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 9.1%; Score 12; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 CCAGAGCTGCT 26
|||||
14 CCAGAGCTGCT 3

RESULT 26
CO617445/c 17 bp DNA linear PAT 02-FEB-2004
LOCUS Sequence 2185 from Patent WO0192524.
DEFINITION CO617445
ACCESSION CO617445
VERSION GI:4167663
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2185 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN /mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 9.1%; Score 12; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 CCAGAGCTGCT 26
|||||
13 CCAGAGCTGCT 2

RESULT 27
CO617446/c 17 bp DNA linear PAT 02-FEB-2004
LOCUS Sequence 2186 from Patent WO0192524.
DEFINITION CO617446
ACCESSION CO617446
VERSION GI:4167664
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2186 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN /mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AR266071
LOCUS AR266071 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 443 from patent US 6528640.
ACCESSION AR266071
VERSION AR266071.1 GI:29723667
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpelsky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 443 04-MAR-2003;
FEATURES
LOCATION/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 CAGGACCTGCTG 27
Db 1 CAGGACCTGCTG 12
RESULT 29
AR398061
LOCUS AR398061 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 442 from patent US 6617438.
ACCESSION AR398061
VERSION AR398061.1 GI:40135568
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpelsky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 442 09-SEP-2003;
FEATURES
LOCATION/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 CAGGACCTGCTG 27
Db 1 CAGGACCTGCTG 12
RESULT 30
AR458504/c
LOCUS AR458504 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2181 from patent US 6686188.
ACCESSION AR458504
VERSION AR458504.1 GI:42693561
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed

predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2181 03-FEB-2004;
FEATURES
LOCATION/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CCAGGACCTGCT 26
Db 17 CCAGGACCTGCT 6
RESULT 31
AR458505/c
LOCUS AR458505 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2182 from patent US 6686188.
ACCESSION AR458505
VERSION AR458505.1 GI:42693562
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
JOURNAL Patent: US 6686188-A 2182 03-FEB-2004;
FEATURES
LOCATION/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CCAGGACCTGCT 26
Db 16 CCAGGACCTGCT 5
RESULT 32
AR458506/c
LOCUS AR458506 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2183 from patent US 6686188.
ACCESSION AR458506
VERSION AR458506.1 GI:42693563
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
JOURNAL Patent: US 6686188-A 2183 03-FEB-2004;
FEATURES
LOCATION/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACTGCT 26
DB 15 CCAGGACTGCT 4

RESULT 33
LOCUS AR458507 17 bp DNA
DEFINITION Sequence 2184 from patent US 6686188.
ACCESSION AR458507
VERSION AR458507.1 GI:42693564
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2184 03-FEB-2004;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACTGCT 26
DB 14 CCAGGACTGCT 3

RESULT 34
LOCUS AR458508 17 bp DNA
DEFINITION Sequence 2185 from patent US 6686188.
ACCESSION AR458508
VERSION AR458508.1 GI:42693565
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2185 03-FEB-2004;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACTGCT 26
DB 13 CCAGGACTGCT 2

RESULT 35
LOCUS AR458509 17 bp DNA
DEFINITION Sequence 2186 from patent US 6686188.
ACCESSION AR458509

VERSION AR458509.1 GI:42693566
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2186 03-FEB-2004;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACTGCT 26
DB 12 CCAGGACTGCT 1

RESULT 36
LOCUS AX579068 17 bp RNA
DEFINITION Sequence 906 from Patent WO0211674.
ACCESSION AX579068
VERSION AX579068.1 GI:27648270
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Thompson, J., Mewisigen, J., McKenzie, T., Ayers, D., Szymkowski, D. E. and Grube, A.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 906 14-FEB-2002;
FEATURES
source RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 GCTGGATGAGC 97
DB 12 GCTGGATGAGC 1

RESULT 37
LOCUS AX579465 17 bp RNA
DEFINITION Sequence 1303 from Patent WO0211674.
ACCESSION AX579465
VERSION AX579465.1 GI:27648667
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D. E.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (Clca-1)
JOURNAL Patent: WO 0211674-A 1303 14-FEB-2002;
RIZOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 89 GGATGAGCGCT 100
17 GGATGAGCGCT 6
Db 17 GGATGAGCGCT 6
RESULT 38
AX731734 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 3368 from Patent WO03025175.
DEFINITION AX731734
ACCESSION AX731734.1 GI:30511077
VERSION AX731734.1 GI:30511077
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 3368 27-MAR-2003;
Molecular Engines Laboratories (PR)
FEATURES location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 84 GGGCTGATGGA 95
14 GGGCTGATGGA 3
Db 14 GGGCTGATGGA 3
RESULT 39
BD012743 18 bp DNA linear PAT 02-AUG-2002
LOCUS A novel fizzled family gene, 584.
DEFINITION BD012743
ACCESSION BD012743.1 GI:22092932
VERSION BD012743.1 GI:22092932
KEYWORDS WO 0112808-A/16.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Seno, C. and Numata, M.
TITLE A novel fizzled family gene, 584
JOURNAL Patent: WO 0112808-A 16 22-FEB-2001;
CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, CHIKAI SENO,
MARIKO NUMATA

COMMENT OS Artificial Sequence
PN WO 0112808-A/16
PD 22-FEB-2001
PF 18-AUG-2000 WO 2000JP005552
PR 18-AUG-1999 JP 99P 232018
PI CHIKAI SENO, MARIKO NUMATA
PC C12N1/5.12, C12N5/10, C12N1/15, C12N1/19, C12N1/21, C12Q1/02, PC
C07K14/705
PC C07K16/28, C12P21/02
CC Description of Artificial Sequence: artificially synthesized
primer
CC sequence C07K14/705,
FH key
FEATURES location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 119 GCCGCTGTCCG 130
16 GCCGCTGTCCG 5
Db 16 GCCGCTGTCCG 5
RESULT 40
A51892 19 bp DNA linear PAT 10-MAR-1997
LOCUS Sequence 56 from Patent WO9620011.
DEFINITION A51892
ACCESSION A51892
VERSION A51892.1 GI:2304640
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Blakey, D.C., Davies, D.H., Dowell, R.I., Hennam, J.F., Marsham, P.R.,
Slater, Anthony M. and Hennequin, L.F.
TITLE CHEMICAL COMPOUNDS CHEMICAL COMPOUNDS
JOURNAL Patent: WO 9620011-A 56 04-JUL-1996;
ZENECA LTD (GB)
COMMENT Other publication AU 4269796 960719.
FEATURES location/Qualifiers
source 1..19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 GGACCTGCTGCA 29
1 GGACCTGCTGCA 12
Db 1 GGACCTGCTGCA 12
RESULT 41
A67354 19 bp DNA linear PAT 05-MAY-1999
LOCUS Sequence 110 from Patent WO9742323.
DEFINITION A67354
ACCESSION A67354
VERSION A67354.1 GI:4756298
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 19)
AUTHORS Copley, C.G., Edge, M.D. and Emery, S.C.
TITLE MONOCLONAL ANTIBODY TO CEA, CONJUGATES COMPRISING SAID ANTIBODY,
AND THEIR THERAPEUTIC USE IN AN ADEPT SYSTEM
JOURNAL Patent: WO 9742329-A 110 13-NOV-1997;
ZENECA LTD (GB)
FEATURES Location/Qualifiers
source 1..19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 GGACCTGCTGCA 29
Db 1 GGACCTGCTGCA 12
RESULT 42
LOCUS A87526 19 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 7 from Patent WO9835988.
ACCESSION A87526
VERSION A87526.1 GI:6736175
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Edge, M.D.
TITLE PROTEINS
JOURNAL Patent: WO 9835988-A 7 20-AUG-1998;
ZENECA LTD (GB); EDGE MICHAEL DEREK (GB)
FEATURES Location/Qualifiers
source 1..19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 GGACCTGCTGCA 29
Db 1 GGACCTGCTGCA 12
RESULT 43
LOCUS AR085857 19 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 52 from patent US 5985281.
ACCESSION AR085857
VERSION AR085857.1 GI:10012623
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Taylorson, C.John., Eggelte, H.Johannes., Taragona-Fiol, A.,
Rabin, B.Robert., Boyle, F.Thomas., Hennam, J.Frederick.,
Blakey, D.Charles., Marsham, P.Robert., Heaton, D.William.,
Davies, D.Huw., Slater, A.Michael. and Hennequin, L.Francois. Andre.
TITLE Chemical compounds
JOURNAL Patent: US 5985281-A 52 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"

ORIGIN /mol_type="unassigned DNA"
Query Match 9.1%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 GGACCTGCTGCA 29
Db 1 GGACCTGCTGCA 12
RESULT 44
LOCUS I46738 19 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 717 from patent US 5639612.
ACCESSION I46738
VERSION I46738.1 GI:2470703
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Mitsuhashi, M. and Cooper, A.
TITLE Method for detecting polynucleotides with immobilized
JOURNAL polynucleotide probes identified based on T.sub.m
Patent: US 5639612-A 717 17-JUN-1997;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CCAGGACCTGCT 26
Db 6 CCAGGACCTGCT 17
RESULT 45
LOCUS AR166750/c 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 6 from patent US 6281412.
ACCESSION AR166750
VERSION AR166750.1 GI:16242219
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Murata, N.
TITLE Method for creating osmotic-pressure-tolerant plant
JOURNAL Patent: US 6281412-A 6 28-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86 GCTGGATGGAGC 97
Db 12 GCTGGATGGAGC 1
RESULT 46
BD250342

LOCUS BD250342 20 bp DNA linear PAT 17-JUN-2003
DEFINITION Antisense modulation of p38 mitogen activated protein kinase
expression.
ACCESSION BD250342
VERSION BD250342.1 GI:33060112
KEYWORDS JP 2002540781-A/94.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Gaarde,W.A., Nero,P.S., McKay,R. and Popoff,I.
TITLE Antisense modulation of p38 mitogen activated protein kinase
JOURNAL Patent: JP 2002540781-A 94 03-DEC-2002;
ISIS :PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002540781-A/94
PD 03-DEC-2002
PF 04-APR-2000 JP 2000609429
PR 06-APR-1999 US 09/286904
PI BRETT P MONIA, WILLIAM A GAARDE, PAMELA S NERO, ROBERT MCKAY, IAN
POPOFF
PC C12N15/09,A61K31/711,A61P19/02,A61P29/00,A61P37/06,
A61P43/00,
PC C12N5/10,C12N9/99,C12N15/00,C12N5/00
CC Antisense modulation of p38 mitogen activated protein kinase
expression
FH Key
FT source
FEATURES
source 1..20
location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 ACGTTCTGCGCG 72
DB 3 ACGTTCTGCGCG 14

RESULT 47
LOCUS AR228892 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 99 from patent US 6448079.
ACCESSION AR228892
VERSION AR228892.1 GI:27268031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Gaarde,W.A., Nero,P. and McKay,R.
TITLE Antisense modulation of p38 mitogen activated protein kinase
expression
JOURNAL Patent: US 6448079-A 99 10-SEP-2002;
FEATURES
source 1..20
location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 ACGTTCTGCGCG 72
DB 3 ACGTTCTGCGCG 14

RESULT 48
LOCUS AR300685 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 53 from patent US 6537811.
ACCESSION AR300685
VERSION AR300685.1 GI:31688234
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Freier,S.M.
TITLE Antisense inhibition of SAP-1 expression
JOURNAL Patent: US 6537811-A 53 25-MAR-2003;
FEATURES
source 1..20
location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 GGGCTGGATGCA 95
DB 15 GGGCTGGATGCA 4

RESULT 49
LOCUS AR314616 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5153 from patent US 6559294.
ACCESSION AR314616
VERSION AR314616.1 GI:31708042
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Grifflais,R., Hoiseh,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 5153 06-MAY-2003;
FEATURES
source 1..20
location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGCCAGAGCCTG 24
DB 5 TGCCAGAGCCTG 16

RESULT 50
LOCUS AR314724 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5261 from patent US 6559294.
ACCESSION AR314724
VERSION AR314724.1 GI:31708150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Grifflais,R., Hoiseh,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,

TITLE Sankaran, B. and Fletcher, L.D.
JOURNAL Chlamydia pneumoniae polynucleotides and uses thereof
FEATURES Patent: US 6559294-A 5261 06-MAY-2003;
SOURCE Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GCATCATCTGCC 16
DB 18 GCATCATCTGCC 7

RESULT 51
AX511476 20 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 5 from Patent WO0238143.
DEFINITION AX511476
ACCESSION AX511476.1 GI:23392345
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bulavina, D.V. and Fornace, A.J.
TITLE Enhanced efficacy and safety of genotoxic therapy by p38 mapk modulation
JOURNAL Patent: WO 0238143-A 5 16-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 ACCTTCTGCCGC 72
DB 3 ACCTTCTGCCGC 14

RESULT 52
CO802500 21 bp DNA linear PAT 10-MAY-2004
LOCUS Sequence 13 from Patent WO2004035615.
DEFINITION CO802500
ACCESSION CO802500.1 GI:47109466
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Klippel-Giese, A., Kaufmann, J. and Schwarzer, R.
TITLE Factor involved in metastasis and uses thereof
JOURNAL Patent: WO 2004035615-A 13 29-APR-2004;
FEATURES actugen AG (DE)
Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="artificial oligonucleotide"

misc_feature 1..6

misc_feature 7..15
misc_feature 16..21
misc_feature /note="DNA linked through phosphorothioate linkages"
misc_feature /note="RNA"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 GCTCGTCCCTGT 109
DB 1 GCTCGTCCCTGT 12

RESULT 53
AR487575 21 bp DNA linear PAT 14-MAY-2004
LOCUS Sequence 29 from patent US 6706505.
DEFINITION AR487575
ACCESSION AR487575
VERSION AR487575.1 GI:47252825
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE 1
AUTHORS Unclassified.
TITLE 1 (bases 1 to 21)
Hao, H.-Q. and Kwak, K.
JOURNAL Human E3.alpha. ubiquitin ligase family
FEATURES Patent: US 6706505-A 29 16-MAR-2004;
Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 CCTGCGATGCAC 60
DB 5 CCTGCGATGCAC 16

RESULT 54
AX057523 21 bp DNA linear PAT 17-JAN-2001
LOCUS Sequence 59 from Patent WO0077204.
DEFINITION AX057523
ACCESSION AX057523
VERSION AX057523.1 GI:12310257
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Lorenz, E., Schwartz, D.A. and Schutte, B.C.
TITLE Variant c174 nucleic acid and uses thereof
JOURNAL Patent: WO 0077204-A 59 21-DEC-2000;
FEATURES University of Iowa Research Foundation (US); Lorenz, Eva (US)
Location/Qualifiers
source 1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 45 GCAGCCCTGCAT 56

Db 6 GCAGCCTGCTG 17

RESULT 55
LOCUS AX179541/c 21 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 2 from Patent WO0132841.
ACCESSION AX179541
VERSION AX179541.1 GI:14599153
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ruiz,M., Kinter,A., Dybul,M., Catanzaro,A. and Fauci,A.S.
TITLE Method of in vitro T cell differentiation of cd34+ progenitor cells
JOURNAL Patent: WO 0132841-A 2 10-MAY-2001;
The Secretary of the Department of Health and Human Services (US)
FEATURES
SOURCE location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer"

ORIGIN

Query Match 9.1%; Score 12; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GCCAGGACCTGC 25
Db 12 GCCAGGACCTGC 1

RESULT 56
LOCUS AX740333 21 bp DNA linear PAT 10-MAY-2003
DEFINITION Sequence 67 from Patent EP1300419.
ACCESSION AX740333
VERSION AX740333.1 GI:30523506
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Buettner,C., Schwarz,M., Knackmuss,S., Peter,K., Roettgen,P. and Little,M.
TITLE Antibody of human origin for inhibiting thrombocyte aggregation
JOURNAL Patent: EP 1300419-A 67 09-APR-2003;
Affirmed Therapeutics AG (DE)
FEATURES
SOURCE location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

ORIGIN

Query Match 9.1%; Score 12; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 GACTGCGTGA 42
Db 20 GACTGCGTGA 9

RESULT 57
LOCUS CQ802965 22 bp DNA linear PAT 10-MAY-2004

DEFINITION Sequence 83 from Patent EP1415996.
ACCESSION CQ802965
VERSION CQ802965.1 GI:47109960
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Nakajima,H.
TITLE Transformed cell with enhanced sensitivity to antifungal compound and use thereof
JOURNAL Patent: EP 1415996-A 83 06-MAY-2004;
Sumitomo Chemical Company, Limited (JP)
FEATURES
SOURCE location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 9.1%; Score 12; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CAGGACCTGCTG 27
Db 8 CAGGACCTGCTG 19

RESULT 58
LOCUS AX553601 22 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 5 from Patent WO02074946.
ACCESSION AX553601
VERSION AX553601.1 GI:25897599
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Serup,P., Heimborg,H. and Gradwohl,G.
TITLE Method for generating insulin-secreting cells suitable for transplantation
JOURNAL Patent: WO 02074946-A 5 26-SEP-2002;
NOVO NORDISK A/S (DK)
FEATURES
SOURCE location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 9.1%; Score 12; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CATCATCTGCCA 17
Db 6 CATCATCTGCCA 17

RESULT 59
LOCUS AX955623 22 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 22 from Patent WO03095491.
ACCESSION AX955623
VERSION AX955623.1 GI:40784281
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1

AUTHORS Brekke,O.H., Stacy,J. and Kaunsmally,L.
TITLE Patent: WO 03095491-A 22 20-NOV-2003;
JOURNAL Affitech AS (NO) ; Brekke, Ole Henrik (NO)
FEATURES
source 1.22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9
RESULT 60
A27365/c 23 bp DNA linear PAT 23-MAY-1995
LOCUS Oligonucleotide primer for HuVKSABACK.
A27365
ACCESSION A27365.1 GI:905169
VERSION A27365.1
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 23)
AUTHORS
TITLE METHODS FOR PRODUCING MEMBERS OF SPECIFIC BINDING PAIRS
JOURNAL Patent: WO 9220791-A 60 26-NOV-1992;
FEATURES
source 1.23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9
RESULT 61
A32959/c 23 bp DNA linear PAT 11-DEC-1996
LOCUS Synthetic PCR primer HuVKSABACK.
A32959
ACCESSION A32959.1 GI:1926608
VERSION A32959.1
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 23)
AUTHORS
TITLE METHODS FOR PRODUCING MEMBERS OF SPECIFIC BINDING PAIRS
JOURNAL Patent: WO 9201047-A 82 23-JAN-1992;
FEATURES
source 1.23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9
RESULT 62
A33878/c 23 bp DNA linear PAT 02-SEP-2002
LOCUS Synthetic primer HuVKSABACK.
A33878
ACCESSION A33878.1 GI:21694125
VERSION A33878.1
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 23)
AUTHORS
TITLE Jespers,L.S.A., Winter,G.P., Baier,M. and Hoogenboom,H.R.J.
JOURNAL Production of chimeric antibodies - a combinatorial approach
Patent: WO 9306213-A 76 01-APR-1993;
FEATURES
source 1.23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9
RESULT 63
A38170/c 23 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 14 from Patent WO9408008.
A38170
ACCESSION A38170.1 GI:2294776
VERSION A38170.1
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 23)
AUTHORS
TITLE IMPROVEMENTS IN OR RELATING TO IMMUNE RESPONSE MODIFICATION
JOURNAL MEDICAL RES COUNCIL (GB)
Patent: WO 9408008-A 14 14-APR-1994;
COMMENT Other publication CA 2145064 940414
Other publication AU 4832493 940426
Other publication JP 8501699T 960227.
FEATURES
source 1.23
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9
RESULT 64

AS1842/c
LOCUS AS1842 23 bp DNA linear PAT 10-MAR-1997
DEFINITION Sequence 6 from Patent WO9620011.
ACCESSION AS1842
VERSION AS1842.1 GI:4530005
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Blakey,D.C., Davies,D.H., Dowell,R.I., Hennam,J.F., Marsham,P.R., Slater,Anthony,M. and Hennequin,L.F.
TITLE CHEMICAL COMPOUNDS CHEMICAL COMPOUNDS
JOURNAL Patent: WO 9620011-A 6 04-JUL-1996;
COMMENT ZENECA LTD (GB)
On Mar 27, 1999 this sequence version replaced gi:2304590.
Other publication AU 4269796 960719.
FEATURES
source
1..23
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 GGACCTGCTGCA 29
19 GGACCTGCTGCA 8
Db

RESULT 65
LOCUS AS1879 23 bp DNA linear PAT 10-MAR-1997
DEFINITION Sequence 43 from Patent WO9620011.
ACCESSION AS1879
VERSION AS1879.1 GI:2304627
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 23)
AUTHORS Blakey,D.C., Davies,D.H., Dowell,R.I., Hennam,J.F., Marsham,P.R., Slater,Anthony,M. and Hennequin,L.F.
TITLE CHEMICAL COMPOUNDS CHEMICAL COMPOUNDS
JOURNAL Patent: WO 9620011-A 43 04-JUL-1996;
COMMENT ZENECA LTD (GB)
Other publication AU 4269796 960719.
FEATURES
source
1..23
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 GGACCTGCTGCA 29
19 GGACCTGCTGCA 8
Db

RESULT 66
LOCUS AS1891 23 bp DNA linear PAT 10-MAR-1997
DEFINITION Sequence 55 from Patent WO9620011.
ACCESSION AS1891
VERSION AS1891.1 GI:2304639
KEYWORDS

SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 23)
AUTHORS Blakey,D.C., Davies,D.H., Dowell,R.I., Hennam,J.F., Marsham,P.R., Slater,Anthony,M. and Hennequin,L.F.
TITLE CHEMICAL COMPOUNDS CHEMICAL COMPOUNDS
JOURNAL Patent: WO 9620011-A 55 04-JUL-1996;
COMMENT ZENECA LTD (GB)
Other publication AU 4269796 960719.
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 9.1%; Score 12; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 GGACCTGCTGCA 29
19 GGACCTGCTGCA 8
Db

RESULT 67
LOCUS A87525 23 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 6 from Patent WO9835988.
ACCESSION A87525
VERSION A87525.1 GI:6736174
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 23)
AUTHORS Edge,M.D.
TITLE PROTEINS
JOURNAL Patent: WO 9835988-A 6 20-AUG-1998;
COMMENT ZENECA LTD (GB); EDGE MICHAEL DREK (GB)
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Query Match 9.1%; Score 12; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 GGACCTGCTGCA 29
19 GGACCTGCTGCA 8
Db

RESULT 68
LOCUS A87543 23 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 24 from Patent WO9835988.
ACCESSION A87543
VERSION A87543.1 GI:6736191
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 23)
AUTHORS Edge,M.D.
TITLE PROTEINS
JOURNAL Patent: WO 9835988-A 24 20-AUG-1998;
COMMENT ZENECA LTD (GB); EDGE MICHAEL DREK (GB)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"


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QY      31 GACTGCGTGACT 42
Db      20 GACTGCGTGACT 9

RESULT 73
CO846582/c
LOCUS   CO846582      23 bp      DNA      linear      PAT 02-AUG-2004
DEFINITION
Sequence 103 from Patent EP1433846.
ACCESSION
CO846582
VERSION
CO846582.1 GI:50895812
KEYWORDS
SOURCE
synthetic construct
ORGANISM
artificial sequence.

REFERENCE
1
AUTHORS
McCaferry,J., Pope,A.R., Johnson,K.S., Hoogenboom,H.R.,
Griffiths,A.D., Jackson,R.H., Holliger,K.P., Marks,J.D.,
Jackson,T.P., Chiswell,D.J., Winter,G.P. and Bonner,T.P.
Phagemid-based method of producing filamentous bacteriophage
particles displaying antibody molecules and the corresponding
bacteriophage particles
Patent: EP 1433846-A 103 30-JUN-2004;
Cambridge Antibody Technology LTD (GB); Medical Research Council
(GB)

FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer"

ORIGIN
Query Match      9.1%; Score 12; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 GACTGCGTGACT 42
Db      20 GACTGCGTGACT 9

RESULT 74
E09118/c
LOCUS   E09118      23 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION
Synthetic oligonucleotides for primer.
ACCESSION
E09118
VERSION
E09118.1 GI:22025744
KEYWORDS
JP 1995115978-A/13.
SOURCE
unidentified
ORGANISM
unclassified.

REFERENCE
1 (bases 1 to 23)
AUTHORS
Katou,T., Yamamoto,K., Nishio,K. and Mizushima,Y.
METHOD FOR DETECTING AND CLONING ANTIBODY GENE
Patent: JP 1995115978-A 13 09-MAY-1995;
L T T KENKYUSHO:KK

COMMENT
OS None
OC Artificial sequences.
PN JP 1995115978-A/13
PD 09-MAY-1995
PE 22-OCT-1993 JP 1993287628
PI KATOU TOMOHIRO, YAMAMOTO KAZUHIKO, NISHIOKA KUZUKI, PI
MIZUSHIMA YUTAKA
PC C12N15/09, C1201/68, G01N33/53;
CC strandedness: Single;
CC topology: Linear;
CC Key
FH Location/Qualifiers
FT source
FT 1..23
FT /organism='Artificial sequences' FT
misc_feature 1..23

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FT
FT      /note='Synthetic oligonucleotide for primer of
5'-side'.
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 GACTGCGTGACT 42
Db      20 GACTGCGTGACT 9

RESULT 75
I27562/c
LOCUS   I27562      23 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION
Sequence 76 from Patent US 5565332.
ACCESSION
I27562
VERSION
I27562.1 GI:1818338
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Hoogenboom,H.R,J.M., Baier,M., Jespers,L.S.A.T. and Winter,G.P.
TITLE
Production of chimeric antibodies - a combinatorial approach
JOURNAL
Patent: US 5565332-A 76 15-OCT-1996;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      9.1%; Score 12; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 GACTGCGTGACT 42
Db      20 GACTGCGTGACT 9

Search completed: February 2, 2005, 20:26:02
Job time : 564.527 secs

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C 94	12	3.8	12	6	AR084606
C 95	12	3.8	12	6	CQ828576
C 96	12	3.8	13	6	CQ828577
C 97	12	3.8	14	6	I711106
C 98	12	3.8	14	6	AR403419
C 99	12	3.8	14	6	BD068919
C 100	12	3.8	15	6	A88671
C 101	12	3.8	15	6	A90638
C 102	12	3.8	15	6	AR084532
C 103	12	3.8	15	6	AR201669
C 104	12	3.8	15	6	AR201675
C 105	12	3.8	15	6	AR278935
C 106	12	3.8	15	6	AX300964
C 107	12	3.8	15	6	BD06184
C 108	12	3.8	16	6	BD274529
C 109	12	3.8	16	6	AR201673
C 110	12	3.8	16	6	AR234357
C 111	12	3.8	16	6	AR328248
C 112	12	3.8	16	6	AX046980
C 113	12	3.8	17	6	A27313
C 114	12	3.8	17	6	A27314
C 115	12	3.8	17	6	A88670
C 116	12	3.8	17	6	A90637
C 117	12	3.8	17	6	AR052186
C 118	12	3.8	17	6	AR164080
C 119	12	3.8	17	6	AR164081
C 120	12	3.8	17	6	CQ623533
C 121	12	3.8	17	6	CQ623534
C 122	12	3.8	17	6	CQ623535
C 123	12	3.8	17	6	CQ623536
C 124	12	3.8	17	6	CQ623537
C 125	12	3.8	17	6	CQ623538
C 126	12	3.8	17	6	AR234417
C 127	12	3.8	17	6	AR242713
C 128	12	3.8	17	6	AR242714
C 129	12	3.8	17	6	AR326995
C 130	12	3.8	17	6	AR318186
C 131	12	3.8	17	6	AR318189
C 132	12	3.8	17	6	AR464596
C 133	12	3.8	17	6	AR464597
C 134	12	3.8	17	6	AR464598
C 135	12	3.8	17	6	AR464599
C 136	12	3.8	17	6	AR464600
C 137	12	3.8	17	6	AR464601
C 138	12	3.8	17	6	AX262904
C 139	12	3.8	17	6	AX262905
C 140	12	3.8	17	6	AX423623
C 141	12	3.8	17	6	AX423627
C 142	12	3.8	17	6	AX475354
C 143	12	3.8	17	6	AX475355
C 144	12	3.8	17	6	AX475356
C 145	12	3.8	17	6	AX475357
C 146	12	3.8	17	6	AX475358
C 147	12	3.8	17	6	AX475359
C 148	12	3.8	17	6	AX498902
C 149	12	3.8	17	6	AX498908
C 150	12	3.8	17	6	AX530591

ALIGNMENTS

RESULT 1
 LOCUS AR026494/c
 DEFINITION Sequence 1 from patent US 5856099.
 ACCESSION AR026494
 VERSION AR026494.1 GI:5937334
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Miraglia, L., Bennett, C., Frank, N., Dean, N. and Geiger, T.
 TITLE Antisense compositions and methods for modulating type I
 interleukin-1 receptor expression
 JOURNAL Patent: US 5856099-A 1 05-JAN-1999;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 5.0%; Score 16; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCCGCGCAGCCCTGG 58
 DB 19 GCCGCGCAGCCCTGG 4

RESULT 2

LOCUS AR196702 18 bp DNA
 DEFINITION Sequence 1167 from patent US 6350934.
 ACCESSION AR196702
 VERSION AR196702.1 GI:20246139
 KEYWORDS
 ORGANISM Unknown.
 Unclassified.

REFERENCE

1 (bases 1 to 18)
 Zwick, M.G., Edington, B.E., McSwiggen, J.A., Merlo, P. Ann. Owens, J.
 TITLE Nucleic acid encoding delta-9 desaturase
 JOURNAL Patent: US 6350934-A 1167 26-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 4.7%; Score 15; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 GCCCGCCCGCAGC 53
 DB 4 CGCCCGCCCGCAGC 18

RESULT 3

LOCUS AR196704 18 bp DNA
 DEFINITION Sequence 1169 from patent US 6350934.
 ACCESSION AR196704
 VERSION AR196704.1 GI:20246141
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Zwick, M.G., Edington, B.E., McSwiggen, J.A., Merlo, P. Ann. Owens, J.
 TITLE Nucleic acid encoding delta-9 desaturase
 JOURNAL Patent: US 6350934-A 1169 26-FEB-2002;
 FEATURES Location/Qualifiers
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 /mol_type="unassigned DNA"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCGCAGC 53
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Db 1 CGCGCGCGCGCGCAGC 15

RESULT 4
AR084538
LOCUS AR084538 24 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 27 from patent US 5981185.
ACCESSION AR084538
VERSION AR084538.1 GI:10011309
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Watson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 27 09-NOV-1999;
FEATURES
source location/Qualifiers
1. .24
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 4.4%; Score 15; DB 6; Length 24;
Best Local Similarity 100.0%; Pred.No.3.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCGCAGC 53
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Db 3 CGCGCGCGCGCGCAGC 17

RESULT 5
AX739218/c
LOCUS AX739218 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4808 from Patent WO03025177.
ACCESSION AX739218
VERSION AX739218.1 GI:30518515
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Teلمان,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 4808 27-MAR-2003;
FEATURES
source location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 4.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred.No.1.4e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 GGTCTCTGGAGATC 188
|||||
Db 14 GGTCTCTGGAGATC 1

RESULT 6
AX452047
LOCUS AX452047 19 bp DNA linear PAT 06-JUL-2002

DEFINITION Sequence 24 from Patent EP1211314.
ACCESSION AX452047
VERSION AX452047.1 GI:21712050
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Annibali,N.
TITLE Expression of a human insulin precursor in p. Pastoris
JOURNAL Patent: EP 1211314-A 24 05-JUN-2002;
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source location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"

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Best Local Similarity 100.0%; Pred.No.1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 CAGCACCGATGGA 254
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Db 3 CAGCACCGATGGA 16

RESULT 7
AR026495/c
LOCUS AR026495 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5856099.
ACCESSION AR026495
VERSION AR026495.1 GI:5937335
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L., Bennett,C.Frank., Dean,N. and Geiger,T.
TITLE Antisense compositions and methods for modulating type I
interleukin-1 receptor expression
JOURNAL Patent: US 5856099-A 2 05-JAN-1999;
FEATURES
source location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCGCGCGCAGCCT 56
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Db 14 GCGCGCGCAGCCT 1

RESULT 8
AR312017/c
LOCUS AR312017 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2554 from patent US 6559294.
ACCESSION AR312017
VERSION AR312017.1 GI:31705443
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoisei,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof

JOURNAL Patent: US 6559294-A 2554 06-MAY-2003;
 FEATURES Location/Qualifiers
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ORIGIN /organism="unknown"
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Query Match 4.4%; Score 14; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 GGAGACGAGGTGC 148
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 17 GGAGACGAGGTGC 4

RESULT 9
 AX686350 20 bp DNA linear PAT 29-MAR-2003
 LOCUS Sequence 159 from Patent WO02059315.
 DEFINITION AX686350
 ACCESSION AX686350
 VERSION AX686350.1 GI:29372089

KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS

1 Shimkets, R.A., Patturajan, M., Vernet, C.A., Casman, S.J.,
 Malynka, U., Shenoy, S., Spytek, K.A., Gangoli, E., Miller, C.,
 Boldog, F., Li, L., Taupier, R.J., Kekuda, R., Smithson, G.,
 Zornhagen, B.D., Liu, X., Colman, S.D., Tchernev, V., St, J., Edinger, S.,
 Stone, D., Sciore, P., Millet, I. and Rothenberg, M.
 Human nucleic acids and polypeptides and methods of use thereof
 Patent: WO 02059315-A 159 01-AUG-2002;
 Curagen Corporation (US)
 Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="PCR Primer sequence"

ORIGIN

Query Match 4.4%; Score 14; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 CAGCACCAGTGAA 254
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 Db 7 CAGCACCAGTGAA 20

RESULT 10
 AX354407/c 22 bp DNA linear PAT 06-FEB-2002
 LOCUS Sequence 53 from Patent WO0196523.
 DEFINITION AX354407
 ACCESSION AX354407
 VERSION AX354407.1 GI:18619249
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 CHIRON CORPORATION (US)
 Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Primer"

FEATURES

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 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Primer"

ORIGIN

Query Match 4.4%; Score 14; DB 6; Length 22;
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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 GAAGCGGAGGTGA 125
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 Db 22 GAAGCGGAGGTGA 9

RESULT 11
 ATH524428 27 bp DNA linear PAT 29-MAR-2003
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 DEFINITION 075A07.
 ACCESSION AJ524428
 VERSION AJ524428.1 GI:26792664
 KEYWORDS left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS
 1 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Bechold, N., Cruaud, C., Derose, R., Pelletier, G.,
 Lepoint, L., Caboche, M. and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites
 EMBL Rep. 3 (12), 1152-1157 (2002)

JOURNAL

MEDLINE
 22363535
 2 (bases 1 to 27)
 Balzerque, S.
 Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
 Direct Submision
 Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
 Gastron Crepeux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
 http://dbgap.versailles.inra.fr/publiclines/. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplante' (http://www.genoplante.com and
 http://genoplante-info.infobiogen.fr).

COMMENT

LOCATION/Qualifiers
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 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="Wassilewskija"
 /db_xref="taxon:3702"
 /clone="075A07"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 1..27
 /note="T-DNA flanking sequence
 left border"

FEATURES

source
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 /cultivar="Wassilewskija"
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 /clone="075A07"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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 /note="T-DNA flanking sequence
 left border"

ORIGIN

Query Match 4.4%; Score 14; DB 8; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 ATGAATAATCAGGT 220
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 Db 8 ATGAATAATCAGGT 21

RESULT 12
 AX791502

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LOCUS       AX791502               30 bp    DNA             linear    PAT 17-JUL-2003
DEFINITION  Sequence 3966 from Patent WO2066501.
ACCESSION   AX791502
VERSION     AX791502.1   GI:32956949
KEYWORDS
SOURCE      Helicobacter pylori
            Helicobacter pylori
            Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
            Helicobacteraceae; Helicobacter.
REFERENCE   1
  AUTHORS   Legrain, P., Rain, J.C., Colland, F., de Reuse, H. and Labigne, A.
  TITLE     Protein-protein interactions in Helicobacter pylori
  JOURNAL   Patent: WO 02066501-A 1966 29-AUG-2002;
            Hybridgenics (FR); INSTITUT PASTEUR (FR)
FEATURES
  source    1..30
            /organism="Helicobacter pylori"
            /mol_type="unassigned DNA"
            /db_xref="taxon:210"

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Query Match      4.4%; Score 14; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      201 TAGTGGATGAAAA 214
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        14 TAGTGGATGAAAA 27

RESULT 13
LOCUS       AX431364/c             14 bp    DNA             linear    PAT 28-JUN-2002
DEFINITION  Sequence 11 from Patent WO240711.
ACCESSION   AX431364
VERSION     AX431364.1   GI:21656219
KEYWORDS
SOURCE      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Moughn, B.
  TITLE     Method for analysing a patient's predisposition to
            insulin-dependent diabetes, device and set of primers
            Patent: WO 0240711-A 11 23-MAY-2002;
            BIOMERIEUX SA (FR)
FEATURES
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

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Query Match      4.1%; Score 13; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      96 CGCAGCTCTCTCT 108
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        13 CGCAGCTCTCTCT 1

Db      13 CGCAGCTCTCTCT 1

RESULT 14
LOCUS       AR033424/c             15 bp    DNA             linear    PAT 29-SEP-1999
DEFINITION  Sequence 190 from patent US 5869253.
ACCESSION   AR033424
VERSION     AR033424.1   GI:5949029
KEYWORDS
SOURCE      Unknown.
            Unknown.
            Unclassified.

LOCUS       AR113246/c             15 bp    DNA             linear    PAT 16-MAY-2001
DEFINITION  Sequence 190 from patent US 6132966.
ACCESSION   AR113246
VERSION     AR113246.1   GI:14093568
KEYWORDS
SOURCE      Unknown.
            Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 15)
  AUTHORS   Draper, K.G.
  TITLE     Method and reagent for inhibiting hepatitis C virus replication
  JOURNAL   Patent: US 6132966-A 190 17-OCT-2000;
            Location/Qualifiers
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  source    1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      4.1%; Score 13; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      129 TCGGGCGGAGACG 141
        |||||
        15 TCGGGCGGAGACG 3

Db      15 TCGGGCGGAGACG 3

RESULT 16
LOCUS       BD207157/c             15 bp    RNA             linear    PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD207157
VERSION     BD207157.1   GI:33016927
KEYWORDS    UP 2002512791-A/747.
SOURCE      unidentified
            unidentified
            unclassified.
REFERENCE   1 (bases 1 to 15)
  AUTHORS   Blatt, L., Mcsvigen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
            Patent: JP 2002512791-A 747 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
            OS Hepatitis virus (hepatitis C virus)
            PN JP 2002512791-A/747
            PD 08-MAY-2002
            PF 26-APR-1999 JP 2000545991
            PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
            25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
            LAWRENCE BLATT, JAMES A MCSWIGEN, ELISABETH ROBERTS, PAMELA A PI
            PAVCO.

COMMENT
  JOURNAL
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FEATURES	source	Location/Qualifiers
CC	hepatitis C virus infection.	
EH	Key	1..15
FT	source	Location/Qualifiers
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		virus)'
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		/organism="unidentified"
		/mol_type="genomic RNA"
		/db_xref="taxon:32644"
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Query Match	4.1%; Score 13; DB 6; Length 15;	
Best Local Similarity	100.0%; Pred. No. 5.6e+04;	
Matches 13; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	129 TCGGCGGAGACG 141	
Db	15 TCGGCGGAGACG 3	
RESULT 17		
LOCUS	157653	15 bp DNA
DEFINITION	Sequence 190 from patent US 5610054.	linear PAT 07-OCT-1997
ACCESSION	157653	
VERSION	157653.1	GI:248217
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 15)	
AUTHORS	Draper,K.G.	
TITLE	Enzymatic RNA molecule targeted against Hepatitis C virus	
JOURNAL	Patent: US 5610054-A 190 11-MAR-1997;	
FEATURES	Location/Qualifiers	
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	/organism="unknown"	
	/mol_type="unassigned DNA"	
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Query Match	4.1%; Score 13; DB 6; Length 15;	
Best Local Similarity	100.0%; Pred. No. 5.6e+04;	
Matches 13; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	129 TCGGCGGAGACG 141	
Db	15 TCGGCGGAGACG 3	
RESULT 18		
LOCUS	BD104567	16 bp DNA
DEFINITION	Kit and method for determining HUA type.	linear PAT 27-AUG-2002
ACCESSION	BD104567	
VERSION	BD104567.1	GI:22650141
KEYWORDS	WO 0192572-A/671.	
SOURCE	synthetic construct	
ORGANISM	artificial construct	
REFERENCE	1 (bases 1 to 16)	
AUTHORS	Inoko,H., Kagiyu,T., Ichihara,T., Matsumura,Y., Moriya,S. and	
TITLE	Nishida,M.	
JOURNAL	Kit and method for determining HUA type	
	Patent: WO 0192572-A 671 06-DEC-2001;	
	NISSHINO INDUSTRIES INC./SYSTEM RESEARCH INC./HIDETOSHI INOKO, TAEKO	
	KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO	

COMMENT	NISHIDA	OS	Artificial Sequence
	PN	WO 0192572-A/671	
	PD	06-DEC-2001	
	PF	01-JUN-2001 WO 2001JP004662	
	PI	HIDEFOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,	PI
	PC	SHOGO MORIYA,MICHO NISHIDA	
	CC	C12Q1/68,C12M1/00,C12N15/09,G01N33/53	
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Best Local Similarity		100.0%; Pred. No. 5.7e+04;	
Matches	13; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	96 CGCAGCTCTCTCT 108		
Db	15 CGCAGCTCTCTCT 3		
RESULT 19			
AX423624/c		17 bp RNA	PAT 18-JUN-2002
LOCUS	AX423624		
DEFINITION	Sequence 1960 from Patent WO0188124.		
ACCESSION	AX423624		
VERSION	AX423624.1 GI:21527006		
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	Jarvis,T., von Carlowitz,I., Mcswigen,J.A., McLaughlin,F.G. and Randi,A.M.		
AUTHORS			
TITLE	Method and reagent for the inhibition of erg		
JOURNAL	Patent: WO 0188124-A 1960 22-NOV-2001;		
	RIBOZYME PHARMACEUTICALS, INC.(US) ; GLAXO GROUP LIMITED (GB)		
FEATURES	Location/Qualifiers		
source	1..17		
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	/mol_type="unassigned RNA"		
	/db_xref="taxon:9606"		
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Best Local Similarity		100.0%; Pred. No. 5.7e+04;	
Matches	13; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	154 TTCTTTCCTCCGAGC 166		
Db	17 TTCTTTCCTCCGAGC 5		
RESULT 20			
AX423625/c		17 bp RNA	PAT 18-JUN-2002
LOCUS	AX423625		
DEFINITION	Sequence 1961 from Patent WO0188124.		
ACCESSION	AX423625		
VERSION	AX423625.1 GI:21527007		
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 Jarvis, T., von Carlwicz, I., Mcswigen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 018124-A 1961 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES location/Qualifiers
source 1..17
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/db_xref="taxon:9606"
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Query Match 4.1%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 154 TTCTTCCCGCAG 166
Db 16 TTCTTCCCGCAG 4
RESULT 21
AX423626/c 17 bp RNA linear PAT 18-JUN-2002
LOCUS Sequence 1962 from Patent WO0189124.
ACCESSION AX423626
VERSION AX423626.1 GI:21527008
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 018124-A 1962 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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Query Match 4.1%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 154 TTCTTCCCGCAG 166
Db 15 TTCTTCCCGCAG 3
RESULT 22
AX498903 17 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 210 from Patent EP1229046.
ACCESSION AX498903
VERSION AX498903.1 GI:23381196
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 210 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers

source 1..17
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 GGAAGCGACGACG 37
Db 5 GGAAGCGACGACG 17
RESULT 23
AX498904 17 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 211 from Patent EP1229046.
ACCESSION AX498904
VERSION AX498904.1 GI:23381197
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 211 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 GGAAGCGACGACG 37
Db 4 GGAAGCGACGACG 16
RESULT 24
AX498905 17 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 212 from Patent EP1229046.
ACCESSION AX498905
VERSION AX498905.1 GI:23381198
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 212 07-AUG-2002;
Aeomica, Inc. (US)
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 GGAAGGCAAGCAG 37
|||||
Db 3 GGAAGGCAAGCAG 15

RESULT 25
LOCUS AX498906 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 213 from Patent EP1229046.
ACCESSION AX498906
VERSION AX498906.1 GI:23381199
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Human testis expressed patched like protein
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 213 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 GGAAGGCAAGCAG 37
|||||
Db 2 GGAAGGCAAGCAG 14

RESULT 26
LOCUS AX498907 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 214 from Patent EP1229046.
ACCESSION AX498907
VERSION AX498907.1 GI:23381200
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Human testis expressed patched like protein
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 214 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 GGAAGGCAAGCAG 37
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Db 1 GGAAGGCAAGCAG 13

RESULT 27
LOCUS AX530592 17 bp DNA linear PAT 22-NOV-2002

DEFINITION Sequence 101 from Patent EP1239051.
ACCESSION AX530592
VERSION AX530592.1 GI:25252558
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Human posh-like protein 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 101 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 4.1%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 GCGCGGAGGAGGG 90
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Db 5 GCGCGGAGGAGGG 17

RESULT 28
LOCUS AX530593 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 102 from Patent EP1239051.
ACCESSION AX530593
VERSION AX530593.1 GI:25252560
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Human posh-like protein 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 102 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
source 1..17
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Query Match 4.1%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 GCGCGGAGGAGGG 90
|||||
Db 4 GCGCGGAGGAGGG 16

RESULT 29
LOCUS AX530594 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 103 from Patent EP1239051.
ACCESSION AX530594
VERSION AX530594.1 GI:25252561
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Human testis expressed patched like protein
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 213 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

AUTHORS Shannon,M.
TITLE Human poosh-like protein 1
JOURNAL Patent: EP 1239051-A 103 11-SEP-2002;
Aecomica, Inc. (US)
FEATURES
SOURCE Location/Qualifiers
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/db_xref="taxon:9606"
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Query Match 4.1%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 GCGCGGAGAGGCGG 90
|||||
3 GCGCGGAGAGGCGG 15
Db
RESULT 30
AX530595 17 bp DNA linear PAT 22-NOV-2002
LOCUS
DEFINITION Sequence 104 from Patent EP1239051.
AX530595
ACCESSION
VERSION AX530595.1 GI:25252562
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M.
1
TITLE Human poosh-like protein 1
JOURNAL Patent: EP 1239051-A 104 11-SEP-2002;
Aecomica, Inc. (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 GCGCGGAGAGGCGG 90
|||||
2 GCGCGGAGAGGCGG 14
Db
RESULT 31
AX530596 17 bp DNA linear PAT 22-NOV-2002
LOCUS
DEFINITION Sequence 105 from Patent EP1239051.
AX530596
ACCESSION
VERSION AX530596.1 GI:25252563
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M.
1
TITLE Human poosh-like protein 1
JOURNAL Patent: EP 1239051-A 105 11-SEP-2002;
Aecomica, Inc. (US)
FEATURES
SOURCE Location/Qualifiers
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/db_xref="taxon:9606"

ORIGIN
Query Match 4.1%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 GCGCGGAGAGGCGG 90
|||||
1 GCGCGGAGAGGCGG 13
Db
RESULT 32
A68426/c 18 bp DNA linear PAT 06-MAY-1999
LOCUS
DEFINITION Sequence 31 from Patent WO9746700.
A68426
ACCESSION
VERSION A68426.1 GI:4759503
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 18)
AUTHORS Mouglin,B.
TITLE NCLEOTIDE PROBES AND METHOD FOR DETERMINING HLA DQB1 TYPING
JOURNAL Patent: WO 9746700-A 31 11-DEC-1997;
BIO MERIEUX (FR)
COMMENT Other publication FR 2749308 19971205.
FEATURES
SOURCE Location/Qualifiers
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/db_xref="taxon:32644"
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Query Match 4.1%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 96 CGCAGCTCTCTCT 108
|||||
15 CGCAGCTCTCTCT 3
Db
RESULT 33
AX926753 18 bp DNA linear PAT 19-DEC-2003
LOCUS
DEFINITION Sequence 36 from Patent WO03085133.
AX926753
ACCESSION
VERSION AX926753.1 GI:40247115
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1
AUTHORS Nagaraju,J.G.
TITLE Novel fischer-pcr primers and method of identifying genotyping
diverse genomes of plant and animal systems including rice
varieties, a kit thereof
Patent: WO 03085133-A 36 16-OCT-2003;
Centre for DNA Fingerprinting and Diagnostics, Centre for the
Department of Biotechnology, Ministry of Science & Technology (IN)
FEATURES
SOURCE Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="A novel FISSR-PCR primer for genotyping eukaryotes"
ORIGIN
Query Match 4.1%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCCGCCGCCGCA 51
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 DB 3 CGCCGCCGCCGCA 15

RESULT 34
 BD087791/c
 LOCUS BD087791 18 bp DNA linear PAT 27-AUG-2002
 DEFINITION A method of arraying genome clone.
 ACCESSION BD087791
 VERSION BD087791.1 GI:22633401
 KEYWORDS JP 2001321190-A/35.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Soeda,E.
 TITLE A method of arraying genome clone
 JOURNAL Patent: JP 2001321190-A 35 20-NOV-2001;
 THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
 GENOTECHS

COMMENT
 OS Artificial Sequence
 PN JP 2001321190-A/35
 PD 20-NOV-2001
 PF 12-MAR-2001 JP 2001068285
 PI EICHI SOEDA
 PC C12N15/09,C12M15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
 C12N15/00
 CC Description of Artificial Sequence: Synthetic DNA FH Key
 FT Location/Qualifiers
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 /organism='Artificial Sequence'.
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 /organism='synthetic construct'
 /mol_type='genomic DNA'
 /db_xref='taxon:32630'

ORIGIN
 Query Match 4.1%; Score 13; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 GAGGAGCGGAG 121
 |||||
 DB 16 GAGGAGCGGAG 4

RESULT 35
 BD103980/c
 LOCUS BD103980 18 bp DNA linear PAT 27-AUG-2002
 DEFINITION Kit and method for determining HLA type.
 ACCESSION BD103980
 VERSION BD103980.1 GI:22649554
 KEYWORDS WO 0192572-A/84.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
 Nishida,M.
 TITLE Kit and method for determining HLA type
 JOURNAL Patent: WO 0192572-A 84 06-DEC-2001;
 NISSHINO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
 KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
 NISHIDA

COMMENT
 OS Artificial Sequence
 PN WO 0192572-A/84
 PD 06-DEC-2001
 PF 01-JUN-2001 WO 2001JP004662
 PR 01-JUN-2000 JP 00P 164798
 PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI

FEATURES
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 1..18
 /organism='synthetic construct'
 /mol_type='genomic DNA'
 /db_xref='taxon:32630'

ORIGIN
 Query Match 4.1%; Score 13; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 CGCAGCTCCTCT 108
 |||||
 DB 16 CGCAGCTCCTCT 4

RESULT 36
 BD104081/c
 LOCUS BD104081 18 bp DNA linear PAT 27-AUG-2002
 DEFINITION Kit and method for determining HLA type.
 ACCESSION BD104081
 VERSION BD104081.1 GI:22649655
 KEYWORDS WO 0192572-A/185.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
 Nishida,M.
 TITLE Kit and method for determining HLA type
 JOURNAL Patent: WO 0192572-A 185 06-DEC-2001;
 NISSHINO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
 KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
 NISHIDA

COMMENT
 OS Artificial Sequence
 PN WO 0192572-A/185
 PD 06-DEC-2001
 PF 01-JUN-2001 WO 2001JP004662
 PR 01-JUN-2000 JP 00P 164798
 PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI
 MATSUMURA,
 PI SHOGO MORIYA, MICHIO NISHIDA
 PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
 CC Description of Artificial Sequence: capture
 FH Key Location/Qualifiers
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 /db_xref='taxon:32630'

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 Best Local Similarity 100.0%; Pred. No. 5.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 CGCAGCTCCTCT 108
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 DB 16 CGCAGCTCCTCT 4

RESULT 37
 BD104190/c
 LOCUS BD104190 18 bp DNA linear PAT 27-AUG-2002


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DEFINITION   Kit and method for determining HLA type.
ACCESSION    BD104190
VERSION      WO 0192572-A/294.
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Inoko,H., Kagiyama,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
TITLE        Kit and method for determining HLA type
JOURNAL      Patent: WO 0192572-A 294 06-DEC-2001.
NISHIMOTO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA
COMMENT      OS Artificial Sequence
              PN WO 0192572-A/294
              PD 06-DEC-2001
              PF 01-JUN-2001 WO 2001JP004662
              PR 01-JUN-2000 JP 00P 164798
              PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,
              PI SHOGO MORIYA, MICHIO NISHIDA
              PC C1201/68, C12M1/00, C12N15/09, G01N33/53
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FEATURES
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Best Local Similarity 100.0%; Pred. No. 5.8e+04;
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QY 96 CGCAGCTCTCTCT 108
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Db 15 CGCAGCTCTCTCT 3

RESULT 38
AB068646/c
LOCUS       AB068646
DEFINITION Synthetic construct DNA, forward primer for human STS seqs-DIS2459
ACCESSION   AB068646
VERSION     AB068646.1 GI:15129450
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE    1
AUTHORS      Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
              Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
              Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
              and Soeda,E.
              A BAC-based STS-content map spanning a 35-Mb region of human
              chromosome 1p35-p36
              Genomics 74 (1), 55-70 (2001)
              21269192
              11374902
              2 (bases 1 to 18)
              Horii,A.
              Direct Submision
              Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
              Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
              Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
              Tel:81-22-717-8042, Fax:81-22-717-8047)
              Location/Qualifiers

FEATURES

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source
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      /db_xref="taxon:32630"
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          sts-DIS2459 obtained from clones B79P10, B23OH10, B23TP6,
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Db      16 GAGGAGCGGAG 4

RESULT 39
AR077249      20 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION Sequence 7 from patent US 5962233.
ACCESSION AR077249
VERSION AR077249.1 GI:10003995
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Liyak,K.U. and Goodsaid,F.
JOURNAL Determination of a genotype of an amplification product at multiple
FEATURES allelic sites
SOURCE Patent: US 5962233-A 7 05-OCT-1999;
Location/Qualifiers
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ORIGIN
Query Match      4.1%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+04; Indels 0; Gaps 0;
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QY      96 CGCAGGTCTCTCT 108
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Db      7 CGCAGTCTCTCT 19

RESULT 40
LOCUS AR120194 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 7 from patent US 6154707.
ACCESSION AR120194
VERSION AR120194.1 GI:14102893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Liyak,K.U. and Goodsaid,F.
JOURNAL Computer logic for fluorescence genotyping at multiple allelic
FEATURES sites
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QY      96 CGCAGGTCTCTCT 108
       |||||
Db      7 CGCAGTCTCTCT 19

RESULT 40
LOCUS AR120194 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 7 from patent US 6154707.
ACCESSION AR120194
VERSION AR120194.1 GI:14102893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Liyak,K.U. and Goodsaid,F.
JOURNAL Computer logic for fluorescence genotyping at multiple allelic
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SOURCE Patent: US 6154707-A 7 28-NOV-2000;
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Matches 13; Conservative 0; Mismatches 0;

QY      96 CGCAGGTCTCTCT 108
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Db      7 CGCAGTCTCTCT 19

RESULT 40
LOCUS AR120194 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 7 from patent US 6154707.
ACCESSION AR120194
VERSION AR120194.1 GI:14102893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Liyak,K.U. and Goodsaid,F.
JOURNAL Computer logic for fluorescence genotyping at multiple allelic
FEATURES sites
SOURCE Patent: US 6154707-A 7 28-NOV-2000;
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RESULT 40
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Liyak,K.U. and Goodsaid,F.
JOURNAL Computer logic for fluorescence genotyping at multiple allelic
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RESULT 40
LOCUS AR120194 20 bp DNA linear PAT 16-MAY-2001
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VERSION AR120194.1 GI:14102893
KEYWORDS
SOURCE Unknown.
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REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Liyak,K.U. and Goodsaid,F.
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QY      96 CGCAGGTCTCTCT 108
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RESULT 40
LOCUS AR120194 20 bp DNA linear PAT 16-MAY-2001
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VERSION AR120194.1 GI:14102893
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TITLE Liyak,K.U. and Goodsaid,F.
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QY      96 CGCAGGTCTCTCT 108
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Db      7 CGCAGTCTCTCT 19

RESULT 40
LOCUS AR120194 20 bp DNA linear PAT 16-MAY-2001
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VERSION AR120194.1 GI:14102893
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ORGANISM Unknown.
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AUTHORS 1 (bases 1 to 20)
TITLE Liyak,K.U. and Goodsaid,F.
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RESULT 40
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VERSION AR120194.1 GI:14102893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Liyak,K.U. and Goodsaid,F.
JOURNAL Computer logic for fluorescence genotyping at multiple allelic
FEATURES sites
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Matches 13; Conservative 0; Mismatches 0;

QY      96 CGCAGGTCTCTCT 108
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Db      7 CGCAGTCTCTCT 19

RESULT 40
LOCUS AR120194 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 7 from patent US 6154707.
ACCESSION AR120194
VERSION AR120194.1 GI:14102893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Liyak,K.U. and Goodsaid,F.
JOURNAL Computer logic for fluorescence genotyping at multiple allelic
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SOURCE Patent: US 6154707-A 7 28-NOV-2000;
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RESULT 40
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DEFINITION Sequence 7 from patent US 6154707.
ACCESSION AR120194
VERSION AR120194.1 GI:14102893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Liyak,K.U. and Goodsaid,F.
JOURNAL Computer logic for fluorescence genotyping at multiple allelic
FEATURES sites
SOURCE Patent: US 6154707-A 7 28-NOV-2000;
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QY      96 CGCAGGTCTCTCT 108
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Db      7 CGCAGTCTCTCT 19

RESULT 40
LOCUS AR120194 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 7 from patent US 6154707.
ACCESSION AR120194
VERSION AR120194.1 GI:14102893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Liyak,K.U. and Goodsaid,F.
JOURNAL Computer logic for fluorescence genotyping at multiple allelic
FEATURES sites
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 Db 7 CGCAGCTCTCTCT 19

RESULT 41
 E13797/c E13797 20 bp DNA linear PAT 27-APR-1998
 DEFINITION PCR primer for discriminating genotype 1a of HCV (Hepatitis C virus).
 ACCESSION E13797
 VERSION E13797.1 GI:3252565
 KEYWORDS JP 1997234072-A/49.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE
 AUTHORS Ono, T., Mukai, M., Hiki, K. and Mizogami, M.
 TITLE NEW OLIGONUCLEOTIDE PRIMER FOR DISCRIMINATION IN GENOTYPE OF HEPATITIS C VIRUS COMPRISING THE SAME AND DISCRIMINATION IN GENOTYPE OF HEPATITIS C VIRUS BY USING THE PRIMER
 JOURNAL Patent: JP 1997234072-A 49 09-SEP-1997;
 S R L:KK

COMMENT
 OS None
 OC Artificial sequences.
 PN JP 1997234072-A/49
 PD 09-SEP-1997
 PF 01-FEB-1996 JP 1996038875
 PR 01-FEB-1995 JP 95P 35997, 30-DEC-1995 JP 95P 352511 PI
 ONO TOMOYOSHI, MUKAI MASAOKA, HIKI KAZUMASA, MI MIZOGAMI MASAFUMI
 PC C12N15/09, C07H21/04, C12Q1/68, C12Q1/70, (C12N15/09, C12R1:92); CC
 strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: Yes;
 FH Key Location/Qualifiers

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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 CGAGGTGCGACC 152
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 Db 16 CGAGGTGCGACC 4

RESULT 42
 AR266141/c AR266141 20 bp DNA linear PAT 10-APR-2003
 LOCUS Sequence 40 from patent US 6492172.
 DEFINITION AR266141
 ACCESSION AR266141.1 GI:29694987
 VERSION AR266141.1
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE
 AUTHORS Bennett, C.F., Busch, H., and Wyatt, J.
 TITLE Antisense modulation of GU protein expression

JOURNAL Patent: US 6492172-A 40 10-DEC-2002;
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QY 307 TGGGATGTCATC 319
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 Db 16 TGGGATGTCATC 4

RESULT 43
 AX292891 AX292891 20 bp DNA linear PAT 21-NOV-2001
 LOCUS Sequence 4653 from Patent WO0179548.
 DEFINITION AX292891
 ACCESSION AX292891
 VERSION AX292891.1 GI:17054574
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

REFERENCE
 AUTHORS Barany, F., Zivvi, M., Gerry, N.P., Favis, R., and Kliman, R.
 TITLE Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction
 JOURNAL Patent: WO 0179548-A 4653 25-OCT-2001;
 CORNELL RESEARCH FOUNDATION, INC. (US)
 FEATURES Location/Qualifiers
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 /db_xref="taxon:32630"
 /note="Hypothetical Probe Sequence"

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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 GAGTGACCATCG 131
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 Db 4 GAGTGACCATCG 16

RESULT 44
 BD087778/c BD087778 20 bp DNA linear PAT 27-AUG-2002
 LOCUS A method of arraying genome clone.
 DEFINITION BD087778
 ACCESSION BD087778
 VERSION BD087778.1 GI:22633388
 KEYWORDS JP 2001321190-A/22.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

REFERENCE
 AUTHORS Soeda, E.
 TITLE A method of arraying genome clone
 JOURNAL Patent: JP 2001321190-A 22 20-NOV-2001;
 THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
 GENOTECHS

COMMENT
 OS Artificial Sequence
 PN JP 2001321190-A/22
 PD 20-NOV-2001
 PF 12-MAR-2001 JP 2001068285
 PI EIICHI SOEDA
 PC C12N15/09, C12N15/00, C12M1/68, G01N33/53, G01N33/566, PC
 C12N15/00

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Gaps 0;			
QY	304	GACTGGGGATGTC 316	
DB	16	GACTGGGGATGTC 4	
RESULT 45			
AB068593/c			
LOCUS	AB068593	20 bp	DNA
DEFINITION	Synthetic construct DNA, reverse primer for human STS sts-wi-13136		
ACCESSION	AB068593		
VERSION	AB068593.1	GI:15129397	
KEYWORDS			
SOURCE	Synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1	artificial sequences.	
AUTHORS	Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,		
	Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,		
	Morohashi, A., Ohira, M., Nakagawara, A., Iiu, S., Hoashi, M., Horii, A.		
	and Seeda, E.		
TITLE	A BAC-based STS-content map spanning a 35-kb region of human		
JOURNAL	chromosome 1p35-p36		
MEDLINE	Genomics 74 (1), 55-70 (2001)		
PUBMED	11374902		
REFERENCE	2	(bases 1 to 20)	
AUTHORS	Horii, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-AUG-2001)		
	Akira Horii, Tohoku University School of		
	Medicine, Molecular Pathology, 2-1 Seiryomachi, Aoba-ku, Sendai,		
	Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,		
	Tel: 81-22-717-8042; Fax: 81-22-717-8047)		
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1..20	/note="reverse primer for human STS sts-wi-13136		
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	library RPC1-11"		
ORIGIN			
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Best Local Similarity	100.0%;	Pred. No. 5.8e+04;	
Matches 13;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps 0;			
QY	304	GACTGGGGATGTC 316	
DB	16	GACTGGGGATGTC 4	
RESULT 46			
AB068593/c			
LOCUS	AB068593	21 bp	DNA
DEFINITION	PCR primer for discriminating genotype 1a of HCV (Hepatitis C		

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ACCESSION      E137281
VERSION        E13781.1 GI:3252549
KEYWORDS       JP 1997234072-A/33.
SOURCE         unidentified
ORGANISM       unclassified.

REFERENCE      1 (bases 1 to 21)
AUTHORS        Ono,T., Mukaiide,M., Hikichi,K. and Mizogami,M.
TITLE          NEW OLIGONUCLEOTIDE, PRIMER FOR DISCRIMINATION IN GENOTYPE OF
               HEPATITIS C VIRUS COMPRISING THE SAME AND DISCRIMINATION IN
               GENOTYPE OF HEPATITIS C VIRUS BY USING THE PRIMER
               Patent: JP 1997234072-A 33 09-SEP-1997;
JOURNAL        S R L:KK

COMMENT        OS None
               OC Artificial sequences.
               PN JP 1997234072-A/33
               PD 09-SEP-1997
               PR 01-FEB-1996 JP 1996038875
               PR 01-FEB-1995 JP 95P 35997, 30-DEC-1995 JP 95P 352511 PI
               ONO TOMOYOSHI, MUKAIDE MASAKAZU, HIKICHI KAZUMASA, PI MIZOGAMI
               MASAFUMI
               PC C12N15/09, C07H21/04, C12Q1/68, C12Q1/70, (C12N15/09, C12R1:92); CC
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               CC topology: Linear;
               CC hypothetical: No;
               CC anti-sense: Yes;
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FEATURES
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Location/Qualifiers
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Query Match 4.1%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 CGAGGTTCGACC 152
Dbb 14 CGAGGTTCGACC 2

RESULT 47
E13793/c
LOCUS          E13793          21 bp          DNA          linear          PAT 27-APR-1998
DEFINITION     PCR primer for discriminating genotype of HCV (Hepatitis C virus).
ACCESSION      E13793
VERSION        E13793.1 GI:3252561
KEYWORDS       JP 1997234072-A/45.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Ono,T., Mukaiide,M., Hikichi,K. and Mizogami,M.
TITLE          NEW OLIGONUCLEOTIDE, PRIMER FOR DISCRIMINATION IN GENOTYPE OF
               HEPATITIS C VIRUS COMPRISING THE SAME AND DISCRIMINATION IN
               GENOTYPE OF HEPATITIS C VIRUS BY USING THE PRIMER
               Patent: JP 1997234072-A 45 09-SEP-1997;
JOURNAL        S R L:KK

COMMENT        OS None
               OC Artificial sequences.
               PN JP 1997234072-A/45
               PD 09-SEP-1997
               PR 01-FEB-1996 JP 1996038875
               PR 01-FEB-1995 JP 95P 35997, 30-DEC-1995 JP 95P 352511 PI
               ONO TOMOYOSHI, MUKAIDE MASAKAZU, HIKICHI KAZUMASA, PI MIZOGAMI
               MASAFUMI
               PC C12N15/09, C07H21/04, C12Q1/68, C12Q1/70, (C12N15/09, C12R1:92); CC

```

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strandness: Single;
CC topology: Linear;
CC hypothetical: No;
FH Key Location/Qualifiers
FT source 1..21
FT Location/Qualifiers
FEATURES
source 1..21
/organism="Artificial sequences"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Query Match 4.1%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 140 CGAGGTTGCGACC 152
14 CGAGGTTGCGACC 2
RESULT 48
AX015616/c 21 bp DNA linear PAT 07-SEP-2000
LOCUS AX015616
DEFINITION Sequence 2 from Patent WO951261.
ACCESSION AX015616
VERSION AX015616.1 GI:10041448
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stephanou, A., Brar, B., Knight, R. and Latchman, D.
TITLE Use of urocortin and like polypeptides in therapy
JOURNAL Patent: WO 951261-A 2 14-OCT-1999;
STEPHANOU ANASTASIS (GB); BRAR BHAWAN (GB); UNIV LONDON (GB);
KNIGHT RICHARD (GB); LATCHMAN DAVID (GB)
FEATURES
source 1..21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
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Query Match 4.1%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 42 CGCGCGCGCAGCC 54
13 CGCGCGCGCAGCC 1
RESULT 49
AX458691/c 21 bp DNA linear PAT 08-JUL-2002
LOCUS AX458691
DEFINITION Sequence 8 from Patent WO0246462.
ACCESSION AX458691
VERSION AX458691.1 GI:21725355
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Greaves, D., Price, S. and Watkins, H.
TITLE Functional genetic variants
JOURNAL Patent: WO 0246462-A 8 13-JUN-2002;
1818 Innovation Limited (GB)
FEATURES
source 1..21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Amplification Primer"
ORIGIN
Query Match 4.1%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 GAGGAGGCGCGAG 94
17 GAGGAGGCGCGAG 5
RESULT 50
BD012872 21 bp DNA linear PAT 02-AUG-2002
LOCUS BD012872
DEFINITION Nucleus localizing RecQ5-type DNA helicase.
ACCESSION BD012872
VERSION BD012872.1 GI:22093061
KEYWORDS WO 0125425-A/45.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Furuchi, Y., Shimamoto, A., Kitao, S. and Nishikawa, K.
TITLE Nucleus localizing RecQ5-type DNA helicase
JOURNAL Patent: WO 0125425-A 45 12-APR-2001;
AGENE RESEARCH INSTITUTE CO LTD, YASUHIRO FURUCHI, AKIRA SHIMAMOTO,
SAORI KITAO, KAORI NISHIKAWA
COMMENT OS Artificial sequence
EN WO 0125425-A/45
PD 12-APR-2001
PF 25-AUG-2000 WO 2000JP005757
PR 05-OCT-1999 JP 99P 284001
PI YASUHIRO FURUCHI, AKIRA SHIMAMOTO, SAORI KITAO, KAORI NISHIKAWA
PC C12N15/12, C12N9/14, C12Q1/68, C07K16/18, G01N33/53, A01K67/00 CC
Description of Artificial Sequence: Artificially synthesized CC
Primer Sequence
FH Key Location/Qualifiers
FEATURES
source 1..21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Query Match 4.1%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 113 AAGCGGAGGTGGA 125
4 AAGCGGAGGTGGA 16
RESULT 51
AR236424 22 bp DNA linear PAT 20-DEC-2002
LOCUS AR236424
DEFINITION Sequence 10 from patent US 6465185.
ACCESSION AR236424
VERSION AR236424.1 GI:27280403
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
AUTHORS Goldfine, I., Trischitta, V., Vigneri, R., Pizzuti, A. and
Fritticita, L. A.
TITLE Polymorphic human PC-1 sequences associated with insulin resistance
JOURNAL Patent: US 6465185-A 10 15-OCT-2002;
FEATURES
source 1..21
Location/Qualifiers
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source 1..22
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 4.1%; Score 13; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 TGAAGATACCAAG 243
|||||
6 TGAAGATACCAAG 18

Db

RESULT 52
AR090653
LOCUS AR090653 23 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 773 from patent US 5994076.
ACCESSION AR090653
VERSION AR090653.1 GI:10017408
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Chenchik,A., Jokhadze,G. and Biblilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 773 30-NOV-1999;
FEATURES
source 1..23
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 4.1%; Score 13; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CGGCTCCTGGCGTC 74
|||||
7 CGGCTCCTGGCGTC 19

Db

RESULT 53
I22162
LOCUS I22162 23 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 21 from patent US 5527669.
ACCESSION I22162
VERSION I22162.1 GI:1602516
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Resnick,R.M. and Young,K.K.Y.
TITLE Methods, primers and probes for detection of hepatitis C and novel
JOURNAL Patent: US 5527669-A 21 18-JUN-1996;
FEATURES
source 1..23
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 4.1%; Score 13; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 CGAGTTGCGACC 152
|||||
1 CGAGTTGCGACC 13

Db

RESULT 54
AR197688
LOCUS AR197688 23 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 773 from patent US 6352829.
ACCESSION AR197688
VERSION AR197688.1 GI:20247537
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Chenchik,A., Jokhadze,G. and Biblilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 773 05-MAR-2002;
FEATURES
source 1..23
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 4.1%; Score 13; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CGGCTCCTGGCGTC 74
|||||
7 CGGCTCCTGGCGTC 19

Db

RESULT 55
AR259842
LOCUS AR259842 23 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 773 from patent US 6489455.
ACCESSION AR259842
VERSION AR259842.1 GI:27310353
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Chenchik,A., Jokhadze,G. and Biblilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 773 03-DEC-2002;
FEATURES
source 1..23
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 4.1%; Score 13; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CGGCTCCTGGCGTC 74
|||||
7 CGGCTCCTGGCGTC 19

Db

RESULT 56
I22155/c
LOCUS I22155 24 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 14 from patent US 5527669.
ACCESSION I22155
VERSION I22155.1 GI:1602509
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Resnick,R.M. and Young,K.K.Y.
TITLE Methods, primers and probes for detection of hepatitis C and novel
JOURNAL Patent: US 5527669-A 14 18-JUN-1996;

FEATURES
source
Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 4.1%; Score 13; DB 6; Length 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 140 CGAGCTTGGACC 152
DB 24 CGAGCTTGGACC 12

RESULT 57
LOCUS AX288258 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 20 from Patent WO0179548.
ACCESSION AX288258
VERSION AX288258.1 GI:17049941
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Barany, F., Zilvi, M., Gerry, N. P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
Patent: WO 0179548-A 20 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
LOCATION/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN

Query Match
Best Local Similarity 4.1%; Score 13; DB 6; Length 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 119 GAGTGAACCATCG 131
DB 8 GAGTGAACCATCG 20

RESULT 58
LOCUS AX042498 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 64 from Patent WO065088.
ACCESSION AX042498
VERSION AX042498.1 GI:11341106
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ulfendahl, P. J. and Wong, K. C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 64 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
LOCATION/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DBQ heterozygote typing primer sequence"

ORIGIN
Query Match
Best Local Similarity 4.1%; Score 13; DB 6; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 96 CGCAGCTCTCTCT 108
DB 12 CGCAGCTCTCTCT 24

RESULT 59
LOCUS AX043378 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 944 from Patent WO065088.
ACCESSION AX043378
VERSION AX043378.1 GI:11341986
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ulfendahl, P. J. and Wong, K. C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 944 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
LOCATION/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DOBI Heterozygote Primer Sequence"

ORIGIN

Query Match
Best Local Similarity 4.1%; Score 13; DB 6; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 96 CGCAGCTCTCTCT 108
DB 25 CGCAGCTCTCTCT 13

RESULT 60
LOCUS AX150396 25 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3 from Patent EP118677.
ACCESSION AX150396
VERSION AX150396.1 GI:14532944
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS
TITLE Oligonucleotides useful in identifying fungicide resistant plant
JOURNAL pathogenic fungi
Patent: EP 118677-A 3 25-JUN-2001;
Novartis AG (CH)
LOCATION/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"

ORIGIN

Query Match
Best Local Similarity 4.1%; Score 13; DB 6; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 266 AAGCTGAAGTTG 278
DB 15 AAGCTGAAGTTG 3

RESULT 61

AX202155/c
LOCUS AX202155 25 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 3 from Patent WO0153521.
ACCESSION AX202155
VERSION AX202155.1 GI:15391949
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Sierotzki, H., Gisl, U. and Wille, P.
TITLE Oligonucleotides identifying fungicide resistant fungi
JOURNAL Patent: WO 0153521-A 3 26-JUL-2001;
Syngenta Participations AG (CH)
FEATURES
Source location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"

ORIGIN
Query Match 4.1%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 AAGCTGAAGCTTG 278
|||||
15 AAGCTGAAGCTTG 3

Db

RESULT 62
AX354462/c
LOCUS AX354462 25 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 108 from Patent WO0196523.
ACCESSION AX354462
VERSION AX354462.1 GI:18619304
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Kennedy, G.C., Kang, S., Reinhard, C. and Jefferson, A.B.
TITLE Polynucleotides related to colon cancer
JOURNAL Patent: WO 0196523-A 108 20-DEC-2001;
CHIRON CORPORATION (US)
FEATURES
Source location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN
Query Match 4.1%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 AAGCGGAGTGA 125
|||||
25 AAGCGGAGTGA 13

Db

RESULT 63
AX500900
LOCUS AX500900 25 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 2207 from Patent EP1229046.
ACCESSION AX500900
VERSION AX500900.1 GI:23383193
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Homo sapiens (human)
TITLE Homo sapiens
JOURNAL Homo sapiens
FEATURES
Source location/Qualifiers
1..25
/organism="Homo sapiens"

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 2207 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
Source location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 4.1%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GGAAGGCAAGCAG 37
|||||
13 GGAAGGCAAGCAG 25

Db

RESULT 64
AX500901
LOCUS AX500901 25 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 2208 from Patent EP1229046.
ACCESSION AX500901
VERSION AX500901.1 GI:23383194
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 2208 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
Source location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 4.1%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GGAAGGCAAGCAG 37
|||||
12 GGAAGGCAAGCAG 24

Db

RESULT 65
AX500902
LOCUS AX500902 25 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 2209 from Patent EP1229046.
ACCESSION AX500902
VERSION AX500902.1 GI:23383195
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 2209 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
Source location/Qualifiers
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/organism="Homo sapiens"

ORIGIN /mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 4.1%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GGAAGGCAAGCAG 37
|||||
11 GGAAGGCAAGCAG 23

RESULT 66
AX500903 25 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 2210 from Patent EP1229046.
DEFINITION AX500903
ACCESSION AX500903.1 GI:23383196
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 2210 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN /mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 4.1%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GGAAGGCAAGCAG 37
|||||
10 GGAAGGCAAGCAG 22

RESULT 67
AX500904 25 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 2211 from Patent EP1229046.
DEFINITION AX500904
ACCESSION AX500904
VERSION AX500904.1 GI:23383197
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 2211 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 4.1%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GGAAGGCAAGCAG 37

Db 9 GGAAGGCAAGCAG 21
|||||

RESULT 68
AX500905 25 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 2212 from Patent EP1229046.
DEFINITION AX500905
ACCESSION AX500905
VERSION AX500905.1 GI:23383198
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 2212 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 4.1%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GGAAGGCAAGCAG 37
|||||
8 GGAAGGCAAGCAG 20

RESULT 69
AX500906 25 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 2213 from Patent EP1229046.
DEFINITION AX500906
ACCESSION AX500906
VERSION AX500906.1 GI:23383199
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 2213 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 4.1%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GGAAGGCAAGCAG 37
|||||
7 GGAAGGCAAGCAG 19

RESULT 70
AX500907 25 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 2214 from Patent EP1229046.
DEFINITION AX500907
ACCESSION

VERSION AX500907.1 GI:23383200
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 2214 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 4.1%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 GGAAGGCAAGCAG 37
|||||
Db 6 GGAAGGCAAGCAG 18
RESULT 71
AX500908 25 bp DNA linear PAT 27-SEP-2002
LOCUS
DEFINITION Sequence 2215 from Patent EP1229046.
ACCESSION AX500908
VERSION AX500908.1 GI:23383201
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 2215 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 4.1%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 GGAAGGCAAGCAG 37
|||||
Db 5 GGAAGGCAAGCAG 17
RESULT 72
AX500909 25 bp DNA linear PAT 27-SEP-2002
LOCUS
DEFINITION Sequence 2216 from Patent EP1229046.
ACCESSION AX500909
VERSION AX500909.1 GI:23383202
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 2216 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

JOURNAL Patent: EP 1229046-A 2216 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
source 1..25
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 GGAAGGCAAGCAG 37
|||||
Db 4 GGAAGGCAAGCAG 16
RESULT 73
AX500910 25 bp DNA linear PAT 27-SEP-2002
LOCUS
DEFINITION Sequence 2217 from Patent EP1229046.
ACCESSION AX500910
VERSION AX500910.1 GI:23383203
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 2217 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 GGAAGGCAAGCAG 37
|||||
Db 3 GGAAGGCAAGCAG 15
RESULT 74
AX500911 25 bp DNA linear PAT 27-SEP-2002
LOCUS
DEFINITION Sequence 2218 from Patent EP1229046.
ACCESSION AX500911
VERSION AX500911.1 GI:23383204
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 2218 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES location/Qualifiers
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/db_xref="taxon:9606"
ORIGIN

Query Match 4.1%; Score 13; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GGAAGGCAAGCAG 37
 |||||
 DB 2 GGAAGGCAAGCAG 14

RESULT 75

AX500912
 LOCUS AX500912 25 bp DNA linear PAT 27-SEP-2002
 DEFINITION Sequence 2219 from Patent EP1229046.
 ACCESSION AX500912
 VERSION AX500912.1 GI:23383205
 KEYWORDS

SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 1 Zhan, J.
 Human testis expressed patched like protein
 Patent: EP 1229046-A 2219 07-AUG-2002;
 Aeomica, Inc. (US)
 Location/Qualifiers

FEATURES
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 1..25
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 6e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 GGAAGGCAAGCAG 37
 |||||
 DB 1 GGAAGGCAAGCAG 13

Search completed: February 2, 2005, 20:25:58
 Job time : 1357.61 secs

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OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:06:25 ; Search time 1259.01 Seconds
(without alignments)
11170.029 Million cell updates/sec

Title: US-10-048-046-1

Perfect score: 2679
Sequence: 1 aagattcgcgcagcagcgcg.....acaaaaaaaaaaaaaaaaa 2679

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3366436

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	21	0.8	21	2	ADK01311 Rat DNA m
c 3	20	0.7	20	2	AAQ75570 Reverse t
c 4	20	0.7	20	5	AAAF30361 Human che
c 5	20	0.7	20	5	AAAF30363 Human che
c 6	20	0.7	20	5	AAAF30354 Human che
c 7	20	0.7	20	5	AAAF30359 Human che
c 8	20	0.7	21	2	AAQ75651 Reverse t
c 9	20	0.7	21	2	AAQ75653 Reverse t
c 10	20	0.7	21	2	AAQ75654 Reverse t
c 11	20	0.7	21	10	ADK01309 Rat DNA m
c 12	20	0.7	21	10	ADK01312 Rat DNA m
c 13	20	0.7	21	10	ADK01310 Rat DNA m
c 14	20	0.7	21	10	ADK01336 Rat DNA m
c 15	20	0.7	28	5	AAAF30355 Human che
c 16	20	0.7	28	5	AAAF30356 Human che
c 17	20	0.7	30	2	AAQ833940 Oligonuci
c 18	20	0.7	30	5	AAAF60462 Oligonuci
c 19	20	0.7	19	2	AAQ75549 Reverse t
c 20	19	0.7	20	2	AAQ75569 Reverse t
c 21	19	0.7	20	2	AAQ75568 Reverse t

c 22	19	0.7	20	2	AAQ75567 Reverse t	Aag75567 Reverse t
c 23	19	0.7	20	2	AAT04917 Mammalian	Aat04917 Mammalian
c 24	19	0.7	20	3	AAA13752 Stem cell	Aaa13752 Stem cell
c 25	19	0.7	20	4	AAH41331 Universal	Aah41331 Universal
c 26	19	0.7	20	4	AAAS04111 Human SCF	Aas04111 Human SCF
c 27	19	0.7	20	4	AAAF89091 Mammalian	Aaf89091 Mammalian
c 28	19	0.7	20	5	AAH23889 Human SCF	Aah23889 Human SCF
c 29	19	0.7	20	5	AAAS04212 Human SCF	Aas04212 Human SCF
c 30	19	0.7	20	5	AAAS10447 Human ste	Aas10447 Human ste
c 31	19	0.7	20	6	AAAS3464 Rat SCF 5	Aas3464 Rat SCF 5
c 32	19	0.7	20	6	ABST73848 SCF univ	Abst73848 SCF univ
c 33	19	0.7	20	10	ADBS2460 Stem cell	Adbs2460 Stem cell
c 34	19	0.7	20	10	ABZ88618 Human o1i	Abz88618 Human o1i
c 35	19	0.7	20	11	ABD24848 AT092623-	Abd24848 AT092623-
c 36	19	0.7	20	12	ADH67348 Human gltu	Adh67348 Human gltu
c 37	19	0.7	20	12	ADH67400 Human gltu	Adh67400 Human gltu
c 38	19	0.7	20	12	ADK74647 Chimeric	Adk74647 Chimeric
c 39	19	0.7	20	12	ADK74442 Chimeric	Adk74442 Chimeric
c 40	19	0.7	20	12	ADM14246 Human mPG	Adm14246 Human mPG
c 41	19	0.7	20	12	ADM14467 Human mPG	Adm14467 Human mPG
c 42	19	0.7	20	12	ADP93302 Stem cell	Adp93302 Stem cell
c 43	19	0.7	21	2	AAQ75648 Reverse t	Aaq75648 Reverse t
c 44	19	0.7	21	2	AAQ75639 Reverse t	Aaq75639 Reverse t
c 45	19	0.7	21	2	AAQ75643 Reverse t	Aaq75643 Reverse t
c 46	19	0.7	21	2	AAQ75646 Reverse t	Aaq75646 Reverse t
c 47	19	0.7	21	2	AAQ75650 Reverse t	Aaq75650 Reverse t
c 48	19	0.7	21	2	AAQ75641 Reverse t	Aaq75641 Reverse t
c 49	19	0.7	21	2	AAQ75642 Reverse t	Aaq75642 Reverse t
c 50	19	0.7	21	2	AAQ75649 Reverse t	Aaq75649 Reverse t
c 51	19	0.7	21	2	AAQ75645 Reverse t	Aaq75645 Reverse t
c 52	19	0.7	21	2	AAQ75640 Reverse t	Aaq75640 Reverse t
c 53	19	0.7	21	2	AAQ75644 Reverse t	Aaq75644 Reverse t
c 54	19	0.7	21	2	AAQ75647 Reverse t	Aaq75647 Reverse t
c 55	19	0.7	21	2	AAV35395 HIV-1 gag	Aav35395 HIV-1 gag
c 56	19	0.7	21	10	ADK01333 Rat DNA m	Adk01333 Rat DNA m
c 57	19	0.7	21	10	ADK01297 Rat DNA m	Adk01297 Rat DNA m
c 58	19	0.7	21	10	ADK01335 Rat DNA m	Adk01335 Rat DNA m
c 59	19	0.7	21	10	ADK01302 Rat DNA m	Adk01302 Rat DNA m
c 60	19	0.7	21	10	ADK01334 Rat DNA m	Adk01334 Rat DNA m
c 61	19	0.7	21	10	ADK01303 Rat DNA m	Adk01303 Rat DNA m
c 62	19	0.7	21	10	ADK01307 Rat DNA m	Adk01307 Rat DNA m
c 63	19	0.7	21	10	ADK01304 Rat DNA m	Adk01304 Rat DNA m
c 64	19	0.7	21	10	ADK01306 Rat DNA m	Adk01306 Rat DNA m
c 65	19	0.7	21	10	ADK01289 Rat DNA m	Adk01289 Rat DNA m
c 66	19	0.7	21	10	ADK01301 Rat DNA m	Adk01301 Rat DNA m
c 67	19	0.7	21	10	ADK01298 Rat DNA m	Adk01298 Rat DNA m
c 68	19	0.7	21	10	ADK01300 Rat DNA m	Adk01300 Rat DNA m
c 69	19	0.7	21	10	ADK01305 Rat DNA m	Adk01305 Rat DNA m
c 70	19	0.7	21	10	ADK01342 Rat DNA m	Adk01342 Rat DNA m
c 71	19	0.7	21	10	ADK01308 Rat DNA m	Adk01308 Rat DNA m
c 72	19	0.7	22	6	ABA93238 PolyA ada	Aba93238 PolyA ada
c 73	19	0.7	23	2	AAQ75028 LCR oligo	Aaq75028 LCR oligo
c 74	19	0.7	23	2	AAQ75029 LCR oligo	Aaq75029 LCR oligo
c 75	19	0.7	24	2	AAZ00877 PCR prime	Aaz00877 PCR prime
c 76	19	0.7	24	4	AAH43079 Nucleotid	Aah43079 Nucleotid
c 77	19	0.7	24	6	ABU78878 Nucleotid	Abu78878 Nucleotid
c 78	19	0.7	24	6	ABL55130 Human gon	AbL55130 Human gon
c 79	19	0.7	24	10	ADG16131 Compound	Adg16131 Compound
c 80	19	0.7	25	2	AAAX84258 PCR prime	Aax84258 PCR prime
c 81	19	0.7	25	6	AAAD34264 Human CYP	Aad34264 Human CYP
c 82	19	0.7	25	6	AAAD26900 Bacterial	Aad26900 Bacterial
c 83	19	0.7	25	6	ABK86170 Oligo dt	Abk86170 Oligo dt
c 84	19	0.7	26	2	AAAX07466 Human BSI	Aax07466 Human BSI
c 85	19	0.7	26	2	AAAX78723 Human pan	Aax78723 Human pan
c 86	19	0.7	26	6	AAAD26899 Bacterial	Aad26899 Bacterial
c 87	19	0.7	26	6	AAAD39650 PolypNP o	Aad39650 PolypNP o
c 88	19	0.7	27	2	AAV71936 Anchored	Aav71936 Anchored
c 89	19	0.7	27	4	AAH43080 Nucleotid	Aah43080 Nucleotid
c 90	19	0.7	27	6	ABO79879 Nucleotid	AbO79879 Nucleotid
c 91	19	0.7	27	10	ADG75074 Biosensor	Adg75074 Biosensor
c 92	19	0.7	27	12	ADG75349 RT-PCR pr	Adg75349 RT-PCR pr
c 93	19	0.7	27	12	AAAS7856 Deoxy-T22	Aas7856 Deoxy-T22
c 94	19	0.7	28	3	AAAS7856 Deoxy-T22	Aas7856 Deoxy-T22

PS Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

SO Query Match 0.8%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2659 GACCAAAAAAAAAAAAAA 2679
DB 21 GACCAAAAAAAAAAAAAA 1

RESULT 3
AAQ75570/c
ID AAQ75570 standard; DNA; 20 BP.
XX
AC AAQ75570;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
JP0630397-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX
PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily

XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

SO Query Match 0.7%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2659 GACCAAAAAAAAAAAAAA 2678
DB 20 GACCAAAAAAAAAAAAAA 1

RESULT 4
AAF30361
ID AAF30361 standard; DNA; 20 BP.
XX
AC AAF30361;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human checkpoint gene chr 5' PCR primer.

XX Checkpoint with forkhead associated domain and ring finger; Chfr; human;
KM mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;
KM ubiquitin-protein ligase; PCR primer; ss.
XX
OS Homo sapiens.
XX
WO200109150-A2.
XX
PD 08-FEB-2001.
XX
PF 14-JUN-2000; 2000MO-US016391.
XX
PR 29-JUL-1999; 99US-0146194P.
XX
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
PI Halazonetis T, Scolnick D;
XX
DR WPI; 2001-182927/18.
XX
PT Novel nucleic acid sequence of mitotic checkpoint gene encoding a
PT checkpoint with forkhead-associated domain and ring finger protein, for
PT diagnosing tumorigenic cells and in screening for anticancer drugs.

XX Example 3; Page 38; 85pp; English.

XX The present sequence is that of a 5' PCR primer, used with the 3' primer
CC given in AAF30362, to amplify a cDNA fragment corresponding to
CC nucleotides 904-1772 of the human chr sequence given in AAF30352. The
CC chr gene encodes the human mitotic checkpoint protein Chfr (see
CC AAB20219), which is required for regulation of the transition of cells
CC from prophase to metaphase during mitosis. Loss of expression of Chfr is
CC associated with a predisposition to tumorigenesis upon exposure to
CC mitotic stress. A set of primers (see AAF30353-76) was used to amplify
CC regions spanning the entire chr coding region in order to determine
CC whether the chr gene is mutated in any of the human cancer cell lines
CC SW480, DLD1, HT29, HCT116, SAOS2, U2OS, IMR5 and NGP. A mutation leading
CC to a Val-580 to Met amino acid substitution was identified in the chr
CC gene of U2OS cells. Chr polypeptides and chr nucleic acids are used in
CC methods of diagnosing tumorigenic cells and of screening for drugs which

CC can inhibit the activity of Chfr in a cancer cell, rendering it more
 CC sensitive to additional antitumour therapies
 XX
 SQ Sequence 20 BP; 10 A; 0 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 AAGAAAATGAGAGAGATGG 881
 |||||
 DB 1 AAGAAAATGAGAGAGATGG 20

RESULT 5
 AAF30363
 ID AAF30363 standard; DNA; 20 BP.

XX AAF30363;

DT 14-MAY-2001 (first entry)

DE Human checkpoint gene chr 5' PCR primer.

KW Checkpoint with forkhead associated domain and ring finger; Chfr; human;
 KM ublquitin-protein ligase; tumour; diagnosis; antitumour; drug screening;
 KW ublquitin-protein ligase; PCR primer; ss.

OS Homo sapiens.

PN WO200109150-A2.

PD 08-FEB-2001.

PF 14-JUN-2000; 2000WO-US016391.

PR 29-JUL-1999; 99US-0146194P.

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.

PI Halazonetis T, Scolnick D;

DR WPI; 2001-182927/18.

PT Novel nucleic acid sequence of mitotic checkpoint gene encoding a
 PT checkpoint with forkhead-associated domain and ring finger protein, for
 PT diagnosing tumorigenic cells and in screening for anticancer drugs.

PS Example 3; Page 38; 85pp; English.

CC The present sequence is that of a 5' PCR primer, used with the 3' primer
 CC given in AAF30364, to amplify a cDNA fragment corresponding to
 CC nucleotides 904-1902 of the human chr sequence given in AAF30352. The
 CC chr gene encodes the human mitotic checkpoint protein Chfr (see
 CC AAB20219), which is required for regulation of the transition of cells
 CC from prophase to metaphase during mitosis. Loss of expression of Chfr is
 CC associated with a predisposition to tumorigenesis upon exposure to
 CC mitotic stress. A set of primers (see AAF30353-76) was used to amplify
 CC regions spanning the entire chr coding region in order to determine
 CC whether the chr gene is mutated in any of the human cancer cell lines
 CC SW480, DLD1, HT29, HCT116, SMO2, U2OS, IMR5 and NGP. A mutation leading
 CC to a Val-580 to Met amino acid substitution was identified in the chr
 CC gene of U2OS cells. Chfr polypeptides and chr nucleic acids are used in
 CC methods of diagnosing tumorigenic cells and of screening for drugs which
 CC can inhibit the activity of Chfr in a cancer cell, rendering it more
 CC sensitive to additional antitumour therapies

SQ Sequence 20 BP; 10 A; 0 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 AAGAAAATGAGAGAGATGG 881
 |||||
 DB 1 AAGAAAATGAGAGAGATGG 20

RESULT 6
 AAF30354/C
 ID AAF30354 standard; DNA; 20 BP.

XX AAF30354;

DT 14-MAY-2001 (first entry)

DE Human checkpoint gene chr 3' PCR primer.

KW Checkpoint with forkhead associated domain and ring finger; Chfr; human;
 KM ublquitin-protein ligase; tumour; diagnosis; antitumour; drug screening;
 KW ublquitin-protein ligase; PCR primer; ss.

OS Homo sapiens.

PN WO200109150-A2.

PD 08-FEB-2001.

PF 14-JUN-2000; 2000WO-US016391.

PR 29-JUL-1999; 99US-0146194P.

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.

PI Halazonetis T, Scolnick D;

DR WPI; 2001-182927/18.

PT Novel nucleic acid sequence of mitotic checkpoint gene encoding a
 PT checkpoint with forkhead-associated domain and ring finger protein, for
 PT diagnosing tumorigenic cells and in screening for anticancer drugs.

PS Example 3; Page 38; 85pp; English.

CC The present sequence is that of a 3' PCR primer, used with the 5' primer
 CC given in AAF30353, to amplify a cDNA fragment corresponding to
 CC nucleotides 66-562 of the human chr sequence given in AAF30352. The chr
 CC gene encodes the human mitotic checkpoint protein Chfr (see AAB20219),
 CC which is required for regulation of the transition of cells from prophase
 CC to metaphase during mitosis. Loss of expression of Chfr is associated
 CC with a predisposition to tumorigenesis upon exposure to mitotic stress.
 CC A set of primers (see AAF30353-76) was used to amplify regions spanning
 CC the entire chr coding region in order to determine whether the chr gene
 CC is mutated in any of the human cancer cell lines SW480, DLD1, HT29,
 CC HCT116, SMO2, U2OS, IMR5 and NGP. A mutation leading to a Val-580 to Met
 CC amino acid substitution was identified in the chr gene of U2OS cells.
 CC Chfr polypeptides and chr nucleic acids are used in methods of
 CC diagnosing tumorigenic cells and of screening for drugs which can
 CC inhibit the activity of Chfr in a cancer cell, rendering it more
 CC sensitive to additional antitumour therapies

SQ Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 501 CAAGAAAATGTGTCATG 520
 |||||
 DB 20 CAAGAAAATGTGTCATG 1

RESULT 7
 AAF30359
 ID AAF30359 standard; DNA; 20 BP.

XX

AC AAF30359;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Human checkpoint gene chr 5' PCR primer.
 XX
 KW Checkpoint with forkhead associated domain and ring finger; Chfr; human;
 KW mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;
 KW ubiquitin-protein ligase; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200109150-A2.
 XX
 PD 08-FEB-2001.
 XX
 PF 14-JUN-2000; 2000WO-US016391.
 XX
 PR 29-JUL-1999; 99US-0146194P.
 XX
 PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 XX
 PI Halazonetis T, Scolnick D;
 XX
 DR WPI; 2001-182927/18.
 XX
 PT Novel nucleic acid sequence of mitotic checkpoint gene encoding a
 PT checkpoint with forkhead-associated domain and ring finger protein, for
 PT diagnosing tumorigenic cells and in screening for anticancer drugs.
 XX
 PS Example 3; Page 38; 85pp; English.
 XX
 CC The present sequence is that of a 5' PCR primer, used with the 3' primer
 CC given in AAF30360, to amplify a cDNA fragment corresponding to
 CC nucleotides 904-1753 of the human chr sequence given in AAF30352. The
 CC chr gene encodes the human mitotic checkpoint protein Chfr (see
 CC AAB20219), which is required for regulation of the transition of cells
 CC from prophase to metaphase during mitosis. Loss of expression of Chfr is
 CC associated with a predisposition to tumorigenesis upon exposure to
 CC mitotic stress. A set of primers (see AAF30353-76) was used to amplify
 CC regions spanning the entire chr coding region in order to determine
 CC whether the chr gene is mutated in any of the human cancer cell lines
 CC SW480, DLD1, HT29, HCT116, SAOS2, U2OS, IMR5 and NGP. A mutation leading
 CC to a Val-580 to Met amino acid substitution was identified in the chr
 CC gene of U2OS cells. Chr polypeptides and chr nucleic acids are used in
 CC methods of diagnosing tumorigenic cells and of screening for drugs which
 CC can inhibit the activity of Chfr in a cancer cell, rendering it more
 CC sensitive to additional antitumour therapies
 XX
 SQ Sequence 20 BP; 10 A; 0 C; 8 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 0.7%; Score 20; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 862 AAGAAATGAGAGAGATGC 861
 DB 1 AAGAAATGAGAGAGATGC 20
 XX
 RESULT 8
 ID AAO75651/c
 AC AAO75651; standard; DNA; 21 BP.
 XX
 AC AAO75651;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX

OS Synthetic;
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAO75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
 XX
 Query Match 0.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 2659 GACCAAAAAAAAAAAAAAAAAA 2678
 DB 20 GACCAAAAAAAAAAAAAAAAAA 1
 XX
 RESULT 9
 ID AAO75653/c
 AC AAO75653; standard; DNA; 21 BP.
 XX
 AC AAO75653;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESCO files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2659 GACCAAAAAAAAAAAAAA 2678
 DB 20 GACCAAAAAAAAAAAAAA 1

RESULT 10
 AAQ75654/C
 ID AAQ75654 standard; DNA; 21 BP.

AC AAQ75654;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.

KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 6; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESCO files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2659 GACCAAAAAAAAAAAAAA 2678
 DB 20 GACCAAAAAAAAAAAAAA 1

RESULT 11
 ADK01309/c
 ID ADK01309 standard; DNA; 21 BP.

XX
 AC ADK01309;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Rat DNA microarray capture oligonucleotide #29.

KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KM blood; nerve; germ cell; food additive; food supplement.

OS Rattus sp.

PN DE10208794-A1.

PD 04-SEP-2003.

PF 28-FEB-2002; 2002DE-01008794.

PR 28-FEB-2002; 2002DE-01008794.

PA (DEGSA) DEGUSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

DR WPI; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.

PS Example; Page 5; 8pp; German.

CC This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC additives or supplements, especially minerals, trace elements, organic
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.

Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2660 ACACAAAAAAAAAAAAA 2679
 DB 20 ACACAAAAAAAAAAAAA 1

07 2660 AAAAAAAAAAAAAAAAAA 2679
ID 20 AAAAAAAAAAAAAAAAAA 1

RESULT 13
ADK01310/C
ID ADK01310 standard; DNA, 21 BP.
AC ADK01310;
XX 06-MAY-2004 (first entry)
DT
DE Rat DNA microarray capture oligonucleotide #30.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
PM DE10208794-A1.
PN
PD 04-SEP-2003.
PE 28-FEB-2002; 2002DE-01008794.
PF 28-FEB-2002; 2002DE-01008794.
PR
PS (DEGS) DEGUSBA BIOACTIVES GMBH.
PA Boekenkamp D, Dieck HT, Hoppe H;
PI WPI; 2003-714082/68.
PP
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PR patterns and screening active agents, uses capture agent with variable
PT and constant regions.
PT
PS Example; Page 5; bpp: German.

This invention describes a novel method for sorting single-stranded nucleic acids by isolation and hybridisation of nucleic acid pools, then reading out, where the nucleic acids are selectively bound using capture agents that are (a) immobilised on the surface of a solid matrix and (b) comprise variable and non-variable regions. The capture oligonucleotides have a 5'-invariable anchor region, the complement of which is present at least once in each nucleic acid and a 3'-variable, discriminatory region that comprises all possible combinations of up to 10 nucleotides to allow binding of particular sorts of single stranded nucleic acids. The capture agents are particularly locked nucleic acids (LNA) and the anchor region comprises a sequence of 10-50, particularly 15-25, T residues. The capture oligonucleotides are biotinylated and immobilised on a surface by interaction with streptavidin. The matrix is of plastic, ceramic, glass, metal, resin, gel, crystalline material and/or membrane, having semi-conducting properties and especially in the form of a chip. Its surface is particularly a layer of (bio)molecular filaments and binding of single stranded nucleic acids to the surface is (quasi)covariant, supramolecular, physical, stimulated by an electrical field or through a molecular sieve. The method is used (i) for analysis of patterns, especially in mucosal, hair root, blood, nerve or germ cells and (ii) for determining the activity of pharmaceuticals and/or nutritional compounds, e.g. food additives or supplements, especially minerals, trace elements, organic acids (amino, carboxylic or fatty acid) or their derivatives, salts and mixtures. The method provides rapid, inexpensive and reproducible representation of differences in pools of nucleic acids from cells. It allows imaging of the complete pattern of all nucleic acid in a cell, and can detect very small differences in the nucleic acid pool. Since the method is based on comparison of nucleic acid probes, not individual genes, matrix miniaturisation is possible. ADK01261-ADK01344 represent capture probes used in the method of the invention.

Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

```
Query Match      0.7%; Score 20; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	2660	ACCAAAAAAAAAAAAAA	2679
Db	20	ACAAAAAAAAAAAAAA	1

RESULT 14	
ADK01336/c	✓
ID ADK01336 standard; DNA; 21 BP.	

AC ADK01336;

DT 06-MAY-2004 (first entry)
xx

Rat DNA microarray capture oligonucleotide #56.

KW ss: hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
KW
YY

OS Rattus sp.

PN DE10208794-A1.

PD 04-SEP-2003.

PF 28-FEB-2002; 2002DE-01008794.

PR 28-FEB-2002; 2002DE-01008794.

PA (DEGS) DEGUSSA BIOACTIVES GMBH.

PI Boekenkamp D, Dieck HT, Hoppe H;

DR WPI; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression patterns and screening active agents, uses capture agent with variable PT and constant regions.

PS Example; Page 6; Bpp; German.

This invention describes a novel method for sorting single-stranded nucleic acids by isolation and hybridisation of nucleic acid pools, then reading out, where the nucleic acids are selectively bound using capture agents that are (a) immobilised on the surface of a solid matrix and (b) comprise variable and non-variable regions. The capture oligonucleotides have a 5'-invariable anchor region, the complement of which is present at least once in each nucleic acid and a 3'-variable, discriminatory region that comprises all possible combinations of up to 10 nucleotides to allow binding of particular sorts of single stranded nucleic acids. The capture agents are particularly locked nucleic acids (LNA) and the anchor region comprises a sequence of 10-50, particularly 15-25, T residues. The capture oligonucleotides are biotinylated and immobilised on a surface by interaction with streptavidin. The matrix is of plastic, ceramic, glass, metal, resin, gel, crystalline material and/or membrane, having semi-conducting properties and especially in the form of a chip. Its surface is particularly a layer of (bio)molecular filaments and binding of single stranded nucleic acids to the surface is (quasi)covalent, supramolecular, physical, stimulated by an electrical field or through a molecular sieve. The method is used (i) for analysis of patterns, especially in mucosal, hair root, blood, nerve or germ cells and (ii) for determining the activity of pharmaceuticals and/or nutritional compounds, e.g. food additives or supplements, especially minerals, trace elements, organic acids (amino, carboxylic or fatty acid) or their derivatives, salts and mixtures. The method provides rapid, inexpensive and reproducible representation of differences in pools of nucleic acids from cells. It allows imaging of the complete pattern of all nucleic acids in a cell, and can detect very small differences in the nucleic acid pool. Since the method is based on comparison of nucleic acid pools, not individual genes, matrix miniaturisation is possible. ADRK01281-ADRK01344 represent

CC	capture probes used in the method of the invention.
XX	
SQ	Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

Query Match	0.7%	Score 20;	DB 10;	Length 21;
Best Local Similarity	100.0%	Pred. No.	2.5e+03;	
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	2660	ACAAAAAAAAAAAAAAAAAAAAA	2679
D_b	21	ACAAAAAAAAAAAAAAAAAAAAA	2

RESULT 15
AAF30355
ID AAF30355 standard; DNA; 28 BP.
vv

AC AAF30355;

DT 14-MAY-2001 (first entry)

Human checkpoint gene chr 5' PCR primer.

KM Checkpoint with forkhead associated domain and ring finger; Chfr; human;
KM mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;
KM ubiquitin-protein ligase; PCR primer; 88.

OS Homo sapiens.

PN WO200109150-A2.

PD 08-FEB-2001.

PF 14-JUN-2000; 2000WO-US016391.

PR 29-JUL-1999; 99US-0146194P.

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.

PI Halazonetis T, Scolnick D;
vv

DR WPI; 2001-182927/18.

PT Novel nucleic acid sequence of mitotic checkpoint gene encoding a
PT checkpoint with forkhead-associated domain and ring finger protein, for
PT diagnosing tumorigenic cells and in screening for anticancer drugs.

PS Example 3; Page 38; 85pp; English.

The present sequence is that of a 5' PCR primer, used with the 3' primer given in AAF30356, to amplify a cDNA fragment corresponding to nucleotides 352-1055 of the human cfr gene sequence given in AAF30352. The cfr gene encodes the human mitotic checkpoint protein Cfr (see AAB20219), which is required for regulation of the transition of cells from prophase to metaphase during mitosis. Loss of expression of Cfr is associated with a predisposition to tumorigenesis upon exposure to mitotic stress. A set of primers (see AAF30353-76) was used to amplify regions spanning the entire cfr coding region in order to determine whether the cfr gene is mutated in any of the human cancer cell lines SW480, DLD1, HT29, HCT116, SRA052, U2OS, IMR5 and NGP. A mutation leading to a Val-580 to Met amino acid substitution was identified in the cfr gene of U2OS cells. Cfr polypeptides and cfr nucleic acids are used in methods of diagnosing tumourigenic cells and of screening for drugs which can inhibit the activity of Cfr in a cancer cell, rendering it more sensitive to additional antitumour therapies

Sequence 28 BP; 12 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match	0.7%	Score 20;	DB 5;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.4e+03;		
Matches	20;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY 310 CTGGAAGATACCAGCACCAG 329

Db 9 CTGGAAGATACCAGCAGCAG 28

RESULT 16

AAf30356/c

ID AAF30356 standard; DNA; 28 BP.

AC AAF30356;

DT 14-MAY-2001 (first entry)

XX Human checkpoint gene chr3' PCR primer.

XX Checkpoint with forkhead associated domain and ring finger; Chfr; human;

XX mtosis; cell cycle; tumour; diagnosis; antitumour; drug screening;

XX Ubiquitin-protein ligase; PCR primer; ss.

XX Homo sapiens.

XX WO200109150-A2.

XX 08-FEB-2001.

XX 14-JUN-2000; 2000WO-US016391.

XX 29-JUL-1999; 99US-0146194P.

XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.

XX Halazoneis T, Scolnick D;

XX WPI: 2001-182927/18.

XX Example 3; Page 38; 85pp; English.

XX The present sequence is that of a 3' PCR primer, used with the 5' primer
 CC given in AAF30355, to amplify a cDNA fragment corresponding to
 CC nucleotides 352-1055 of the human chr sequence given in AAF30352. The
 CC chr gene encodes the human mitotic checkpoint protein Chfr (see
 CC AAB20119), which is required for regulation of the transition of cells
 CC from prophase to metaphase during mitosis. Loss of expression of Chfr is
 CC associated with a predisposition to tumorigenesis upon exposure to
 CC mitotic stress. A set of primers (see AAF30353-76) was used to amplify
 CC regions spanning the entire chr coding region in order to determine
 CC whether the chr gene is mutated in any of the human cancer cell lines
 CC SM480, DDD1, HT29, HCT116, SAOS2, U2OS, IMR5 and NGP. A mutation leading
 CC to a Val-580 to Met amino acid substitution was identified in the chr
 CC gene of U2OS cells. Chr polypeptides and chr nucleic acids are used in
 CC methods of diagnosing tumorigenic cells and of screening for drugs which
 CC can inhibit the activity of Chfr in a cancer cell, rendering it more
 CC sensitive to additional antitumour therapies

XX Sequence 28 BP; 10 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 5; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 994 CTGACATGATCATCTGCCA 1013

Db 28 CTGACATGATCATCTGCCA 9

RESULT 17
 AAQ83940
 ID AAQ83940 standard; DNA; 30 BP.
 XX
 AC AAQ83940;

XX 25-MAR-2003. (revised)
 DT 04-OCT-1995 (first entry)

XX Oligonucleotide clamp o, for producing comb-type brached polymer.

XX HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified_base 1 /*tag= a /note= "Modified with SP(O-)-(=O)-"

XX WO9501365-A1.

XX 12-JAN-1995.

XX 05-JUL-1994; 94WO-US007557.

XX 02-JUL-1993; 93US-00087386.

XX (LYNX-) LYNX THERAPEUTICS INC.

XX GYAZNOV SM;

XX WPI: 1995-060944/08.

XX Synthesis of branched polymers and novel branched polymeric structures -
 XX used as molecular probes esp. for detecting poly-nucleotide(s).

XX Example 8; Page 33; 52pp; English.

XX The sequences given in AAQ83938, AAQ83952 and AAQ83940 are used in the
 CC construction of an oligonucleotide clamp. The clamp is a comb-type
 CC branched polymer which has 3' termini and was used to bind a target
 CC sequence comprising a segment of the HIV pol and nef genes in single
 CC stranded or double stranded forms. An oligonucleotide clamp is a compound
 CC capable of forming a covalently closed macromolecule or a stable circular
 CC oligonucleotide clamps generally comprise one or more oligonucleotide
 CC moieties capable of specific binding to the target molecule and one or
 CC more pairs of binding moieties covalently linked to the oligonucleotide
 CC moieties. Upon annealing of the oligonucleotide moieties to the target
 CC polynucleotide, the binding moieties of a pair are brought into
 CC juxtaposition so that they form a stable covalent or non-covalent linkage
 CC or complex. The interaction of the binding moieties effectively clamps
 CC the specifically annealed oligonucleotide moieties to the target
 CC polynucleotide. (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 AAAAAAAAAAAAAAAAAA 2679

Db 4 AAAAAAAAAAAAAAAAAA 23

RESULT 18

AAf60462

ID AAF60462 standard; DNA; 30 BP.

AC AAF60462;

DT 27-APR-2001 (first entry)

XX Oligonucleotide clamp #22.

XX Oligonucleotide clamp; ds.

XX	Unidentified.
XX	
XX	US6180777-B1.
XX	
XX	30-JAN-2001.
XX	
XX	03-JAN-1997; 97US-00787321.
XX	
XX	12-JAN-1996; 96US-0009918P.
XX	
XX	(FARB) BAYER CORP.
XX	
XX	Horn T;
XX	
XX	WPI, 2001-201911/20.
XX	
XX	Synthesizing branched nucleic acids useful as diagnostic and molecular
XX	PT probes, involves combining first units having haloalkylamino groups and
XX	second units having thiol or phosphorothioate groups.
XX	
XX	Example 8; Col 19; 20pp; English.
XX	
XX	The present invention relates to a method for synthesizing a branched or
XX	multilinked connected macromolecular structure, comprising oligonucleotide
XX	clamps (OC). The macromolecular structure is capable of specifically
XX	binding to a target molecule, and can therefore be used as probes. At
XX	least one OC comprises a target binding sequence that binds specifically
XX	and stably with the target molecule, and at least two OCs comprise signal
XX	generation moieties capable of generating a detectable signal in the
XX	presence of the target molecule. In addition the OCs are connected to one
XX	another by thioalkylamino, or thiophosphorylalkylamino bridges. The
XX	present sequence is an OC used in the present invention
XX	
XX	Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
XX	
XX	Query Match 0.7%; Score 20; DB 5; Length 30;
XX	Best Local Similarity 100.0%; Pred.No. 2.4e+03;
XX	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	2660 AAAAAAAAAAAAAAAAAAAAAA 2679
Db	4 AAAAAAAAAAAAAAAAAAAAAA 23
RESULT 19	
AAQ75549/C	
ID	AAQ75549 standard; DNA; 19 BP.
XX	
XX	AAQ75549;
XX	
XX	04-AUG-1995 (first entry)
XX	
XX	Reverse transcription primer used in cDNA analysis technique.
XX	
XX	Analysis; gene expression; reverse transcription; primer; cDNA;
XX	aggregate; restriction enzyme; ss.
XX	
OS	Synthetic.
XX	
XX	JP06303997-A.
XX	
XX	01-NOV-1994.
XX	
XX	16-APR-1993; 93JP-00112515.
XX	
XX	16-APR-1993; 93JP-00112515.
XX	
XX	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX	
XX	WPI, 1995-018287/03.
XX	
XX	Analysis of cDNA and gene expression - by amplification of mRNA followed

```

PT by digestion with restriction enzymes.
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESeq files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match          0.7%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      2660 ACMAAAAAAAAAAAAAA 2678
       |||||
       19 ACMAAAAAAAAAAAAAAA 1

RESULT 20
AAQ75569/c
ID   AAQ75569 standard; DNA; 20 BP.
XX
AC   AAQ75569;
XX
DT   04-AUG-1995 (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KM   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.*
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;    93UP-00112515.
PR   16-APR-1993;    93UP-00112515.
XX
(PNTE ) NIPPON TELEGRAPH & TELEPHONE CORP.
DR   WPI; 1995-018287/03.
XX
AN   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESeq files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match          0.7%; Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2660 ACMAAAAAAAAAAAAAA 2678
       |||||

```

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 21
AAQ75568/C
ID AAQ75568 standard; DNA; 20 BP.
XX
AC AAQ75568;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENBSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 AAAAAAAAAAAAAAAAAA 2678
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 22
AAQ75567/C
ID AAQ75567 standard; DNA; 20 BP.
XX
AC AAQ75567;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 01-NOV-1994.
XX

XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENBSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 AAAAAAAAAAAAAAAAAA 2678
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 23
AAT04917/C
ID AAT04917 standard; cDNA; 20 BP.
XX
AC AAT04917;
XX
DT 25-MAY-2003 (revised)
XX
DR 15-MAY-1996 (first entry)
XX
DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3.
XX
KM Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
XX chromocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
XX transplant; neoplasia; myeloidsuppression; bone marrow; ss.
XX
OS Synthetic.
XX
PN EP676470-A1.
XX
PD 11-OCT-1995.
XX
PF 04-OCT-1990; 95EP-00105391.
XX
PR 16-OCT-1989; 89US-00422383.
XX
PR 11-JUN-1990; 90US-00537198.
XX
PR 24-AUG-1990; 90US-00573616.
XX
PR 28-SEP-1990; 90WO-US005548.
XX
PR 01-OCT-1990; 90US-00589701.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsabo KM, Suggs SV, Bosselman RA, Martin FH;
XX
DR WPI; 1995-346090/45.
XX
PT New stem cell factor polypeptide(s) - for stimulating the growth of
XX primitive progenitor cells, esp. for treating disorders involving blood
XX cells.
XX

PS Example 3; Fig 12C; 127bp; English.

XX AAT04915-T04922 are oligonucleotide primers and probes used for the

CC amplification and sequencing of mammalian stem cell factor (SCF). Non-

CC naturally occurring SCF and C-terminally truncated polypeptides, having

CC amino acid sequences sufficiently duplicative of naturally occurring SCF,

CC stimulate growth of primitive progenitors such as haematopoietic

CC progenitor cells, neural stem cells and primordial germ stem cells. The

CC peptides can be used in a composition for treating leucopenia, anaemia or

CC thrombocytopenia, for enhancing engraftment of bone marrow during

CC transplantation or for bone marrow recovery after chemotherapy or

CC radiation-induced bone marrow aplasia or myelosuppression. They can also

CC be used for treating neoplasia, nerve damage, infertility, intestinal

CC damage or myeloproliferative disorders. Antibodies may be raised against

CC the peptides for use in detection or neutralisation of SCF in serum. SCF

CC may be useful for the treatment of AIDS and severe combined

CC immunodeficiency (SCID) states alone or in combination with other factors

CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 5.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679

DB 19 CAAAAAAAAAAAAAAAAA 1

RESULT 24

AAH13752/c

ID AAH13752 standard; DNA; 20 BP.

AC AAA13752;

XX

DT 27-JUN-2000 (first entry)

XX

DE Stem cell factor universal oligonucleotide 220-3.

XX

KM Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;

KM primitive progenitor cell; haematopoietic disorder; synergic;

KW allogeneic; autologous bone marrow transplant; gene therapy;

KM transfection; haematopoietic stem cell; acute blood loss; neoplasia;

XX cancer; ss.

XX

OS Synthetic.

XX

EP92579-A1.

PN EP92579-A1.

XX

PD 12-APR-2000.

XX

PF 04-OCT-1990; 99EP-00122861.

XX

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 28-SEP-1990; 90WO-US005548.

PR 01-OCT-1990; 90US-00589701.

PR 04-OCT-1990; 90EP-00310899.

XX

PA (AMGE-) AMGEN INC.

XX

PI Zeebo KM, Suggs SV, Besselmann RA, Martin FH;

XX

DR WPI; 2000-259135/23.

XX

PT Production of hematopoietic cells suitable for administration to a

PT subject using progenitor cells and expanding the cells using stem cell

PT factor.

XX

PS Example 3; Fig 12C; 123bp; English.

XX

CC A method has been developed of making haematopoietic cells suitable for

CC administration to a subject. The method comprises: (a) obtaining

CC haematopoietic progenitor cells from a donor; and (b) expanding the cells

CC by adding to the cells a haematopoietically effective dose of a

CC polypeptide product having at least part of the primary structural

CC configuration and one or more of the biological properties of naturally

CC occurring stem cell factor (SCF). The method is useful for stimulating

CC primitive progenitor cells including early haematopoietic progenitor

CC cells which are capable of maturing to erythroid, megakaryocyte,

CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute

CC increases in haematopoietic cells of both myeloid and lymphoid lineages

CC SCF is useful for treating haematopoietic disorders. The method is useful

CC for expanding early haematopoietic progenitors in synergic, allogeneic

CC or autologous bone marrow transplant. SCF is useful for enhancing the

CC efficiency of gene therapy based on transfecting haematopoietic stem

CC cells. SCF is also useful for combating the myelosuppressive effects of

CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery

CC after acute blood loss and as a boost to the immune system for fighting

CC neoplasia (cancer). The present sequence represents a universal

CC oligonucleotide which is used in an example from the present invention

XX

SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 5.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679

DB 19 CAAAAAAAAAAAAAAAAA 1

RESULT 25

AAH1331/c

ID AAH1331 standard; DNA; 20 BP.

AC AAH1331;

XX

DT 21-AUG-2001 (first entry)

XX

DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID No.32.

XX

KM Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;

KW gene therapy; PCR primer; mutagenesis; probe; ss.

XX

OS Synthetic.

XX

US6207454-B1.

PN US6207454-B1.

XX

PD 27-MAR-2001.

XX

PF 31-DEC-1998; 98US-00224681.

XX

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 25-NOV-1992; 92US-00982255.

PR 21-DEC-1993; 93US-00172329.

PR 24-MAY-1995; 95US-00449653.

PR 12-JAN-1998; 98US-00005893.

XX

PA (AMGE-) AMGEN INC.

XX

PI Zeebo KM, Besselman RA, Suggs SV, Martin FH;

XX

DR WPI; 2001-366062/38.

XX

PT Enhancing efficiency of transfer of polynucleotide into a target

PT mammalian cell in vitro, involves exposing cell that expresses a stem

PT cell factor receptor to stem cell factor, and introducing polynucleotide

PT into cell in vitro.

XX

PS Example 3; Fig 12C; 210bp; English.
 XX
 CC The present invention describes a method for enhancing (E) the efficiency
 CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in
 CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
 CC receptor to a biologically active SCF, its analogue or fragment, which
 CC induces cell proliferation, and introducing (I) to (II) in vitro.
 CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.
 CC The method is useful for enhancing the efficiency of the transfer of a
 CC polynucleotide into a target mammalian cell in vitro. The method is
 CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAH98351 to
 CC AAH98390 represent sequences used in the exemplification of the present
 CC invention.
 XX
 SO Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 0.7%; Score 19; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2661 CAAAAAAAAAAAAAAAAA 2679
 DB 19 CAAAAAAAAAAAAAAAAA 1
 RESULT 26
 AAS04111/C
 ID AAS04111 standard; DNA; 20 BP.
 XX
 AC AAS04111;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
 XX
 KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 KW PCR primer; 88.
 XX
 OS Homo sapiens.
 XX
 PN US6207417-B1.
 XX
 PD 27-MAR-2001.
 XX
 PF 07-JUN-1995; 95US-00482918.
 XX
 PR 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 21-DEC-1993; 93US-00172329.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN P H.
 XX
 PI Zeebo KM, Bosseelman RA, Suggs SV, Martin FH;
 XX
 DR WPI; 2001-298941/31.
 XX
 PT Novel nucleic acids encoding stem cell factor useful for treating
 PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
 PT disease, Kala azar, anemia and septicemia.
 XX
 PS Example 3; Fig 12C; 209bp; English.
 XX
 CC The present sequence for universal PCR primer 220-3 is 1 of 8 universal
 CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the

CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
 CC including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in
 CC gene therapy. It is useful for treating disorders involving blood cells
 CC such as myelofibrosis, metastatic carcinoma, acute leukemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, fulminating septicemia, malaria, vitamin B12
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
 CC disorders such as piebaldism and vitiligo.
 XX
 SO Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 0.7%; Score 19; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2661 CAAAAAAAAAAAAAAAAA 2679
 DB 19 CAAAAAAAAAAAAAAAAA 1
 RESULT 27
 AAF89091/C
 ID AAF89091 standard; DNA; 20 BP.
 XX
 AC AAF89091;
 XX
 DT 13-JUL-2001 (first entry)
 XX
 DE Mammalian stem cell factor PCR primer SEQ ID NO: 32.
 XX
 KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
 KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
 KW neurological damage; intestinal damage; interillity; AIDS; SCID;
 KW severe combined immunodeficiency; PCR primer; 88.
 XX
 OS Mammalia.
 XX
 PN US6207802-B1.
 XX
 PD 27-MAR-2001.
 XX
 PF 09-NOV-1994; 94US-00336728.
 XX
 PR 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 25-NOV-1992; 92US-00982255.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Zeebo KM, Bosseelman RA, Suggs SV, Martin FH;
 XX
 DR WPI; 2001-353108/37.
 XX
 PT Novel isolated non-human mammalian stem cell factor polypeptide
 PT stimulating growth of early hematopoietic progenitor cells, useful for
 PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
 PT sarcoidosis.
 XX
 PS Example 3; Fig 12C; 209bp; English.
 XX
 CC The present invention provides the protein and coding sequences of
 CC mammalian stem cell factors (SCFs). These are capable of stimulating the
 CC growth of early haematopoietic progenitor cells, neural stem cells and
 CC plurimordial germ stem cells. The sequences are useful in the treatment of
 CC leukaemia, haematopoietic disorders, aplastic anaemia, paroxysmal
 CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
 CC and intestinal damage, interillity, AIDS and severe combined

CC Immunodeficiency (SCID). The present sequence is primer used to amplify
 CC an SCF in the exemplification of the invention
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 0.7%; Score 19; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DY 2661 CAAAAAAAAAAAAAAAAA 2679
 Db 19 CAAAAAAAAAAAAAAAAA 1
 RESULT 28
 AAH23889/c
 ID AAH23889 standard; DNA; 20 BP.
 AC AAH23889;
 XX
 XX 07-AUG-2001 (first entry)
 DT
 DE Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
 XX
 XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX US6204363-B1.
 PN 20-MAR-2001.
 PD 25-NOV-1992; 92US-00982255.
 XX
 XX 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 10-APR-1991; 91US-00684535.
 XX
 XX (AMGE-) AMGEN INC.
 PA Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI WPI; 2001-256683/26.
 DR
 XX
 PT New stem cell factor polypeptides and their analogs which stimulate
 PT growth of early hematopoietic progenitors, useful for treating aplastic
 PT anemia, carcinoma, multiple myeloma, vitiligo, Kala azar, Hodgkin's
 PT disease.
 PT
 XX
 XX Example 3; Fig 12C; 166bp; English.
 PS
 PS The present sequence for universal PCR primer 220-3 is 1 of 8 universal
 CC oligonucleotides (AAH23889-AAH23895) used in the isolation of the human
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the
 CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
 CC including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides
 CC (AAH2859-AAH2867) used in the isolation of human and rat SCF sequences.
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in
 CC gene therapy. It is useful for treating disorders involving blood cells
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, fulminating septicemia, malaria, vitamin B12
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
 CC disorders such as piebaldism and vitiligo
 CC
 CC hypopigmentation disorders such as piebaldism and vitiligo

SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 0.7%; Score 19; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DY 2661 CAAAAAAAAAAAAAAAAA 2679
 Db 19 CAAAAAAAAAAAAAAAAA 1
 RESULT 29
 AAS04212/c
 ID AAS04212 standard; DNA; 20 BP.
 AC AAS04212;
 XX
 XX 29-AUG-2001 (first entry)
 DT
 DE Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
 XX
 XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX US6218148-B1.
 PN 17-APR-2001.
 PD 21-DEC-1993; 93US-00172329.
 XX
 XX 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 25-NOV-1992; 92US-00982255.
 XX
 XX (AMGE-) AMGEN INC.
 PA Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI WPI; 2001-281051/29.
 DR
 XX
 PT Isolated DNA sequence, encoding polypeptide product useful for
 PT stimulating growth of early hematopoietic progenitor cells.
 PT
 XX
 XX Example 3; Fig 12C; 167bp; English.
 PS
 PS The present sequence for universal PCR primer 220-3 is 1 of 8 universal
 CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
 CC and the polynucleotides encoding them. SCF stimulate primitive progenitor
 CC cells including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
 CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in
 CC gene therapy. It is useful for treating disorders involving blood cells
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, fulminating septicemia, malaria, vitamin B12
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
 CC disorders such as piebaldism and vitiligo
 CC
 CC Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 SQ
 Query Match 0.7%; Score 19; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2661 CAAAAAAAAAAAAAAAAA 2679
 Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 30
 AAS10447/c
 ID AAS10447 standard; DNA; 20 BP.
 XX AAS10447;
 AC AAS10447;
 XX 24-OCT-2001 (first entry)
 DT 24-OCT-2001 (first entry)
 DE Human stem cell factor (SCF) cDNA universal PCR primer 220-3.
 XX Human; stem cell factor; SCF; haematopoietic progenitor cell;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 PN US6248319-B1.
 XX US6248319-B1.
 PD 19-JUN-2001.
 XX 19-JUN-2001.
 XX 24-MAY-1995; 95US-00449653.
 XX 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 10-APR-1991; 91US-00684535.
 PR 25-NOV-1992; 92US-00982255.
 PR 21-DEC-1993; 93US-00172329.
 XX (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI WPI: 2001-407312/43.
 DR WPI: 2001-407312/43.
 XX Increasing the number of early hematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell factor.
 XX Example 3; Fig 12C; 210pp; English.

XX The present sequence for universal PCR primer 220-3 is 1 of 19 PCR
 CC primers (AAS10435-AAS10453) used to amplify various portions of the human
 CC SCF cDNA sequence. The sequence is described in an invention relating to
 CC novel stem cell factors, the polynucleotides encoding them and methods
 CC for producing the stem cell factors. The methods involve increasing the
 CC number of early haematopoietic progenitor cells in human peripheral blood
 CC by administering a haematopoietically effective human stem cell factor
 CC polypeptide. The methods are useful for the treatment of blood disorders,
 CC including myelofibrosis, myelocleorosis, osteopetrosis, metastatic
 CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
 CC lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
 CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation
 CC disorders i.e. piebaldism and viral induced disorders, including AIDS
 CC XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2661 CAAAAAAAAAAAAAAAAA 2679
 |||||

Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 31
 AAD35464/c
 ID AAD35464 standard; DNA; 20 BP.
 XX AAD35464;
 AC AAD35464;
 XX 25-JUN-2002 (first entry)
 DT 25-JUN-2002 (first entry)
 DE Rat SCF 5' cDNA amplifying PCR primer, 220-3.
 XX Rat SCF 5' cDNA amplifying PCR primer, 220-3.
 KW Rat; stem cell factor; SCF protein; leucopenia; thrombocytopenia;
 KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
 KW infertility; neoplasia; myelofibrosis; myelocleorosis; osteopetrosis;
 KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
 KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
 KW Letterer-Siwe disease; refractory erythroidlastic anaemia; Kala azar;
 KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
 KW disseminated fungus disease; Fulminating septicemia; piebaldism; AIDS;
 KW acquired immune deficiency syndrome; malaria; military tuberculosis;
 KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
 KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
 KW primer; ss.
 XX Rattus sp.
 OS Rattus sp.
 PN US2002018763-A1.
 XX 14-FEB-2002.
 PD 12-JAN-1998; 98US-00005243.
 XX 24-MAY-1995; 95US-00449653.
 XX (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI WPI: 2002-350789/38.
 DR WPI: 2002-350789/38.
 XX Novel non-naturally-occurring stem cell factor polypeptide, useful for
 PT treating leucopenia, thrombocytopenia, anemia and for enhancing
 PT engraftment of bone marrow during transplantation in a mammal.
 XX Example 3; Fig 12C; 217pp; English.

XX The present invention relates to novel non-naturally-occurring stem cell
 CC factor (SCF) polypeptides having an amino acid sequence sufficiently
 CC duplicative of that of naturally-occurring SCF to allow possession of
 CC haematopoietic biological activity of naturally occurring SCF. Sequences
 CC of the invention are useful for treating leucopenia, thrombocytopenia,
 CC anemia and for enhancing bone marrow recovery in treatment of radiation,
 CC or chemotherapy induced bone marrow aplasia or myelosuppression. They
 CC are also useful for treating acquired immune deficiency in a human, nerve
 CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
 CC damage in a mammal. SCF sequences are useful for preparing biologically
 CC active polymer polypeptide adducts, for enhancing transfection of early
 CC haematopoietic progenitor cells with a gene, and transfer of a gene into
 CC a mammal. They are useful for treating myelofibrosis, myelocleorosis,
 CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
 CC Letterer-Siwe disease, refractory erythroidlastic anaemia, Di Guglielmo
 CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
 CC splenic pancytopenia, disseminated fungus disease, malaria, military
 CC tuberculosis, Fulminating septicemia, pyridoxine deficiency, vitamin B12
 CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
 CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)

CC and vitiligo. The present sequence is a PCR primer which is used for
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC exemplification of the invention
XX

Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679

Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 32

AB573848/c
ID AB573848 standard; DNA; 20 BP.

XX AB573848;

XX 05-DEC-2002 (first entry)

XX SCF universal oligonucleotide 220-3.

XX Stem cell factor; SCF; blood-forming system; blood cell disorder;
XX haematopoietic system; metastatic carcinoma; acute leukaemia;
XX multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
XX refractory erythroblastic anaemia; myelary tuberculosis; cytostatic;
XX disseminated fungus disease; haematopoietic; tuberculosis;
XX antianaemic; antifungal; antimalarial; dermatological; ss.

OS Synthetic.

XX EP1241258-A2.

XX 18-SEP-2002.

XX 04-OCT-1990; 2002EP-00008587.

XX 16-OCT-1989; 89US-00422383.
XX 11-JUN-1990; 90US-00537198.
XX 24-AUG-1990; 90US-00573616.
XX 28-SEP-1990; 90MO-US005548.
XX 01-OCT-1990; 90US-00589701.
XX 04-OCT-1990; 90EP-00310899.
XX 04-OCT-1990; 95EP-00105391.

XX (AMGE-) AMGEN INC.

XX Zsebo KM, Suggs SV, Bosselman RA, Martin FH;

XX WPI; 2002-684093/74.

XX Production of a human stem cell factor (SCF) polypeptide for treating
XX disorders involving blood cells, such as leukemia, comprises culturing
XX mammalian cells comprising non-human SCF promoter DNA linked to DNA
XX encoding the human SCF.

XX Example 3; Fig 12C; 120pp; English.

XX The present invention relates to novel stem cell factors (SCFs),
XX polynucleotide sequences encoding the SCFs, and methods of producing
XX them. SCFs are involved in the blood-forming (haematopoietic) system in
XX mammals, particularly humans. The method of the invention is useful for
XX the production of human SCF. The stem cell factors are useful to treat
XX disorders involving blood cells e.g. metastatic carcinoma, acute
XX leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
XX erythroblastic anaemia, myelary tuberculosis, disseminated fungus
XX disease, malaria, and vitiligo. The present sequence representing a
XX universal oligonucleotide for SCF DNA is used in the examples of the
XX present invention

Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679

Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 33

AD552460/c
ID AD552460 standard; DNA; 20 BP.

XX AD552460;

XX 29-JUN-2004 (first entry)

XX Stem cell factor (SCF) related DNA #31.

XX Stem cell factor; SCF; haematopoietic activity; infertility;
XX intestinal damage; myeloproliferative disorder; leucopenia;
XX thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
XX neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
XX myelary tuberculosis; haematopoietic progenitor cell; ss.

OS Synthetic.

XX US2002031491-A1.

XX 14-MAR-2002.

XX 31-DEC-1998; 98US-00224683.

XX 16-OCT-1989; 89US-00422383.
XX 11-JUN-1990; 90US-00537198.
XX 24-AUG-1990; 90US-00573616.
XX 01-OCT-1990; 90US-00589701.
XX 10-APR-1991; 91US-00684535.
XX 25-NOV-1992; 92US-00982255.
XX 21-DEC-1993; 93US-00172329.
XX 24-MAY-1995; 95US-00449653.
XX 12-JAN-1998; 98US-00005893.

XX (ZSEB/) ZSEBO K M.
XX (BOSS/) BOSSSELMAN R A.
XX (SUGS/) SUGGS S V.
XX (MART/) MARTIN F H.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2003-851459/79.

XX New non-natural stem cell factor, useful for treating e.g. leucopenia or
XX immune deficiency, also related nucleic acid and antibodies.
XX Disclosure; SEQ ID NO 32; 217pp; English.

XX The invention relates to stem cell factor (SCF) polypeptides with
XX haematopoietic activity and the polynucleotides encoding them. The
XX polypeptides are used for treating infertility, intestinal damage,
XX myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,
XX for improving engraftment of bone marrow transplants, for enhancing bone
XX marrow recovery after radiotherapy or chemotherapy and in treatment of
XX immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
XX carcinoma, leukaemia and myelary tuberculosis. The SCF polypeptides are
XX also used to expand haematopoietic progenitor cells for transplantation
XX and to prepare such cells for transfection with a gene. The SCF
XX polynucleotides can be used for recombinant expression of the
XX polypeptides and also as probes for mapping of the SCF gene, for
XX identifying SCF-related diseases and as a marker for neighbouring genes.
XX Antibodies raised against the polypeptides are useful in diagnosis and to

CC remove SCF from blood. This sequence represents SCF related DNA of the invention.

SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

DY 2661 CAAAAAAAAAAAAAAAAAAAAA 2679
||| ||| ||| ||| ||| ||| ||| |||
Db 19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 34
ID ABZ88618
XX ABZ88618 standard, DNA; 20 BP.
AC ABZ88618,
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.

KM Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypocensive; immunosuppressive; cytostatic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.

XS Homo sapiens.
OS
PN WO200285308-A2.
PD
PP 31-OCT-2002.
PX
PY 23-APR-2002; 2002WO-US013135.
PR
PS 24-APR-2001; 2001US-0286137P.
PA (EPIC-) EPIGENESIS PHARM INC.
PI Nyce JW, Li Y, Sandrasegara A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S,
XX
DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiqunone.

PS Disclosure: SEQ ID NO 3860; 872bp; English.

XX The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypocensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed document.

CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC the oligonucleotides in the target RNA serves to prevent the breakdown of
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX

SQ Sequence 20 BP, 1 A, 1 C, 0 G, 0 T, 0 U, 0 Other;

Query Match 0.7%; Score 19; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 1 CAAAAAAAAAAAAAAAAA 19

RESULT 36
ADH67348/C
ID ADH67348 standard; DNA; 20 BP.

AC ADH67348;

DT 25-MAR-2004 (first entry)

DE Human glucocorticoid receptor-specific antisense oligonucleotide #4182.

KW antisense oligonucleotide; glucocorticoid receptor; infection;

KW inflammation; tumour formation; diabetes; obesity;

KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;

KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.

OS Homo sapiens.

XX

XX WO2003099215-A2.

XX PD 04-DEC-2003.

XX PF 20-MAY-2003; 2003WO-US016084.

XX PR 20-MAY-2002; 2002US-0381857P.

XX PA (PHAA) PHARMACIA CORP.

XX PI Crosby SD, Nalseth AE;

XX DR WPI; 2004-035034/03.

XX PT New antisense compound targeted to a nucleic acid molecule encoding

XX PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,

XX PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.

XX PS Claim 4; SEQ ID NO 4182; 985pp; English.

XX The invention comprises an antisense oligonucleotides that are targeted
XX to nucleic acids encoding a mammalian glucocorticoid receptor. The
XX antisense oligonucleotides of the invention are useful for preventing or
XX delaying infection, inflammation or tumour formation. The antisense
XX oligonucleotides are also useful for treating diabetes, obesity,
XX cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
XX present DNA sequence represents an antisense oligonucleotide that targets
XX the human glucocorticoid receptor gene. NOTE: The present sequence
XX contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.

SQ Sequence 20 BP, 0 A, 1 C, 1 G, 18 T, 0 U, 0 Other;

Query Match 0.7%; Score 19; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 20 CAAAAAAAAAAAAAAAAA 2

RESULT 37
ADH67400/C
ID ADH67400 standard; DNA; 20 BP.

AC ADH67400;

DT 25-MAR-2004 (first entry)

DE Human glucocorticoid receptor-specific antisense oligonucleotide #4234.

KW antisense oligonucleotide; glucocorticoid receptor; infection;

KW inflammation; tumour formation; diabetes; obesity;

KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;

KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.

OS Homo sapiens.

XX

XX WO2003099215-A2.

XX PD 04-DEC-2003.

XX PF 20-MAY-2003; 2003WO-US016084.

XX PR 20-MAY-2002; 2002US-0381857P.

XX PA (PHAA) PHARMACIA CORP.

XX PI Crosby SD, Nalseth AE;

XX DR WPI; 2004-035034/03.

XX PT New antisense compound targeted to a nucleic acid molecule encoding

XX PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,

XX PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.

XX PS Claim 4; SEQ ID NO 4234; 985pp; English.

XX The invention comprises an antisense oligonucleotides that are targeted
XX to nucleic acids encoding a mammalian glucocorticoid receptor. The
XX antisense oligonucleotides of the invention are useful for preventing or
XX delaying infection, inflammation or tumour formation. The antisense
XX oligonucleotides are also useful for treating diabetes, obesity,
XX cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
XX present DNA sequence represents an antisense oligonucleotide that targets
XX the human glucocorticoid receptor gene. NOTE: The present sequence
XX contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.

SQ Sequence 20 BP, 1 A, 0 C, 1 G, 18 T, 0 U, 0 Other;

Query Match 0.7%; Score 19; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 19 CAAAAAAAAAAAAAAAAA 1

RESULT 38
ADK74647/C
ID ADK74647 standard; DNA; 20 BP.

XX

AC ADK74647;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1981.
 XX
 XX Nav1.3; Analgesic; Noctropic; Neuroprotective; post-herpetic neuralgia;
 KW diabetic neuropathy; arthritic pain; migraine headache;
 KW infantile epilepsy; ataxia; ss.
 XX
 OS Synthetic.
 XX
 PN WO2004016754-A2.
 XX
 PD 26-FEB-2004.
 XX
 DR 14-AUG-2003; 2003WO-US025465.
 XX
 PR 14-AUG-2002; 2002US-0403416P.
 XX
 PA (PHAA) PHARMACIA CORP.
 XX
 PI Roberds SL;
 XX
 PS WPI; 2004-203785/19.
 XX
 PT New antisense compound targeted to a nucleic acid molecule encoding
 PT Nav1.3, useful for treating a disease or condition associated
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
 PT disorder, or ataxia.
 XX
 PS Claim 4; SEQ ID NO 1981; 417pp; English.
 XX
 CC The present invention relates to an antisense compound targeted to a
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The
 CC compound and composition are useful for treating a disease or condition
 CC associated with Nav1.3, e.g. pain including but not limited to
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate
 CC headache; seizure disorder such as childhood seizure disorder, including
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
 CC sequence represents a chimeric phosphorothioate oligonucleotide with
 CC 2'WOE wings and a deoxy gap. Used during the antisense inhibition of
 CC human Nav1.3 expression, the oligonucleotides are designed to target
 CC different regions of the human Nav1.3 RNA.
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
 XX
 Query Match 0.7%; Score 19; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2661 CAAAAAAAAAAAAAAAAA 2679
 DB 20 CAAAAAAAAAAAAAAAAA 2
 XX
 RESULT 39
 ADK74442/c
 ID ADK74442 standard; DNA; 20 BP.
 XX
 AC ADK74442;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1776.
 XX
 KW Nav1.3; Analgesic; Noctropic; Neuroprotective; post-herpetic neuralgia;
 KW diabetic neuropathy; arthritic pain; migraine headache;
 KW infantile epilepsy; ataxia; ss.
 XX

OS Synthetic.
 XX
 PN WO2004016754-A2.
 XX
 PD 26-FEB-2004.
 XX
 DR 14-AUG-2003; 2003WO-US025465.
 XX
 PR 14-AUG-2002; 2002US-0403416P.
 XX
 PA (PHAA) PHARMACIA CORP.
 XX
 PI Roberds SL;
 XX
 PS WPI; 2004-203785/19.
 XX
 PT New antisense compound targeted to a nucleic acid molecule encoding
 PT Nav1.3, useful for treating a disease or condition associated
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
 PT disorder, or ataxia.
 XX
 PS Claim 4; SEQ ID NO 1776; 417pp; English.
 XX
 CC The present invention relates to an antisense compound targeted to a
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The
 CC compound and composition are useful for treating a disease or condition
 CC associated with Nav1.3, e.g. pain including but not limited to
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate
 CC headache; seizure disorder such as childhood seizure disorder, including
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
 CC sequence represents a chimeric phosphorothioate oligonucleotide with
 CC 2'WOE wings and a deoxy gap. Used during the antisense inhibition of
 CC human Nav1.3 expression, the oligonucleotides are designed to target
 CC different regions of the human Nav1.3 RNA.
 XX
 SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
 XX
 Query Match 0.7%; Score 19; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2661 CAAAAAAAAAAAAAAAAA 2679
 DB 19 CAAAAAAAAAAAAAAAAA 1
 XX
 RESULT 40
 ADM14246/c
 ID ADM14246 standard; DNA; 20 BP.
 XX
 AC ADM14246;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human mPGBS-1 chimeric antisense oligonucleotide SEQ ID NO:433.
 XX
 KW chimeric; antisense oligonucleotide; phosphorothioate; human;
 KW microsome1 prostaglandin H2 synthase; mPGBS-1; mPGBS-1 inhibitor;
 KW microsome1 prostaglandin H2 synthase inhibitor; cytosolic; antidiabetic;
 KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
 KW neuroprotective; noctropic; antiarthritic; vasotropic; ophthalmological;
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
 KW reperfusion injury; opthalmic disorder; immunological disorder;
 KW cardiovascular disorder; neurological disorder; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers

```
FT modified_base 1. .20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1. .5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16. .20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 433; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid encoding
XX and inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cyclostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 19; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 5.9e+03;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2661 CAAAAAAAAAAAAAAAAA 2679
XX Db 20 CAAAAAAAAAAAAAAAAA 2
XX
XX RESULT 41
XX ADM14467/c
XX ID ADM14467 standard; DNA; 20 BP.
XX
XX ADM14467;
XX
XX 01-JUL-2004 (first entry)
XX
```

```
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:654.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
XX immunomodulatory; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1. .20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX modified_base 1. .5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX modified_base 16. .20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid encoding
XX and inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cyclostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 19; DB 12; Length 20;
XX
```

Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
 Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 42
 ADP9302/c
 ID ADP9302 standard; DNA; 20 BP.

AC ADP9302;
 DT 23-SEP-2004 (first entry)
 DE Stem cell factor, SCF, universal PCR primer #2.

XX SCF; stem cell factor; gene therapy; haematopoietic progenitor cell;
 KM aplastic anaemia; paroxysmal nocturnal haemoglobinuria; myelofibrosis;
 KM myelodysplasia; osteoporosis; metastatic carcinoma; acute leukaemia;
 KM multiple myeloma; Hodgkin's disease; lymphoma; Gaucher's disease;
 KM Niemann-Pick disease; Letterer-Siwe disease;
 KM refractory erythroidlastic anaemia; Di Guglielmo syndrome;
 KM congestive splenomegaly; Kala awar; sarcoidosis;
 KM primary splenic pancytopenia; miliary tuberculosis;
 KM disseminated fungus disease; fulminating septicemia; malaria;
 KM vitamin B12 deficiency; folate acid deficiency; pyridoxine deficiency;
 KM Diamond Blackfan anaemia; hypopigmentation disorder; piebaldism;
 KM vitiligo; neurological damage; infertility; intestinal damage;
 KM irradiation; chemotherapy; AIDS; haematopoietic recovery;
 KM acute blood loss; neoplasm; cancer; ss; PCR; primer.

XX Mammalia.
 OS
 XX US6759215-B1.
 PN
 XX 06-JUL-2004.
 PD
 XX 07-AUG-2000; 2000US-00635251.
 PF
 XX 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 10-APR-1991; 91US-00684535.
 PR 25-NOV-1992; 92US-00982255.
 PR 21-DEC-1993; 93US-00172329.
 PR 24-MAY-1995; 95US-00449182.
 PA (AMGE-) AMGEN INC.
 XX
 XX Zeebo KM, Bosseiman RA, Suggs SV, Martin FH;
 PI WPI; 2004-497128/47.
 DR
 XX Preparing a human stem cell factor (SCF) polypeptide, useful for treating
 PT hematopoietic disorders, e.g., aplastic anemia, comprises growing host
 PT cells transformed or transfected with DNA encoding a human SCF.

XX Example 3; SEQ ID NO 32; 210pp; English.

XX The invention relates to preparing a (vertebrate) human stem cell factor
 CC (SCF) polypeptide comprising growing host cells transformed or
 CC transfected with DNA encoding a human SCF that stimulates growth of
 CC haematopoietic progenitor cells under nutrient conditions, the DNA being
 CC operatively linked to an expression control sequence, and isolating the
 CC polypeptide produced. Also included is a recombinant host cell
 CC transformed or transfected with an expression construct comprising a
 CC vertebrate SCF polypeptide-encoding DNA operatively linked to a
 CC heterologous expression regulatory sequence, permitting the expression of
 CC the vertebrate SCF polypeptide in the host cell. Disclosed as new are rat
 CC and human nucleic acids encoding SCF, SCF proteins from a number of other

CC mammals and recombinantly expressed SCF protein fragments. The DNA
 CC sequences are useful for effecting the large scale synthesis of SCF by a
 CC variety of recombinant techniques or for generating new and useful viral
 CC and circular plasmid DNA vectors, new and useful transformed and
 CC transfected prokaryotic and eukaryotic host cells, and new and useful
 CC methods for cultured growth of such host cells capable of expression of
 CC SCF and its related products. The DNA sequences are also useful as
 CC labelled probes in isolating human genomic DNA encoding SCF, in methods
 CC of protein synthesis, in genetic therapy in humans and other mammals, and
 CC in developing transgenic mammalian species which may serve as eukaryotic
 CC hosts for production of SCF and SCF products in quantity. The SCF is
 CC useful for treating haematopoietic disorders, e.g., aplastic anaemia,
 CC paroxysmal nocturnal haemoglobinuria, myelofibrosis, myelodysplasia,
 CC osteoporosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
 CC Letterer-Siwe disease, refractory erythroidlastic anaemia, Di Guglielmo
 CC syndrome, congestive splenomegaly, Kala awar, sarcoidosis, primary
 CC splenic pancytopenia, miliary tuberculosis, disseminated fungus disease,
 CC fulminating septicemia, malaria, vitamin B12 and folate acid deficiency,
 CC pyridoxine deficiency, Diamond Blackfan anaemia, and hypopigmentation
 CC disorders such as piebaldism and vitiligo. The SCF are also useful for
 CC treating neurological damage, infertility states, intestinal damage
 CC resulting from irradiation or chemotherapy, and AIDS. SCF is also useful
 CC for enhancing haematopoietic recovery after acute blood loss and as a
 CC boost to the immune system for fighting neoplasia (cancer). The present
 CC sequence is a universal SCF PCR primer used in the isolation of SCF DNA.

XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
 Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 43
 AAQ75648/c
 ID AAQ75648 standard; DNA; 21 BP.

XX AAQ75648;
 AC
 XX 04-AUG-1995 (first entry)
 DT
 XX Reverse transcription primer used in cDNA analysis technique.
 DE
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 KM
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX 16-APR-1993; 93JP-00112515.
 PF
 XX 16-APR-1993; 93JP-00112515.
 PR
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA WPI; 1995-018287/03.
 DR
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.
 PT
 XX Disclosure; Page 6; 11pp; Japanese.
 PS
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENBSEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 ACACAAAAAAAAAAAAAAAA 2678
DB 19 ACACAAAAAAAAAAAAAAAA 1
RESULT 44
AAQ75639/C
ID AAQ75639 standard; DNA; 21 BP.
XX
AC AAQ75639;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 ACACAAAAAAAAAAAAAAAA 2678
DB 19 ACACAAAAAAAAAAAAAAAA 1
RESULT 45
AAQ75643/C
ID AAQ75643 standard; DNA; 21 BP.
XX

AC AAQ75643;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 ACACAAAAAAAAAAAAAAAA 2678
DB 19 ACACAAAAAAAAAAAAAAAA 1
RESULT 46
AAQ75646/C
ID AAQ75646 standard; DNA; 21 BP.
XX
AC AAQ75646;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX

DR WPI; 1995-018287/03.
XX
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
PS Disclosure; Page 6; 11pp; Japanese.
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENSEQ files AAQ75647-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2660 AAAAAAAAAAAAAAAAAA 2678
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 47
AAQ75650/C
ID AAQ75650 standard; DNA; 21 BP.
XX
XX
AC AAQ75650;
XX
XX 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
PS Disclosure; Page 6; 11pp; Japanese.
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENSEQ files AAQ75647-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2660 AAAAAAAAAAAAAAAAAA 2678
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 48
AAQ75641/C
ID AAQ75641 standard; DNA; 21 BP.
XX
XX
AC AAQ75641;
XX
XX 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
PS Disclosure; Page 6; 11pp; Japanese.
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENSEQ files AAQ75647-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2660 AAAAAAAAAAAAAAAAAA 2678
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 49
AAQ75642/C
ID AAQ75642 standard; DNA; 21 BP.
XX
XX
AC AAQ75642;
XX
XX 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.


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XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX 16-APR-1993; 93JP-00112515.
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 AAAAAAAAAAAAAAAAAA 2678
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 53
AAQ75644/c
ID AAQ75644 standard; DNA; 21 BP.
XX
XX AAQ75644;
AC
XX
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX 16-APR-1993; 93JP-00112515.
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
DR

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XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 AAAAAAAAAAAAAAAAAA 2678
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 54
AAQ75647/c
ID AAQ75647 standard; DNA; 21 BP.
XX
XX AAQ75647;
AC
XX
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX 16-APR-1993; 93JP-00112515.
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2660 ACACAAAAAAAAAAAAA 2678
      |||
      19 AAAAAAAAAAAAAAAAAA 1
Db

RESULT 55
AAV53395
ID      AAV53395 standard; DNA; 21 BP.
XX
XX      AAV53395;
XX
XX      13-OCT-1998 (first entry)
XX
XX      HIV-1 gag protein DNA primer #8.
XX
XX      Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
XX      vaccines; infection; protection; primer; ss.
XX
XX      Synthetic.
XX
XX      WO982596-A1.
XX
XX      28-MAY-1998.
XX
XX      19-NOV-1997; 97WO-JP004216.
XX
XX      19-NOV-1996; 96JP-00323412.
XX
XX      (NTNA-) JAPAN NAT INST INFECTIOUS DISEASES.
XX      (JAPG) NIPPON ZEON KK.
XX
XX      Kojima A, Kurata T, Yasuda A;
XX
XX      WPI, 1998-312481/27.
XX
XX      Recombinant vaccinia virus containing fusion HIB gag gene - for
XX      production in host cells of gag protein for use as vaccine.
XX
XX      Example 1; Page 66; 84pp; Japanese.
XX
XX      AAV5388-935414 are primers used in a method which results in a
XX      recombinant vaccinia virus comprising of a gag gene from a retrovirus
XX      such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
XX      region (30-300 bases in length) of a retroviral gene other than the gag
XX      gene. The gag gene may be altered so as to produce a gag protein modified
XX      from the natural sequence by the addition, deletion or substitution of at
XX      least 1 amino acid residue. The fusion gene is inserted into a region of
XX      a vaccinia virus not essential to its propagation, to give a recombinant
XX      vaccinia virus vector which is used to transform a host cell (such as
XX      HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
XX      culturing the host cell produces particulate structures containing the
XX      fusion gag protein. The recombinant vaccinia virus or the fusion gag
XX      protein particles may be used in the production of vaccines for
XX      protecting against infection with retroviruses such as HIV
XX
XX      Sequence 21 BP; 19 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match      0.7%; Score 19; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2661 CAAAAAAAAAAAAAAAAA 2679
      |||
      2 CAAAAAAAAAAAAAAAAA 20
Db

RESULT 56
ADK01333/c
ID      ADK01333 standard; DNA; 21 BP.
XX
XX      ADK01333;
XX
XX      06-MAY-2004 (first entry)
DT

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XX      Rat DNA microarray capture oligonucleotide #53.
XX
XX      ss: hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX      blood; nerve; germ cell; food additive; food supplement.
XX
XX      Rattus sp.
XX
XX      DE10208794-A1.
XX
XX      04-SEP-2003.
XX
XX      28-FEB-2002; 2002DE-01008794.
XX
XX      28-FEB-2002; 2002DE-01008794.
XX
XX      (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
XX      Boekenkamp D, Dieck HT, Hoppe H;
XX
XX      WPI; 2003-714082/68.
XX
XX      Sorting single-stranded nucleic acid, useful for analyzing expression
XX      patterns and screening active agents, uses capture agent with variable
XX      and constant regions.
XX
XX      Example; Page 5; 8pp; German.
XX
XX      This invention describes a novel method for sorting single-stranded
XX      nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX      reading out, where the nucleic acids are selectively bound using capture
XX      agents that are (a) immobilised on the surface of a solid matrix and (b)
XX      comprise variable and non-variable regions. The capture oligonucleotides
XX      have a 5'-invariable anchor region, the complement of which is present at
XX      least once in each nucleic acid and a 3'-variable, discriminatory region
XX      that comprises all possible combinations of up to 10 nucleotides to allow
XX      binding of particular sorts of single stranded nucleic acids. The capture
XX      agents are particularly locked nucleic acids (LNA) and the anchor region
XX      comprises a sequence of 10-50, particularly 15-25, T residues. The
XX      capture oligonucleotides are biotinylated and immobilised on a surface by
XX      interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX      metal, resin, gel, crystalline material and/or membrane, having semi-
XX      conducting properties and especially in the form of a chip. Its surface
XX      is particularly a layer of (bio)molecular filaments and binding of single
XX      stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX      physical, stimulated by an electrical field or through a molecular sieve.
XX      The method is used (i) for analysis of patterns, especially in mucosal,
XX      hair root, blood, nerve or germ cells and (ii) for determining the
XX      activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX      additives or supplements, especially minerals, trace elements, organic
XX      acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX      mixtures. The method provides rapid, inexpensive and reproducible
XX      representation of differences in pools of nucleic acids from cells. It
XX      allows imaging of the complete pattern of all nucleic acid in a cell, and
XX      can detect very small differences in the nucleic acid pool. Since the
XX      method is based on comparison of nucleic acid pools, not individual
XX      genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX      capture probes used in the method of the invention.
XX
XX      Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
SQ
Query Match      0.7%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2661 CAAAAAAAAAAAAAAAAA 2679
      |||
      20 CAAAAAAAAAAAAAAAAA 2
Db

RESULT 57
ADK01297/c
ID      ADK01297 standard; DNA; 21 BP.

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```

XX AC ADR01297;
XX AC
XX DT 06-MAY-2004 (first entry)
XX DE
XX DE Rat DNA microarray capture oligonucleotide #17.
XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX KW blood; nerve; germ cell; food additive; food supplement.
XX OS
XX OS Rattus sp.
XX PN DE10208794-A1.
XX PD
XX PD 04-SEP-2003.
XX PF 28-FEB-2002; 2002DE-01008794.
XX PR 28-FEB-2002; 2002DE-01008794.
XX PA (DEGS ) DEGUSA BIOACTIVES GMBH.
XX PI Boekenkamp D, Dieck HT, Hoppe H;
XX DR WPI; 2003-714082/68.
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX PT patterns and screening active agents, uses capture agent with variable
XX PT and constant regions.
XX PS
XX PS Example; Page 5; 8pp; German.
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (bio)molecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acid in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADR01281-ADR01344 represent
XX CC capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX AC ADR01335;
XX AC
XX DT 06-MAY-2004 (first entry)
XX DE
XX DE Rat DNA microarray capture oligonucleotide #55.
XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX KW blood; nerve; germ cell; food additive; food supplement.
XX OS
XX OS Rattus sp.
XX PN DE10208794-A1.
XX PD
XX PD 04-SEP-2003.
XX PF 28-FEB-2002; 2002DE-01008794.
XX PR 28-FEB-2002; 2002DE-01008794.
XX PA (DEGS ) DEGUSA BIOACTIVES GMBH.
XX PI Boekenkamp D, Dieck HT, Hoppe H;
XX DR WPI; 2003-714082/68.
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX PT patterns and screening active agents, uses capture agent with variable
XX PT and constant regions.
XX PS
XX PS Example; Page 6; 8pp; German.
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (bio)molecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acid in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADR01281-ADR01344 represent
XX CC capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY	2661	C A A A A A A A A A A A A A A A A A	2679
Db	20	C A A A A A A A A A A A A A A A A A	2

RESULT 59
ADK01302/c
ID ADK01302 standard; DNA; 21 BP.
yy

ADK01302; AC

DT 06-MAY-2004 (first entry)
 XX

Rat DNA microarray capture oligonucleotide #22.

XX blood; nerve; germ cell; food additive; food supplement.

OS Rattus sp.

PN DE10208794-A1.

PD 04-SEP-2003.

PF 28-FEB-2002; 2002DE-01008794.
XX

PR 28-FEB-2002; 2002DE-01008794.
XY

PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX

РІ Воєнкамп Д, Дієк НТ, Норре Н, XX

WFL; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression patterns and screening active agents, uses capture agent with variable PT and constant regions.

PS Example; Page 5; 8pp; German.

This invention describes a novel method for sorting single-stranded nucleic acids by isolation and hybridisation of nucleic acid pools, then reading out, where the nucleic acids are selectively bound using capture agents that are (a) immobilised on the surface of a solid matrix and (b) comprise variable and non-variable regions. The capture oligonucleotides have a 5'-invertible anchor region, the complement of which is present at least once in each nucleic acid and a 3'-variable, discriminatory region that comprises all possible combinations of up to 10 nucleotides to allow binding of particular sorts of single stranded nucleic acids. The capture agents are particularly locked nucleic acids (LNA) and the anchor region comprises a sequence of 10-50, particularly 15-25, T residues. The capture oligonucleotides are biotinylated and immobilised on a surface by interaction with streptavidin. The matrix is of plastic, ceramic, glass, metal, resin, gel, crystalline material and/or membrane, having semi-conducting properties and especially in the form of a chip. Its surface is particularly a layer of (bio)molecular filaments and binding of single stranded nucleic acids to the surface is (quasi) covalent, supramolecular, physical, stimulated by an electrical field or through a molecular sieve. The method is used (i) for analysis of patterns, especially in mucosal, hair root, blood, nerve or germ cells and (ii) for determining the activity of pharmaceuticals and/or nutritional compounds, e.g. food additives or supplements, especially minerals, trace elements, organic acids (amino, carboxylic or fatty acid) or their derivatives, salts and mixtures. The method provides rapid, inexpensive and reproducible representation of differences in pools of nucleic acids from cells. It allows imaging of the complete pattern of all nucleic acid in a cell, and can detect very small differences in the nucleic acid pool. Since the method is based on comparison of nucleic acid pools, not individual genes, matrix mislabourisation is possible. ADO01281-ADO01344 represent capture probes used in the method of the invention.

Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

	0.7%;	Score 19;	DB 10;	Length 21;
Query Match				
Best Local Similarity	100.0%;	Pred. No. 5.9e+03;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	2661	CAAAAAAAAAAAAAAAAAA	2679	
Db	19	CAAAAAAAAAAAAAAAAAA	1	

QY 2661 CAAAAAAAAAAAAAAAAA 2679

D6 19 CAAAAA AAAA AAAA AAAA 1

RESULT 60

ADK01334/C
ID ADK01334

AC ADK01334;

DT 06-MAY-2004 (first entry)

Rat DNA microarray capture oligonucleotide #54.

kw BB; hybrid
KW blood; net

AA Ratna sp.
05

PN DE10208794-1

PD 04-SEP-2003.

28-FEB-2002; 2002DE-01008794.

28-FEB-2002; 2002DE-01008794.

PA (DEGS) DEGUSSA BIOACTIVES GMBH.

PI Boekenkamp D, Dieck

PT Sorting single-stranded nucleic acid, useful for analyzing expression patterns and screening active agents, uses capture agent with variable PT and constant regions.

Example; Page 5; 8pp; German.

This invention describes a novel method for sorting single-stranded nucleic acids by isolation and hybridisation of nucleic acid pools, then reading out, where the nucleic acids are selectively bound using capture agents that are (a) immobilised on the surface of a solid matrix and (b) comprise variable and non-variable regions. The capture oligonucleotides have a 5'-invariable anchor region, the complement of which is present at least once in each nucleic acid and a 3'-variable, discriminatory region that comprises all possible combinations of up to 10 nucleotides to allow binding of particular sorts of single stranded nucleic acids. The capture agents are particularly locked nucleic acids (LNA) and the anchor region comprises a sequence of 10-50, particularly 15-25, T residues. The capture oligonucleotides are biotinylated and immobilised on a surface by interaction with streptavidin. The matrix is of plastic, ceramic, glass, metal, resin, gel, crystalline material and/or membrane, having semi-conducting properties and especially in the form of a chip. Its surface is particularly a layer of (bio)molecular filaments and binding of single stranded nucleic acids to the surface is (quasi)covalent, supramolecular, physical, stimulated by an electrical field or through a molecular sieve. The method is used (i) for analysis of patterns, especially in mucosal, hair root, blood, nerve or germ cells and (ii) for determining the activity of pharmaceuticals and/or nutritional compounds, e.g. food additives or supplements, especially minerals, trace elements, organic acids (amino, carboxylic or fatty acid) or their derivatives, salts and mixtures. The method provides rapid, inexpensive and reproducible representation of differences in pools of nucleic acids from cells. It allows imaging of the complete pattern of all nucleic acids in a cell, and can detect very small differences in the nucleic acid pool. Since the method is based on comparison of nucleic acid pools, not individual genes, matrix miniaturisation is possible. ADO101281-A, ADO101344 represent

CC capture probes used in the method of the invention.
 XX Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;
 SQ Query Match 0.7%; Score 19; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2661 CAAAAAAAAAAAAAAAAA 2679
 Db 20 CAAAAAAAAAAAAAAAAA 2
 RESULT 61
 ADK01303/c
 ID ADK01303 standard; DNA; 21 BP.
 AC ADK01303;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Rat DNA microarray capture oligonucleotide #23.
 XX
 KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KW blood; nerve; germ cell; food additive; food supplement.
 XX
 OS Rattus sp.
 XX
 PN DE10208794-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 26-FEB-2002; 2002DE-01008794.
 XX
 PR 28-FEB-2002; 2002DE-01008794.
 XX
 PA (DEGS) DEGUSSA BIOACTIVES GMBH.
 XX
 PI Boekenkamp D, Dieck HT, Hoppe H;
 XX
 DR WPI; 2003-714082/68.
 XX
 PT Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.
 XX
 PS Example; Page 5; 8pp; German.
 XX
 CC This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC additives or supplements, especially minerals, trace elements, organic
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It

CC allows imaging of the complete pattern of all nucleic acid in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.
 XX
 SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
 Oy 2661 CAAAAAAAAAAAAAAAAA 2679
 Db 19 CAAAAAAAAAAAAAAAAA 1
 Query Match 0.7%; Score 19; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 62
 ADK01307/c
 ID ADK01307 standard; DNA; 21 BP.
 AC ADK01307;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Rat DNA microarray capture oligonucleotide #27.
 XX
 KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KW blood; nerve; germ cell; food additive; food supplement.
 XX
 OS Rattus sp.
 XX
 PN DE10208794-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 26-FEB-2002; 2002DE-01008794.
 XX
 PR 28-FEB-2002; 2002DE-01008794.
 XX
 PA (DEGS) DEGUSSA BIOACTIVES GMBH.
 XX
 PI Boekenkamp D, Dieck HT, Hoppe H;
 XX
 DR WPI; 2003-714082/68.
 XX
 PT Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.
 XX
 PS Example; Page 5; 8pp; German.
 XX
 CC This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food

CC additives or supplements, especially minerals, trace elements, organic
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.

SO Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
 Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 63
 ADK01304/C
 ID ADK01304 standard; DNA; 21 BP.
 AC ADK01304;
 DT 06-MAY-2004 (first entry)
 DE Rat DNA microarray capture oligonucleotide #24.
 XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KM blood; nerve; germ cell; food additive; food supplement.
 XX Rattus sp.
 OS DE10208794-A1.
 XX 04-SEP-2003.
 PD 28-FEB-2002; 2002DE-01008794.
 XX 28-FEB-2002; 2002DE-01008794.
 PR 28-FEB-2002; 2002DE-01008794.
 XX (DEGS) DEGUSSA BIOACTIVES GMBH.
 PA Boekenkamp D, Dieck HT, Hoppe H;
 PI WPI; 2003-714082/68.
 DR

PT Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.
 XX

PS Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,

CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC additives or supplements, especially minerals, trace elements, organic
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.

SO Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
 Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 64
 ADK01306/C
 ID ADK01306 standard; DNA; 21 BP.
 AC ADK01306;
 DT 06-MAY-2004 (first entry)
 DE Rat DNA microarray capture oligonucleotide #26.
 XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KM blood; nerve; germ cell; food additive; food supplement.
 XX Rattus sp.
 OS DE10208794-A1.
 XX 04-SEP-2003.
 PD 28-FEB-2002; 2002DE-01008794.
 XX 28-FEB-2002; 2002DE-01008794.
 PR 28-FEB-2002; 2002DE-01008794.
 XX (DEGS) DEGUSSA BIOACTIVES GMBH.
 PA Boekenkamp D, Dieck HT, Hoppe H;
 PI WPI; 2003-714082/68.
 DR

PT Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.
 XX

PS Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,

CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1
RESULT 65
ADK01299/c
ID ADK01299 standard; DNA; 21 BP.
AC ADK01299;
XX 06-MAY-2004 (first entry)
DT
XX
DE Rat DNA microarray capture oligonucleotide #19.
XX
KM sg; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.
DR
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture

CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1
RESULT 66
ADK01301/c
ID ADK01301 standard; DNA; 21 BP.
AC ADK01301;
XX
XX 06-MAY-2004 (first entry)
DT
XX
DE Rat DNA microarray capture oligonucleotide #21.
XX
KM sg; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.
DR
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides

CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.

XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679

DB 19 CAAAAAAAAAAAAAAAAA 1

RESULT 67

ADK01298/C
 ID ADK01298 standard; DNA; 21 BP.

AC ADK01298;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #18.

KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 blood; nerve; germ cell; food additive; food supplement.

OS Rattus sp.

PN DE10208794-A1.

PD 04-SEP-2003.

PF 28-FEB-2002; 2002DE-01008794.

PR 28-FEB-2002; 2002DE-01008794.

PA (DEGS) DEGUSA BIOACTIVES GMBH.

PI Boekenkamp D, Dieck HT, Hoppe H;

DR WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 XX and constant regions.

PS Example; Page 5; Bpp; German.

CC This invention describes a novel method for sorting single-stranded

CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.

XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679

DB 19 CAAAAAAAAAAAAAAAAA 1

RESULT 68

ADK01300/C
 ID ADK01300 standard; DNA; 21 BP.

AC ADK01300;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #20.

KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 blood; nerve; germ cell; food additive; food supplement.

OS Rattus sp.

PN DE10208794-A1.

PD 04-SEP-2003.

PF 28-FEB-2002; 2002DE-01008794.

PR 28-FEB-2002; 2002DE-01008794.

PA (DEGS) DEGUSA BIOACTIVES GMBH.

PI Boekenkamp D, Dieck HT, Hoppe H;

DR WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 XX and constant regions.

XX Example; Page 5; 8bp; German.
PS
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1
RESULT 69
ADK01305/C
ID ADK01305 standard; DNA; 21 BP.
XX
AC ADK01305;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #25.
XX
KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
PT
PS Example; Page 5; 8bp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1
RESULT 70
ADK01342/C
ID ADK01342 standard; DNA; 21 BP.
XX
AC ADK01342;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #62.
XX
KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSA BIOACTIVES GMBH.

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XX  Boekenkamp D, Dieck HT, Hoppe H;
XX  WPI; 2003-714082/68.
XX
XX  Sorting single-stranded nucleic acid, useful for analyzing expression
XX  patterns and screening active agents, uses capture agent with variable
XX  and constant regions.
XX
XX  Example; Page 6; 8pp; German.
XX
XX  This invention describes a novel method for sorting single-stranded
XX  nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX  reading out, where the nucleic acids are selectively bound using capture
XX  agents that are (a) immobilised on the surface of a solid matrix and (b)
XX  comprise variable and non-variable regions. The capture oligonucleotides
XX  have a 5'-invariable anchor region, the complement of which is present at
XX  least once in each nucleic acid and a 3'-variable, discriminatory region
XX  that comprises all possible combinations of up to 10 nucleotides to allow
XX  binding of particular sorts of single stranded nucleic acids. The capture
XX  agents are particularly locked nucleic acids (LNA) and the anchor region
XX  comprises a sequence of 10-50, particularly 15-25, T residues. The
XX  capture oligonucleotides are biotinylated and immobilised on a surface by
XX  interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX  metal, resin, gel, crystalline material and/or membrane, having semi-
XX  conducting properties and especially in the form of a chip. Its surface
XX  is particularly a layer of (bio)molecular filaments and binding of single
XX  stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX  physical, stimulated by an electrical field or through a molecular sieve.
XX  The method is used (i) for analysis of patterns, especially in mucosal,
XX  hair root, blood, nerve or germ cells and (ii) for determining the
XX  activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX  additives or supplements, especially minerals, trace elements, organic
XX  acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX  mixtures. The method provides rapid, inexpensive and reproducible
XX  representation of differences in pools of nucleic acids from cells. It
XX  allows imaging of the complete pattern of all nucleic acids in a cell, and
XX  can detect very small differences in the nucleic acid pool. Since the
XX  method is based on comparison of nucleic acid pools, not individual
XX  genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX  capture probes used in the method of the invention.
XX
XX  Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
XX
XX  Query Match      0.7%; Score 19; DB 10; Length 21;
XX  Best Local Similarity 100.0%; Pred. No. 5.9e+03;
XX  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 2661 CAAAAAAAAAAAAAAAAA 2679
XX  |||||
XX  DB 21 CAAAAAAAAAAAAAAAAA 3
XX
XX  RESULT 71
XX  ADK01308/c
XX  ID ADK01308 standard; DNA; 21 BP.
XX
XX  AC ADK01308;
XX
XX  DT 06-MAY-2004 (first entry)
XX
XX  DE Rat DNA microarray capture oligonucleotide #28.
XX
XX  KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX  blood; nerve; germ cell; food additive; food supplement.
XX
XX  OS Rattus sp.
XX
XX  PN DE10208794-A1.
XX
XX  PD 04-SEP-2003.
XX
XX  PF 28-FEB-2002; 2002DE-01008794.

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XX  28-FEB-2002; 2002DE-01008794.
XX
XX  (DEGS ) DEGUSA BIOACTIVES GMBH.
XX
XX  Boekenkamp D, Dieck HT, Hoppe H;
XX  WPI; 2003-714082/68.
XX
XX  Sorting single-stranded nucleic acid, useful for analyzing expression
XX  patterns and screening active agents, uses capture agent with variable
XX  and constant regions.
XX
XX  Example; Page 5; 8pp; German.
XX
XX  This invention describes a novel method for sorting single-stranded
XX  nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX  reading out, where the nucleic acids are selectively bound using capture
XX  agents that are (a) immobilised on the surface of a solid matrix and (b)
XX  comprise variable and non-variable regions. The capture oligonucleotides
XX  have a 5'-invariable anchor region, the complement of which is present at
XX  least once in each nucleic acid and a 3'-variable, discriminatory region
XX  that comprises all possible combinations of up to 10 nucleotides to allow
XX  binding of particular sorts of single stranded nucleic acids. The capture
XX  agents are particularly locked nucleic acids (LNA) and the anchor region
XX  comprises a sequence of 10-50, particularly 15-25, T residues. The
XX  capture oligonucleotides are biotinylated and immobilised on a surface by
XX  interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX  metal, resin, gel, crystalline material and/or membrane, having semi-
XX  conducting properties and especially in the form of a chip. Its surface
XX  is particularly a layer of (bio)molecular filaments and binding of single
XX  stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX  physical, stimulated by an electrical field or through a molecular sieve.
XX  The method is used (i) for analysis of patterns, especially in mucosal,
XX  hair root, blood, nerve or germ cells and (ii) for determining the
XX  activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX  acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX  mixtures. The method provides rapid, inexpensive and reproducible
XX  representation of differences in pools of nucleic acids from cells. It
XX  allows imaging of the complete pattern of all nucleic acids in a cell, and
XX  can detect very small differences in the nucleic acid pool. Since the
XX  method is based on comparison of nucleic acid pools, not individual
XX  genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX  capture probes used in the method of the invention.
XX
XX  Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
XX
XX  Query Match      0.7%; Score 19; DB 10; Length 21;
XX  Best Local Similarity 100.0%; Pred. No. 5.9e+03;
XX  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 2661 CAAAAAAAAAAAAAAAAA 2679
XX  |||||
XX  DB 19 CAAAAAAAAAAAAAAAAA 1
XX
XX  RESULT 72
XX  ABA93238
XX  ID ABA93238 standard; DNA; 22 BP.
XX
XX  AC ABA93238;
XX
XX  DT 18-APR-2002 (first entry)
XX
XX  DE PolyA adaptor oligonucleotide SEQ ID NO:1.
XX
XX  KW Detection; comparative detection; adaptor; ss.
XX
XX  OS Synthetic.
XX
XX  PN JP2001333800-A.

```

PD 04-DEC-2001.
 XX 30-MAY-2000; 2000JP-00160324.
 XX 30-MAY-2000; 2000JP-00160324.
 XX (UNIT-) UNITECH CO LTD.
 XX WPI; 2002-135950/18.
 XX
 XX Comparative detection of the amounts of RNA and DNA.
 XX
 XX Disclosure; Page 9; 9pp; Japanese.
 XX
 XX The present invention describes a method for the comparative detection of
 CC the amount of an RNA. The method comprises: (a) cDNAs obtained by
 CC transcribing respectively from at least two tissue RNAs are respectively
 CC fragmented by using a same restriction enzyme; (b) each different adaptor
 CC and a common adaptor are added to each of the cDNA fragments derived from
 CC the same or different tissues by the step (a); (c) the resultant adaptor-
 CC added cDNAs are mixed together; (d) an adaptor primer having the common
 CC sequence to said different adaptor and a gene-specific adaptor are used
 CC to amplify said adaptor-added cDNAs containing no region derived from
 CC polyadenylic acid of the mRNA before the addition of the adaptor among
 CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
 CC cDNA amounts are measured between the tissues; (f) the RNA is detected
 CC from the measured result; (g) each different adaptor and a common adaptor
 CC are added to each of the genomic DNA fragments derived from a same or
 CC different individuals; (h) the resultant adaptor-added genomic DNAs are
 CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using
 CC an adaptor primer having the common sequence to the different adaptor and
 CC a sequence-specific adaptor; and (j) the ratios of the amplified amounts
 CC of the genomic DNAs are measured between the individuals. The method is
 CC used for the detection of the amounts of RNA and DNA. The present
 CC sequence represents an oligonucleotide which is used in the
 CC exemplification of the present invention
 XX
 XX Sequence 22 BP; 19 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
 XX
 XX Query Match 0.7%; Score 19; DB 6; Length 22;
 XX Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Oy 2661 CAAAAAAAAAAAAAAAAA 2679
 XX Db 4 CAAAAAAAAAAAAAAAAA 22
 XX
 XX RESULT 73
 XX AAQ75028
 XX ID AAQ75028 standard; DNA; 23 BP.
 XX
 XX AAQ75028;
 XX
 XX 25-MAR-2003 (revised)
 XX DT 03-AUG-1995 (first entry)
 XX
 XX LCR oligo 2.
 XX
 XX Synthetic oligo; solid phase immunoassay; ss.
 XX
 XX Synthetic.
 XX
 XX WO9426932-A1.
 XX
 XX 24-NOV-1994.
 XX
 XX 13-MAY-1994; 94WO-US005407.
 XX
 XX 13-MAY-1993; 93US-00061694.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX

PI Fields HA, Khudyakov YE;
 XX
 XX WPI; 1995-006819/01.
 XX
 XX Solid phase immunoassay using oligo:nucleotide as label - also new
 XX PT conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
 XX PT diagnosing hepatitis C or E virus infection.
 XX
 XX Example; Page 13; 34pp; English.
 XX
 XX AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
 XX CC They are used in a method for detecting an antigen in a subject. The
 CC method involves binding the antigen to a solid support and then reacting
 CC it with an immunoreactive ligand (L) bound to an oligo; removing any
 CC unreacted L, and then detecting the presence of the oligo. A similar
 CC method can be used to detect Abs, in which case the ligand is an oligo-
 CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
 CC to be detected at very low levels. An exemplary oligo is AAQ75024 which
 CC can be covalently attached by the 5'- terminus to the N- or C-terminal of
 CC a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see
 CC AAQ75027-075030) can be used. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 23 BP; 19 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
 XX
 XX Query Match 0.7%; Score 19; DB 2; Length 23;
 XX Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Oy 2661 CAAAAAAAAAAAAAAAAA 2679
 XX Db 5 CAAAAAAAAAAAAAAAAA 23
 XX
 XX RESULT 74
 XX AAQ75029/c
 XX ID AAQ75029 standard; RNA; 23 BP.
 XX
 XX AAQ75029;
 XX
 XX 25-MAR-2003 (revised)
 XX DT 03-AUG-1995 (first entry)
 XX
 XX LCR oligo 3.
 XX
 XX Synthetic oligo; solid phase immunoassay; ss.
 XX
 XX Synthetic.
 XX
 XX WO9426932-A1.
 XX
 XX 24-NOV-1994.
 XX
 XX 13-MAY-1994; 94WO-US005407.
 XX
 XX 13-MAY-1993; 93US-00061694.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Fields HA, Khudyakov YE;
 XX
 XX WPI; 1995-006819/01.
 XX
 XX Solid phase immunoassay using oligo:nucleotide as label - also new
 XX PT conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
 XX PT diagnosing hepatitis C or E virus infection.
 XX
 XX Example; Page 13; 34pp; English.
 XX
 XX AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
 XX CC They are used in a method for detecting an antigen in a subject. The
 CC method involves binding the antigen to a solid support and then reacting
 CC it with an immunoreactive ligand (L) bound to an oligo; removing any

CC unreacted L, and then detecting the presence of the oligo. A similar
 CC method can be used to detect Abg, in which case the ligand is an oligo-
 CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
 CC to be detected at very low levels. An exemplary oligo is AAQ75024 which
 CC can be covalently attached to the 5'-terminus to the N- or C-terminal of
 CC a synthetic peptide. For LCR using oligo AAQ75024, oligos 1-4 (see
 CC AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 CC
 CC
 SQ Sequence 23 BP; 0 A; 0 C; 4 G; 1 T; 18 U; 0 Other;

Query Match 0.7%; Score 19; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAAAAAA 2679
 DB 19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 75
 AA20877/c
 ID AA20877 standard; DNA; 24 BP.

AC AA20877;

DT 27-SEP-1999 (first entry)

DE PCR primer PGRT32 for PGI coding sequence.

XX PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;
 KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
 KW PSA; human; ss.

OS Synthetic.
 OS Homo sapiens.

PN MO993264-A2.

PD 01-JUL-1999.

PF 22-DEC-1998; 98WO-1B002133.

PR 22-DEC-1997; 97US-00996306.
 PR 09-SEP-1998; 98US-0099658P.

PA (GEST) GENSET.

PI Cohen D, Blumenfeld M, Chumakov I, Bougueleret L;
 DR WPI; 1999-405176/34.

PT Use of a prostate cancer associated gene and biallelic markers derived
 PT from it.

PS Example 6; Page 42; 365pp; English.

CC The invention relates to a mammalian PGI gene and protein, and a set of
 CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are
 CC used in a hybridisation assay, a sequencing assay, or in an allele-
 CC specific amplification assay for determining the identity of a nucleotide
 CC at a PGI-related biallelic marker. The methods can be used to detect and
 CC to assess the risk of developing cancer or prostate cancer. Early-stage
 CC diagnosis of prostate cancer relies on prostate specific antigen (PSA)
 CC dosage. However, the effectiveness of this is limited due to its
 CC inability to discriminate between malignant and non-malignant affections
 CC of the organ. A need exists for both a reliable diagnostic procedure
 CC which would enable early-stage diagnosis, and for preventative and
 CC curative treatments of the disease. The PGI gene can be used for
 CC detection of prostate cancer, and the risk of developing it in the
 CC future, and can also be used to determine therapies for the disease
 CC
 CC
 SQ Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAAAAAA 2679
 DB 20 CAAAAAAAAAAAAAAAAAAAAA 2

Search completed: February 2, 2005, 16:08:58
 Job time : 1262.01 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model1

Run on: February 2, 2005, 15:07:30 ; Search time 8226.78 seconds
(without alignments)
11866.381 Million cell updates/sec

Title: US-10-048-046-1

Perfect score: 2679

Sequence: 1 aagatcgcgcagcagcgccg.....acaaaaaaaaaaaaaaaaaaaaa 2679

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size: 0

Total number of hits satisfying chosen parameters: 46458

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: listing first 150 summaries

Database:

EST:
1: gb_est1:
2: gb_est2:
3: gb_hnc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gse1:
9: gb_gse2:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	0.8	25	1	AL048782 DKF2P5660
2	21	0.8	29	1	AL039119 DKF2P566J
3	20	0.7	21	5	BX558161 BX558161
4	20	0.7	21	8	AZ792613 2M0045M12
5	20	0.7	23	1	AL038397 DKF2P566G
6	20	0.7	23	1	AL038592 DKF2P566G
7	20	0.7	23	1	AL038609 DKF2P566G
8	20	0.7	23	1	AL038688 DKF2P566J
9	20	0.7	23	5	BX559898 BX559898
10	20	0.7	26	6	CF336199 JMT--06-C
11	20	0.7	28	7	TS2836
12	20	0.7	28	8	AZ654007 1M0527020
13	20	0.7	29	1	AL038731 DKF2P566L
14	20	0.7	30	1	AL037566 DKF2P564I
15	20	0.7	30	5	BX553986 BX553986
16	20	0.7	30	5	BX554037 BX554037
17	20	0.7	30	6	CF299716 7LEAF--03
18	20	0.7	30	8	AZ458127 1M0261124
19	20	0.7	30	8	CF298396 7LEAF--01
20	19	0.7	19	6	CF302456 7LEAF--07
21	19	0.7	20	1	AL038460 DKF2P566B
22	19	0.7	20	1	AL587572
23	19	0.7	20	1	AL587727
24	19	0.7	20	6	CF282002 14ERTL--09

25	19	0.7	20	6	CF316662
26	19	0.7	20	6	CF320843
27	19	0.7	20	8	AZ579178
28	19	0.7	20	8	AZ821905
29	19	0.7	21	1	AL038582 DKF2P566F
30	19	0.7	21	1	AL038839 DKF2P566P
31	19	0.7	21	6	CF276747 14ERTL--02
32	19	0.7	21	6	CF311914 ABF--07-G
33	19	0.7	22	1	AL048750
34	19	0.7	22	6	CF328832
35	19	0.7	22	8	AZ304806
36	19	0.7	22	8	AZ505769 1M0346A10
37	19	0.7	23	1	AJ666332
38	19	0.7	23	1	AL048745
39	19	0.7	23	6	CF318266
40	19	0.7	23	8	AZ315640
41	19	0.7	24	1	AL048765
42	19	0.7	24	6	CF326993
43	19	0.7	24	8	AZ404871
44	19	0.7	24	8	AZ786257 2M0031H11
45	19	0.7	25	1	AL587718
46	19	0.7	25	7	N27663
47	19	0.7	25	9	CG726337 119089B1
48	19	0.7	26	6	CF280688
49	19	0.7	26	7	CN545723
50	19	0.7	27	6	CF299084
51	19	0.7	27	6	CF310560
52	19	0.7	27	6	CF310745 ABF--05-J
53	19	0.7	27	6	CF311022 ABF--06-B
54	19	0.7	27	7	CN545777
55	19	0.7	27	7	CN545880
56	19	0.7	27	7	N89936
57	19	0.7	27	9	TJ386G03Q
58	19	0.7	28	1	AL037026
59	19	0.7	28	1	AL037270
60	19	0.7	28	1	AL037803
61	19	0.7	28	1	AL039180
62	19	0.7	28	1	AL587582
63	19	0.7	28	5	BX554747
64	19	0.7	28	7	CN545498
65	19	0.7	28	7	CN545659
66	19	0.7	28	8	AZ481286
67	19	0.7	28	8	AZ809971
68	19	0.7	29	1	AL038989
69	19	0.7	29	1	AL039052
70	19	0.7	29	1	AL048747
71	19	0.7	29	5	BQ590537
72	19	0.7	29	5	BX551339
73	19	0.7	29	5	BX553273
74	19	0.7	29	5	BX555108
75	19	0.7	29	5	BX555418
76	19	0.7	29	5	BX556473
77	19	0.7	29	5	BX567852
78	19	0.7	29	6	CF293772
79	19	0.7	29	6	CF310757
80	19	0.7	29	6	CF330960
81	19	0.7	29	7	CN545616
82	19	0.7	30	1	AL036726
83	19	0.7	30	1	AL036800
84	19	0.7	30	1	AL037025
85	19	0.7	30	1	AL038461
86	19	0.7	30	1	AL038840
87	19	0.7	30	5	BX549620
88	19	0.7	30	5	BX551781
89	19	0.7	30	5	BX553141
90	19	0.7	30	5	BX556144
91	19	0.7	30	7	CN545845
92	19	0.7	30	7	CN545523
93	18	0.7	18	1	AL038692
94	18	0.7	18	5	BQ582676
95	18	0.7	18	5	BQ590027
96	18	0.7	18	6	CF277873
97	18	0.7	18	6	CF297446

CF316662	HD--06-A2
CF320843	HD--11-00
AZ579178	1M0363R11
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AL038582	DKF2P566F
AL038839	DKF2P566P
CF276747	14ERTL--02
CF311914	ABF--07-G
AL048750	DKF2P566L
CF328832	NACL--03-
AZ304806	1M0005K17
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AJ666332	AB666332
AL048745	DKF2P566K
CF318266	HD--08-F0
AZ315640	1M0033004
AL048765	DKF2P566M
CF326993	NACL--01-
AZ404871	1M0173J14
AZ786257	2M0031H11
AL587718	AL587718
N27663	YW50G06.B1
CG726337	119089B1
CF280688	14ERTL--07
CN545723	EST 17667
CF299084	EST 17667
CF310560	ABF--05-E
CF310745	ABF--05-J
CF311022	ABF--06-B
CN545777	EST 17721
CN545880	EST 17824
N89936	2b23e12.B1
AL98287	T. Brucei
AL037026	DKF2P564H
AL037270	DKF2P564E
AL037803	DKF2P564F
AL039180	DKF2P566O
AL587582	AL587582
BX554747	BX554747
CN545498	EST 17442
CN545659	EST 17603
AZ481286	1M0303L24
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AL038989	DKF2P566B
AL039052	DKF2P566F
AL048747	DKF2P566K
BQ590537	E012843-0
BX551339	BX551339
BX553273	BX553273
BX555108	BX555108
BX555418	BX555418
BX556473	BX556473
BX567852	BX567852
CF293772	30DGS--03
CF310757	ABF--05-J
CF330960	NACL--06-
CN545616	EST 17560
AL036726	DKF2P564L
AL036800	DKF2P564H
AL037025	DKF2P564B
AL038461	DKF2P566B
AL038840	DKF2P566P
BX549620	BX549620
BX551781	BX551781
BX553141	BX553141
BX556144	BX556144
CN545845	EST 17789
CN545523	EST 18667
AL038692	DKF2P566J
BQ582676	E012281-0
BQ590027	E012844-0
CF277873	14ERTL--03
CF297446	30DGS--08

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C 100	18	0.7	18	6	CF301325	7LEAF--06
C 101	18	0.7	18	6	CF301760	7LEAF--06
C 102	18	0.7	19	1	AJ668179	AJ668179
C 103	18	0.7	19	1	AJ669138	AJ669138
C 104	18	0.7	19	5	BQ588729	BQ588729
C 105	18	0.7	19	6	CB174047	CB174047
C 106	18	0.7	19	6	CF297908	CF297908
C 107	18	0.7	19	6	CF291089	CF291089
C 108	18	0.7	19	6	CF291090	CF291090
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C 110	18	0.7	19	6	CF293167	CF293167
C 111	18	0.7	19	6	CF293167	CF293167
C 112	18	0.7	19	6	CF299598	CF299598
C 113	18	0.7	19	6	CF300327	CF300327
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C 116	18	0.7	19	6	CF309821	CF309821
C 117	18	0.7	19	6	CF309943	CF309943
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C 119	18	0.7	19	6	CF311513	CF311513
C 120	18	0.7	19	6	CF311778	CF311778
C 121	18	0.7	19	6	CF312403	CF312403
C 122	18	0.7	19	6	CF315299	CF315299
C 123	18	0.7	19	6	CF316480	CF316480
C 124	18	0.7	19	6	CF318788	CF318788
C 125	18	0.7	19	6	CF329986	CF329986
C 126	18	0.7	19	6	CF331361	CF331361
C 127	18	0.7	19	6	CF332063	CF332063
C 128	18	0.7	19	6	CF333507	CF333507
C 129	18	0.7	19	6	CF333753	CF333753
C 130	18	0.7	19	6	CF334014	CF334014
C 131	18	0.7	19	6	CF335293	CF335293
C 132	18	0.7	19	7	CN545602	CN545602
C 133	18	0.7	19	7	CN545922	CN545922
C 134	18	0.7	19	7	CN545923	CN545923
C 135	18	0.7	19	7	CN545964	CN545964
C 136	18	0.7	19	8	CN546303	CN546303
C 137	18	0.7	19	8	AZ307313	AZ307313
C 138	18	0.7	19	8	AZ310079	AZ310079
C 139	18	0.7	19	8	AZ310105	AZ310105
C 140	18	0.7	19	8	AZ317743	AZ317743
C 141	18	0.7	19	8	AZ340311	AZ340311
C 142	18	0.7	19	8	AZ350519	AZ350519
C 143	18	0.7	19	8	AZ364226	AZ364226
C 144	18	0.7	19	8	AZ365966	AZ365966
C 145	18	0.7	19	8	AZ374409	AZ374409
C 146	18	0.7	19	8	AZ374619	AZ374619
C 147	18	0.7	19	8	AZ385952	AZ385952
C 148	18	0.7	19	8	AZ391509	AZ391509
C 149	18	0.7	19	8	AZ410050	AZ410050
C 150	18	0.7	19	8	AZ414413	AZ414413
					AZ422604	AZ422604

ALIGNMENTS

RESULT 1
AL048782 25 bp mRNA linear EST 04-SBP-2003
DEFINITION DKFZ5660013_r1 566 (synonym: hfkd2) Homo sapiens CDNA clone
AL048782
AL048782.1 GI:4727853
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 25)
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehrer, et al.)

JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
LOCATION/Qualifiers
1..25
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="DKFZ5660013"
/issue_type="Kidney"
/dev stage="fetal"
/lab_host="X1-2blue"
/clone.lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2659 GACCAAAAAAAAAAAAAA 2679
D 4 GACCAAAAAAAAAAAAAA 24

RESULT 2
AL039119 29 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZ5660034_r1 566 (synonym: hfkd2) Homo sapiens CDNA clone
AL039119
AL039119.1 GI:49682250
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 29)
AUTHORS Blocker, H., Boecker, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Blocker, et al.)
JOURNAL Unpublished (1999).
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
LOCATION/Qualifiers
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/mol_type="mRNA"
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/clone="DKFZ5660034"
/issue_type="Kidney"
/dev stage="fetal"
/lab_host="X1-2blue"
/clone.lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

ORIGIN
Query Match 0.8%; Score 21; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2659 GACCAAAAAAAAAAAAAA 2679
D 9 GACCAAAAAAAAAAAAAA 29

RESULT 3
BX558161 21 bp mRNA linear EST 10-OCT-2003
DEFINITION BX558161 Glosina morsitans morsitans adult infected gut Glosina morsitans morsitans CDNA clone Tse37a05_p1c, mRNA sequence.

ACCESSION BX558161 GI:33429302
 VERSION BX558161.1
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 21)
 REFERENCE Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Bettiman, M.,
 Hamilton, U., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly *Glossina*
morsitans morsitans and expression analysis of putative immune
 response genes
 JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UM
 All clones with suffix g1c are reverse primer reads starting at 5'
 end of the cDNA all p1c reads are from
 the 3' end.
 FEATURES
 source
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 Location/Qualifiers
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
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 /clone="Tse37805_p1c"
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 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T.brucei"

Query Match 0.7% Score 20; DB 5; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2660 AAAAAAAAAAAAAAAAAA 2679
 Db 21 AAAAAAAAAAAAAAAAAA 2

RESULT 4
 A2792613/c 21 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0045M12P Mouse 10kb plasmid UUC1M library Mus musculus genomic
 DEFINITION clone UUCG2M0045M12 P, genomic survey sequence.
 A2792613
 VERSION A2792613.1 GI:12936725
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0045 row: M column: 12
 Seq primer: CGTGTAAACGACGCCACGT
 Class: plasmid ends
 High quality sequence stop: 21.
 FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:10090"
 /clone="UUCG2M0045M12"
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 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g14732114[gb]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.7% Score 20; DB 8; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2660 AAAAAAAAAAAAAAAAAA 2679
 Db 21 AAAAAAAAAAAAAAAAAA 2

RESULT 5
 AL038397 23 bp mRNA linear EST 06-JUL-2004
 LOCUS DKFZps66N082_r1 566 (synonym: hfxd2) Homo sapiens cDNA clone
 DEFINITION DKFZps66N082, mRNA sequence.
 AL038397
 VERSION AL038397.1 GI:49682109
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 23)
 REFERENCE Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
 Wiemann, S.
 EST (Ottenwaelder, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter landstr.1, D-85764 Neuherberg, Germany.
 Location/Qualifiers

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			/lab_host="Xl-2blue"
			/clone_lib="566 (synonym: hfkcd2)"
			/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"
ORIGIN			
Query Match	0.7%; Score 20; DB 1; Length 23;		
Best Local Similarity	100.0%; Pred. No. 5.6e+02;		
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	2660 AAAAAAAAAAAAAAAAAAAAAA 2679		
Db	3 AAAAAAAAAAAAAAAAAAAAAA 22		
RESULT 6			
AL038592			
LOCUS	AL038592	23 bp mRNA	EST 06-JUL-2004
DEFINITION	DKFZps66G1446_r1 566 (synonym: hfkcd2) Homo sapiens cDNA clone		
ACCESSION	AL038592		
VERSION	AL038592.1 GI:49682166		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 23)		
JOURNAL	Ottewaelder,B., Oberwarter,B., Mewes,H.W., Gassenhuber,U. and		
COMMENT	Wiemann,S. EST (Ottewaelder, et al.) Unpublished (1993) Contact: MIPS MIPS Ingolstaedter landstr.1, D-85764 Neuherberg, Germany. Location/Qualifiers 1..23 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="DKFZps66G1446" /issue_type="kidney" /dev_stage="fetal" /lab_host="Xl-2blue" /clone_lib="566 (synonym: hfkcd2)" /note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"		
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source			
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Query Match	0.7%; Score 20; DB 1; Length 23;		
Best Local Similarity	100.0%; Pred. No. 5.6e+02;		
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	2660 AAAAAAAAAAAAAAAAAAAAAA 2679		
Db	3 AAAAAAAAAAAAAAAAAAAAAA 22		
RESULT 7			
AL038609			
LOCUS	AL038609	23 bp mRNA	linear EST 06-JUL-2004
DEFINITION	DKFZps66G0946_r1 566 (synonym: hfkcd2) Homo sapiens cDNA clone		
ACCESSION	AL038609		
VERSION	AL038609.1 GI:49682169		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		

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REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE          1 (bases 1 to 23)
JOURNAL        Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
COMMENT        Wiemann, S.
               EST (Ottenwaelder, et al.)
               Unpublished (1999)
MIPS           Contact: MIPS
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               Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
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ORIGIN
Query Match      0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2660 AAAAAAAAAAAAAAAAAA 2679
        |||||
        3 AAAAAAAAAAAAAAAAAA 22

LOCUS      AL038688                23 bp      mRNA      linear      EST 06-JUL-2004
DEFINITION DKFZps66J0646_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION  AL038688
VERSION    DKFZps66J0646, mRNA sequence.
KEYWORDS   AL038688
SOURCE     AL038688.1 GI:49682188
ORGANISM   EST.
            Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 23)
AUTHORS    Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
            Wiemann, S.
TITLE      EST (Ottenwaelder, et al.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: MIPS
MIPS       MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
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    /dev_stage="fetal"
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    /note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2660 AAAAAAAAAAAAAAAAAA 2679
        |||||
        3 AAAAAAAAAAAAAAAAAA 22

LOCUS      AL038688                23 bp      mRNA      linear      EST 06-JUL-2004
DEFINITION DKFZps66J0646_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION  AL038688
VERSION    DKFZps66J0646, mRNA sequence.
KEYWORDS   AL038688
SOURCE     AL038688.1 GI:49682188
ORGANISM   EST.
            Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 23)
AUTHORS    Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
            Wiemann, S.
TITLE      EST (Ottenwaelder, et al.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: MIPS
MIPS       MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
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    /clone="DKFZps66J0646"
    /tissue_type="kidney"
    /dev_stage="fetal"
    /lab_host="X1-2blue"
    /clone_id="566 (synonym: hfkd2)"
    /note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2660 AAAAAAAAAAAAAAAAAA 2679
        |||||
        3 AAAAAAAAAAAAAAAAAA 22

LOCUS      AL038688                23 bp      mRNA      linear      EST 06-JUL-2004
DEFINITION DKFZps66J0646_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION  AL038688
VERSION    DKFZps66J0646, mRNA sequence.
KEYWORDS   AL038688
SOURCE     AL038688.1 GI:49682188
ORGANISM   EST.
            Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 23)
AUTHORS    Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
            Wiemann, S.
TITLE      EST (Ottenwaelder, et al.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: MIPS
MIPS       MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
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    1..23
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="DKFZps66J0646"
    /tissue_type="kidney"
    /dev_stage="fetal"
    /lab_host="X1-2blue"
    /clone_id="566 (synonym: hfkd2)"
    /note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2660 AAAAAAAAAAAAAAAAAA 2679
        |||||
        3 AAAAAAAAAAAAAAAAAA 22

LOCUS      AL038688                23 bp      mRNA      linear      EST 06-JUL-2004
DEFINITION DKFZps66J0646_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION  AL038688
VERSION    DKFZps66J0646, mRNA sequence.
KEYWORDS   AL038688
SOURCE     AL038688.1 GI:49682188
ORGANISM   EST.
            Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 23)
AUTHORS    Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
            Wiemann, S.
TITLE      EST (Ottenwaelder, et al.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: MIPS
MIPS       MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
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    1..23
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="DKFZps66J0646"
    /tissue_type="kidney"
    /dev_stage="fetal"
    /lab_host="X1-2blue"
    /clone_id="566 (synonym: hfkd2)"
    /note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2660 AAAAAAAAAAAAAAAAAA 2679
        |||||
        3 AAAAAAAAAAAAAAAAAA 22

LOCUS      AL038688                23 bp      mRNA      linear      EST 06-JUL-2004
DEFINITION DKFZps66J0646_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION  AL038688
VERSION    DKFZps66J0646, mRNA sequence.
KEYWORDS   AL038688
SOURCE     AL038688.1 GI:49682188
ORGANISM   EST.
            Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 23)
AUTHORS    Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
            Wiemann, S.
TITLE      EST (Ottenwaelder, et al.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: MIPS
MIPS       MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
  source
    1..23
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    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="DKFZps66J0646"
    /tissue_type="kidney"
    /dev_stage="fetal"
    /lab_host="X1-2blue"
    /clone_id="566 (synonym: hfkd2)"
    /note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2660 AAAAAAAAAAAAAAAAAA 2679
        |||||
        3 AAAAAAAAAAAAAAAAAA 22

LOCUS      AL038688                23 bp      mRNA      linear      EST 06-JUL-2004
DEFINITION DKFZps66J0646_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION  AL038688
VERSION    DKFZps66J0646, mRNA sequence.
KEYWORDS   AL038688
SOURCE     AL038688.1 GI:49682188
ORGANISM   EST.
            Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 23)
AUTHORS    Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
            Wiemann, S.
TITLE      EST (Ottenwaelder, et al.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: MIPS
MIPS       MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
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    1..23
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="DKFZps66J0646"
    /tissue_type="kidney"
    /dev_stage="fetal"
    /lab_host="X1-2blue"
    /clone_id="566 (synonym: hfkd2)"
    /note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2660 AAAAAAAAAAAAAAAAAA 2679
        |||||
        3 AAAAAAAAAAAAAAAAAA 22

LOCUS      AL038688                23 bp      mRNA      linear      EST 06-JUL-2004
DEFINITION DKFZps66J0646_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION  AL038688
VERSION    DKFZps66J0646, mRNA sequence.
KEYWORDS   AL038688
SOURCE     AL038688.1 GI:49682188
ORGANISM   EST.
            Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 23)
AUTHORS    Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
```

RESULT 9
BX559898/c
LOCUS BX559898 23 bp mRNA linear EST 10-OCT-2003
DEFINITION BX559898 Glososina moristans adult infected gut Glososina moristans moristans cDNA clone Tse46d05_p1c, mRNA sequence.
ACCESSION BX559898
VERSION BX559898.1 GI:33367802
KEYWORDS EST.
SOURCE Glososina moristans moristans
ORGANISM Glososina moristans moristans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glososina.
1 (bases 1 to 23)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glososina moristans moristans and expression analysis of putative immune response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2NW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.
FEATURES
source
1..23
Location/Qualifiers
/organism="Glososina moristans moristans"
/mol_type="mRNA"
/db_xref="taxon:37546"
/clone="Tse46d05_p1c"
/tissue_type="adult infected gut"
/clone_id="Glososina moristans moristans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

ORIGIN
Query Match 0.7%; Score 20; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2660 AAAAAAAAAAAAAAAAAA 2679
|||||
22 AAAAAAAAAAAAAAAAAA 3
|||||

RESULT 10
CF336199/c
LOCUS CF336199 26 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--06-C18.g1 AlJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--06-C18, mRNA sequence.
ACCESSION CF336199
VERSION CF336199.1 GI:33820789
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eshartrideae; Oryzaceae; Oryza.
1 (bases 1 to 26)

AUTHORS
TITLE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
LOCATION/Qualifiers
1..26
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--06-C18"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_id="AlJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Usominate Carboxyl methyltransferase overexpression line."

ORIGIN
Query Match 0.7%; Score 20; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2660 AAAAAAAAAAAAAAAAAA 2679
|||||
26 AAAAAAAAAAAAAAAAAA 7
|||||

RESULT 11
T52836/c
LOCUS T52836 28 bp mRNA linear EST 06-FEB-1995
DEFINITION ya1b09.a1 Stratiagene ovary (#937217) Homo sapiens cDNA clone IMAGE:68057 3, similar to similar to gb:XS5463 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (HUMAN), mRNA sequence.
ACCESSION T52836
VERSION T52836.1 GI:654696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 28)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Harkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Martis, E., Moore, B., Norris, W., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierly, M., Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Maira, M.
Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PUBMED 8889549
COMMENT Contact: Wilson R.
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 51
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LINT. This clone is available royalty-free through LINT; contact the IMAGE Consortium (infoimage.lint.gov)

for further information. Trace considered overall poor quality
 Insert length: 51 Std Error: 0.00
 Seq primer: -21m3
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

```
1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:50414"
/db_xref="taxon:9606"
/clone="IMAGE:68057"
/sex="female"
/dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/note="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Total ovary tissue, normal, caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGCAG 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."
```

ORIGIN

Query Match 0.7%; Score 20; DB 7; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 ACMAAAAAAAAAAAAAAAAA 2679

DB 22 ACMAAAAAAAAAAAAAAAAA 3

RESULT 12

AZ654007/c

LOCUS

DEFINITION

1M05270208 Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

AZ654007

VERSION

AZ654007.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 28)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A. and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weis

JOURNAL

University of Utah

COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

COMMENT

Tel: 801 585 5606

COMMENT

Fax: 801 585 7177

COMMENT

Email: ddunn@genetics.utah.edu

COMMENT

Insert length: 10000

COMMENT

Std Error: 0.00

COMMENT

Plate: 0527

COMMENT

row: 0

COMMENT

column: 20

COMMENT

Seq primer: CACACAGAAACAGCTATGACC

COMMENT

Class: plasmid ends

COMMENT

High quality sequence stop: 28.

FEATURES

source

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1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0527020"
/sex="Male"
```

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD22uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (GI:4732114|9d|AF12907.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.7%; Score 20; DB 8; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 ACMAAAAAAAAAAAAAAAAA 2679

DB 27 ACMAAAAAAAAAAAAAAAAA 8

RESULT 13

AL038731

LOCUS

DEFINITION

DKFZps56L2146 r1 566 (synonym: hfk2) Homo sapiens cDNA clone

ACCESSION

AL038731

VERSION

AL038731.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 29)

AUTHORS

Ottensmeyer, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

TITLE

EST (Ottensmeyer, et al.)

JOURNAL

Unpublished (1999)

COMMENT

Contact: MIPS

COMMENT

MIPS

COMMENT

Ingolstraeder Landstr. 1, D-85764 Neuherberg, Germany.

COMMENT

Location/Qualifiers

COMMENT

1..29

COMMENT

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COMMENT

/mol_type="mRNA"

COMMENT

/db_xref="taxon:9606"

COMMENT

/clone="DKFZps56L2146"

COMMENT

/issue_type="Kidney"

COMMENT

/dev_stage="fetal"

COMMENT

/lab_host="X1-2blue"

COMMENT

/clone_lib="566 (synonym: hfk2)"

COMMENT

/note="Vector: pMFP1, Site_1: NotI, Site_2: SalI"

ORIGIN

Query Match 0.7%; Score 20; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 ACMAAAAAAAAAAAAAAAAA 2679

DB 9 ACMAAAAAAAAAAAAAAAAA 28

RESULT 14
AL037566 30 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZP564I1472.F1.564 (synonym: hbr2) Homo sapiens cDNA clone
DEFINITION DKFZP564I1472, mRNA sequence.
ACCESSION AL037566
VERSION AL037566.1 GI:49682018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 30)
AUTHORS Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS.
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..30
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="DKFZP564I1472"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_idb="564 (synonym: hbr2)"
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ORIGIN
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2659 GACAAAAA 2678
DB 10 GACAAAAA 29

RESULT 15
BX553986 30 bp mRNA linear EST 10-OCT-2003
LOCUS BX553986 Glosina morsitans morsitans adult infected gut Glosina
DEFINITION morsitans morsitans cDNA clone Tse13ig02_p1c, mRNA sequence.
ACCESSION BX553986
VERSION BX553986.1 GI:33378096
KEYWORDS EST.
SOURCE Glosina morsitans morsitans
ORGANISM Glosina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glosina.
REFERENCE 1 (bases 1 to 30)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
TITLE Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glosina
morsitans morsitans and expression analysis of putative immune
response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

FEATURES
source
1..30
/organism="Glosina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse13ig02_p1c"
/tissue_type="adult infected gut"
/clone_idb="Glosina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

ORIGIN
Query Match 0.7%; Score 20; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2660 ACAA 2679
DB 30 ACAA 11

RESULT 16
BX554037 30 bp mRNA linear EST 10-OCT-2003
LOCUS BX554037 Glosina morsitans morsitans adult infected gut Glosina
DEFINITION morsitans morsitans cDNA clone Tse13a07_p1c, mRNA sequence.
ACCESSION BX554037
VERSION BX554037.1 GI:33378144
KEYWORDS EST.
SOURCE Glosina morsitans morsitans
ORGANISM Glosina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glosina.
REFERENCE 1 (bases 1 to 30)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
TITLE Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glosina
morsitans morsitans and expression analysis of putative immune
response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.

FEATURES
source
1..30
/organism="Glosina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse13a07_p1c"
/tissue_type="adult infected gut"
/clone_idb="Glosina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.7%; Score 20; DB 5; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2660 ACMAAAAAAAAAAAAAAAAAA 2679
 |||||
 Db 30 ACMAAAAAAAAAAAAAAAAAA 11

RESULT 17
 CF299716/c 30 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--03-N11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--03-N11, mRNA
 sequence.

ACCESSION CF299716 GI:33671477
 VERSION CF299716
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriactoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 30)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE Contact: Nahm B.H.
 JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 COMMENT of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6335
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source 1..30
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--03-N11"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E. coli DH10B"
 /clone_id="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOP0, Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

ORIGIN

Query Match 0.7%; Score 20; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2660 ACMAAAAAAAAAAAAAAAAAA 2679
 |||||
 Db 22 ACMAAAAAAAAAAAAAAAAAA 3

RESULT 18
 AZ458127 30 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M0261124R Mouse 10kb plasmid UUCGM library Mus musculus genomic
 DEFINITION clone UUCGM0261124 R, genomic survey sequence.

ACCESSION AZ458127 GI:10616252
 VERSION AZ458127
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 30)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Dvali,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingay,A., von
 Niederhausen,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 CONTACT Robert B. Weiss
 UNIVERSITY University of Utah Genome Center
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 TEL: 801 585 5606
 FAX: 801 585 7177
 EMAIL: ddunn@genetics.utah.edu
 INSERT LENGTH: 10000 Std Error: 0.00
 PLATE: 0261 row: 1 column: 24
 SEQ PRIMER: CACACAGAAACGCTATGACC
 CLAS: plasmid ends
 HIGH QUALITY sequence stop: 30.
 Location/Qualifiers

FEATURES

source 1..30
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM0261124"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_id="Mouse 10kb plasmid UUCGM library"
 /note="Vector: PMD42n; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 0.7%; Score 20; DB 8; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2660 ACMAAAAAAAAAAAAAAAAAA 2679
 |||||
 Db 24 ACMAAAAAAAAAAAAAAAAAA 5

RESULT 19
 CF298396/c 19 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--01-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--01-M05, mRNA
 sequence.

ACCESSION CF298396 GI:33670157
 VERSION CF298396
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharctoidae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
SOURCE

1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--01-M05"
/issue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
19 CAAAAAAAAAAAAAAAAA 1

RESULT 20
CF302456/c 19 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P22, mRNA
sequence.
ACCESSION CF302456.1 GI:33674217
VERSION CF302456.1
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharctoidae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
SOURCE

1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--07-P22"
/issue_type="leaf"

/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
19 CAAAAAAAAAAAAAAAAA 1

RESULT 21
AL038460 20 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZP566B2246.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DEFINITION DKFZP566B2246, mRNA sequence.
ACCESSION AL038460.1 GI:49682131
VERSION AL038460
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 20)
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
EST (Ostenwaelder, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
SOURCE

1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566B2246"
/issue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
2 CAAAAAAAAAAAAAAAAA 20

RESULT 22
AL587572/c 20 bp mRNA linear EST 02-MAR-2001
LOCUS AU587572 BP Chicken Brain Library Gallus gallus cDNA clone
DEFINITION ROS059B11, mRNA sequence.
ACCESSION AL587572.1 GI:13192606
VERSION AL587572.1
KEYWORDS
SOURCE
ORGANISM
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
1 (bases 1 to 20)

AUTHORS
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
JOURNAL
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
(*6854-)

FEATURES
source
Seq primer: M13F.
Location/Qualifiers
1..20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059B11"
/issue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCACCTCGAG 3' / 3' adaptor sequence: 5'
GCGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
Clontech (*6854-1)"

ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 23
AL587727/c 20 bp mRNA linear EST 02-MAR-2001
LOCUS
DEFINITION
AL587727 BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION
AL587727
VERSION
AL587727.1 GI:13192761
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 20)

REFERENCE
AUTHORS
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
JOURNAL
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech
(*6854-)

FEATURES
source
Seq primer: M13F.
Location/Qualifiers
1..20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS061D01"
/issue_type="Brain"

1..20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS061D01"
/issue_type="Brain"

/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCACCTCGAG 3' / 3' adaptor sequence: 5'
GCGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
Clontech (*6854-1)"

ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 20 CAAAAAAAAAAAAAAAAA 2

RESULT 24
CF282002/c 20 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
CF282002 Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F01,
mRNA sequence.
ACCESSION
CF282002.1 GI:33659389
VERSION
CF282002
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriocaulaceae; Oryzaceae; Oryza.
1 (bases 1 to 20)

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nam, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
Contact: Nam, B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--09-F01"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
14ETL"

/note="Vector: PCR4-TOPO, Site 1: EcoRI, mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 20 CAAAAAAAAAAAAAAAAA 2

RESULT 25
CF316662/c

LOCUS CF316662 20 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--06-A20.g1 OshDACL-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--06-A20, mRNA sequence.
ACCESSION CF316662
VERSION CF316662.1 GI:33688423
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS 1 (bases 1 to 20)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of BioScience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--06-A20"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDACL-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

ORIGIN
 Query Match 0.7%; Score 19; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
 |||||
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 26
CF320843 20 bp mRNA linear EST 15-AUG-2003
LOCUS HD--11-001.g1 OshDACL-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--11-001, mRNA sequence.
ACCESSION CF320843
VERSION CF320843.1 GI:33692604
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS 1 (bases 1 to 20)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division

of BioScience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--11-001"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDACL-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

ORIGIN
 Query Match 0.7%; Score 19; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
 |||||
Db 20 CAAAAAAAAAAAAAAAAA 2

RESULT 27
A2579178 20 bp DNA linear GSS 13-DEC-2000
LOCUS A2579178
DEFINITION IM0363F11F Mouse 10kb plasmid UUC1M1 library Mus musculus genomic clone UUC1M0363F11 F, genomic survey sequence.
ACCESSION A2579178
VERSION A2579178.1 GI:11693523
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 20)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0363 row: F column: 11
 Seq primer: CGTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES
 source
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0363F11"

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.7%; Score 19; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
Db 1 CAAAAAAAAAAAAAAAAA 19

RESULT 28
LOCUS A2821905 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0094D20R Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCG2M0094D20 R, genomic survey sequence.

ACCESSION A2821905
VERSION A2821905.1 GI:12991813
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

REFERENCE Durn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Petersen, T., Niederhausern, A. and Wright, D., Weiser, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA

FEATURES
source
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: D column: 20
Seq primer: CACACGAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0094D20"

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.7%; Score 19; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
Db 2 CAAAAAAAAAAAAAAAAA 20

RESULT 29
LOCUS AL038582 21 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZ0566F0946.r1.566 (synonym: hfkx2) Homo sapiens cDNA clone
DKFZ0566F0946, mRNA sequence.

ACCESSION AL038582
VERSION AL038582.1 GI:49682163
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 21)

REFERENCE Oltmannseder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Oltmannseder, et al.)
Unpublished (1999)

JOURNAL COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ0566F0946"
/tissue_type="kidney"
/dev stage="fetal"
/lab host="X1-2blue"
/clone lib="566 (synonym: hfkx2)"
/note="Vector: pMPL; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
Db 2 CAAAAAAAAAAAAAAAAA 20

RESULT 30
LOCUS AL038839
DEFINITION DKE2p566p1346_x1 566 (synonym: htkd2) Homo sapiens cDNA clone
ACCESSION AL038839
VERSION DKE2p566p1346, mRNA sequence.
KEYWORDS
SOURCE EST. AL038839.1 GI:49682218
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 21)
AUTHORS Otsenwaelder, B., Oberwarter, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Otsenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
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1..21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKE2p566p1346"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: htkd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"
ORIGIN
Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 2 CAAAAAAAAAAAAAAAAA 20
RESULT 31
LOCUS CF276747/c
DEFINITION CF276747 21 bp mRNA linear EST 14-AUG-2003
14FTL--02-A06.b1 Rice etiolated leaf plasmid cDNA library (14FTL)
Oryza sativa (japonica cultivar-group) cDNA clone 14FTL--02-A06,
mRNA sequence.
ACCESSION CF276747
VERSION CF276747.1 GI:33654133
KEYWORDS
SOURCE EST:
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
LOCATION/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
..

ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1
RESULT 32
LOCUS CF311914/c
DEFINITION ABF--07-G07.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--07-G07, mRNA sequence.
ACCESSION CF311914
VERSION CF311914.1 GI:33683675
KEYWORDS
SOURCE EST:
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
LOCATION/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ABF--07-G07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO, Site_1: EcoRI, Site_2: EcoRI; mRNA was capped
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2661 CAAAAAAAAAAAAAAAAA 2679

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Db      21 CAAAAAAAAAAAAAAAAAAAAA 3
|||||
RESULT 33
AL048750                22 bp  mRNA  linear  EST 04-SEP-2003
LOCUS  DKFZPS661123_r1.566 (synonym: hfk42) Homo sapiens cDNA clone
DEFINITION
AK048750                mRNA sequence.
ACCESSION  AL048750.1 GI:4727821
VERSION    .EST.
KEYWORDS   Homo sapiens (human)
SOURCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS    Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE      EST (Koehrer, et al.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: MIPS
MIPS       Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES   Location/Qualifiers
SOURCE     1..22
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKFZPS661123"
            /tissue_type="Kidney"
            /dev_stage="fetal"
            /lab_host="X1-2blue"
            /clone_lib="566 (synonym: hfk42)"
            /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      0.7%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2661 CAAAAAAAAAAAAAAAAAAAAA 2679
|||||
Db      4 CAAAAAAAAAAAAAAAAAAAAA 22
|||||
RESULT 34
CF328832                22 bp  mRNA  linear  EST 18-AUG-2003
LOCUS  NCCL-03-C020.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION  sativa (japonica cultivar-group) cDNA clone NACL-03-C020, mRNA
sequence.
ACCESSION  CF328832
VERSION    CF328832.1 GI:3805905
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 22)
            2 (bases 1 to 22)
REFERENCE  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Yonsei University
            Yongsin, Kyeonggi, Korea
            Tel: 82 31 321 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myonji.ac.kr.
            Location/Qualifiers
            1..22
FEATURES   source

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39847"
/clone="NACL-03-C020"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match      0.7%; Score 19; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2661 CAAAAAAAAAAAAAAAAAAAAA 2679
|||||
Db      19 CAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 35
AZ304806                22 bp  DNA  linear  GSS 29-SEP-2000
LOCUS  IM0005K17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION  clone UUGC1M0005K17 F, genomic survey sequence.
ACCESSION  AZ304806
VERSION    AZ304806.1 GI:10341191
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 22)
REFERENCE  Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
AUTHORS    Islam,H., Longacre,S., Mahmoud,M., Neenan,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0005 row: K column: 17
            Seq primer: CATTGTAAACGACGCGCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
            Location/Qualifiers
            1..22
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            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0005K17"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4

```

ORIGIN

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 1 CAAAAAAAAAAAAAAAAA 19

RESULT 36
AZ505769 22 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0346A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0346A10 R, genomic survey sequence.
ACCESSION AZ505769
VERSION AZ505769.1 GI:10687085
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0346 row: A column: 10
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1..22
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0346A10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passages through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

ORIGIN

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 1 CAAAAAAAAAAAAAAAAA 19

RESULT 37
AUF66332 23 bp mRNA linear EST 28-JUN-2004
LOCUS AUF66332 CSEORAN09 Sus scrofa CDNA clone C0000033_H19, mRNA
DEFINITION AUF66332
ACCESSION AUF66332
VERSION AUF66332.1 GI:49350783
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 23)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.

TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle

JOURNAL
COMMENT Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross-match with the -minscore 20 and -mismatch 12 options. Vector:pbluescriptII(ks+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
source
1..23
Location/Qualifiers

/organism="Sus scrofa"
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/db_xref="taxon:9823"
/clone="C0000033_H19"
/issue_type="placenta"
/clone_lib="CSEORAN09"
/note="Vector: pbluescriptII(ks+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 20 CAAAAAAAAAAAAAAAAA 2

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RESULT 38
AL048745
LOCUS
DEFINITION DKFZP566K213_r1.566 (synonym: hfk42) Homo sapiens cDNA clone
ACCESSION AL048745
VERSION AL048745
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 23)
JOURNAL Koehrer, K., Beyer, A., Mewes, H.W., Gaassenhuber, J. and Wiemann, S.
COMMENT Unpublished (1999)
CONTACT: MIPS
MIS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..23
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566K213"
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/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfk42)"
/notes="Vector: pMPL; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match 0.7%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2661 CAAAAAAAAAAAAAAAAAAAAA 2679
|||||
4 CAAAAAAAAAAAAAAAAAAAAA 22

RESULT 39
CF318266/c
LOCUS CF318266
DEFINITION HD--08-F07.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
ACCESSION HD--08-F07, mRNA sequence.
VERSION CF318266
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE 1 (bases 1 to 23)
JOURNAL Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
COMMENT Song, S.I., Kim, J.K., Kim, J.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Yonsei University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ybio.com, bhnahm@bio.yonsei.ac.kr.
Location/Qualifiers
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"

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/clone="HD--08-F07"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOP0; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2661 CAAAAAAAAAAAAAAAAAAAAA 2679
|||||
19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 40
AZ315640
LOCUS AZ315640
DEFINITION 23 bp DNA linear GSS 29-SEP-2000
ACCESSION clone UGCGIM0033004 F, genomic survey sequence.
VERSION AZ315640
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 23)
JOURNAL Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
COMMENT Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0033 row: 0 column: 04
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0033004"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

```

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.7%; Score 19; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
|||||
Db 3 CAAAAAAAAAAAAAAAAA 21

RESULT 41
AL048765 24 bp mRNA linear EST 04-SEP-2003
LOCUS DKEZP566M233_r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

DEFINITION DKEZP566M233, mRNA sequence.
ACCESSION AL048765
VERSION AL048765.1 GI:4727836

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 24)

AUTHORS Koehler, K., Beyer, A., Mewes, H.W., Gaassenhuber, J. and Wiemann, S.

TITLE EST (Koehler, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

FEATURES

source location/Qualifiers

1..24
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKEZP566M233"
/issue_type="Kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
|||||
Db 4 CAAAAAAAAAAAAAAAAA 22

RESULT 42
CF326993 24 bp mRNA linear EST 18-AUG-2003
LOCUS CF326993
DEFINITION NACL-01-E17.g1 Rice callus plasmid cDNA library (NACL) Oryza

sativa (japonica cultivar-group) cDNA clone NACL-01-E17, mRNA
sequence.

ACCESSION CF326993
VERSION CF326993.1 GI:33802241

KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 24)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source location/Qualifiers

1..24
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:3947"
/clone="NACL-01-E17"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
|||||
Db 2 CAAAAAAAAAAAAAAAAA 20

RESULT 43
AZ404871 24 bp DNA linear GSS 03-OCT-2000

LOCUS AZ404871
DEFINITION IM0173J14R Mouse 10kb plasmid UGCGM library Mus musculus genomic

clone UGCGM0173J14 R, genomic survey sequence.
ACCESSION AZ404871
VERSION AZ404871.1 GI:10528884

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0173 row: J column: 14
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends

FEATURES High quality sequence stop: 24.
Location/Qualifiers
source 1..24

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0173J14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.7%; Score 19; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
Db 4 CAAAAAAAAAAAAAAAAA 22

RESULT 44
LOCUS AZ786257 24 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M003JH1R Mouse 10kb plasmid UUCGM library Mus musculus genomic
ACCESSION AZ786257
VERSION AZ786257.1 GI:12923835
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Jellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: dduan@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: H column: 11
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends

FEATURES High quality sequence stop: 24.
Location/Qualifiers
source 1..24

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0031H11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.7%; Score 19; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
Db 1 CAAAAAAAAAAAAAAAAA 19

RESULT 45
LOCUS AL587718/c 25 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587718 BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION ROS061C02, mRNA sequence.
VERSION AL587718.1 GI:13192752
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
1 (bases 1 to 25)
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCAGCGCGCTTTTCTTTT 3' Poly A RNA purchased from Clontech (*6854-
Seq primer: M13F.
FEATURES Location/Qualifiers
source 1..25
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"

/clone="ROS061C02"
 /tissue_type="Brain"
 /dev_stage="Unknown"
 /lab_host="DH10B"
 /clone_lib="BP Chicken Brain Library"
 /note="Vector: pSPORT1, Site 1: NotI; Site 2: SalI; Cloned
 unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
 GCGGCCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from
 Clontech (*6854-1)"

ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

2661 CAAAAAAAAAAAAAAAAA 2679
 21 CAAAAAAAAAAAAAAAAA 3

DB

RESULT 46
 N27663/c 25 bp mRNA linear EST 30-DEC-1995
 LOCUS yw50g06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone
 DEFINITION IMAGE:255706.3, similar to gb:J05032 ASPARTYL-TRNA SYNTHETASE
 (HUMAN);, mRNA sequence.

ACCESSION N27663
 VERSION N27663.1 GI:1142144
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 25)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chisnoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
 Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
 Trevaeth, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
 and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL 97044478
 MEDLINE
 PUBMED
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: m13 -40 forward
 High quality sequence stop: 1.
 Location/Qualifiers
 1..25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3866115"
 /db_xref="taxon:9606"
 /clone="IMAGE:255706"
 /sex="Female"
 /tissue_type="olfactory epithelium"
 /dev_stage="35 year old"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Weizmann Olfactory Epithelium"
 /note="Organ: nose; Vector: pBluescript SK-; Site_1:"

FEATURES

SOURCE

EsORI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Olfactory epithelium, normal. Average insert
 size: 0.8 kb; Uni-ZAP XR Vector. Library constructed by N.
 Walker, D. Lancelet, Weizmann Institute of Science. ~5'
 adaptor sequence: 5' GAATTCGACGAG 3' ~3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match 0.7%; Score 19; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

2661 CAAAAAAAAAAAAAAAAA 2679
 22 CAAAAAAAAAAAAAAAAA 4

DB

RESULT 47
 CG726337/c 25 bp DNA linear GSS 20-OCT-2003
 LOCUS 11190899E12.2RL_Y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
 DEFINITION survey sequence.
 ACCESSION CG726337
 VERSION CG726337.1 GI:37764992
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 25)
 AUTHORS Walbot, V.
 Maize genomic sequences found using engineered RescueMu transposon
 unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 119089 row: B column: 12
 Class: transposon-tagged.
 Location/Qualifiers
 1..25
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /culturivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="1119 - RescueMu Grid AA"
 /note="Organ: leaf; Vector: RescueMu (engineered from
 pBluescript backbone); Site_1: BamHI; Site_2: BglII;
 RescueMu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on RescueMu, go to the web
 site 'www.zmld.iastate.edu' and follow the links for
 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
 was extracted from leaf strips, double digested using
 BamHI and BglII, and ligated to form circular plasmids.
 DH10B cells were transformed and then screened on LB
 plates with ampicillin."

FEATURES

SOURCE

ORIGIN

Query Match 0.7%; Score 19; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
 Db 23 CAAAAAAAAAAAAAAAAA 5

RESULT 48
 CF280688 26 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ETL--07-H09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-H09,
 mRNA sequence.
 ACCESSION CF280688
 VERSION CF280688.1 GI:33658074
 SOURCE EST.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 26)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..26
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ETL--07-H09"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice etiolated leaf plasmid cDNA library
 (14ETL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

ORIGIN
 Query Match 0.7%; Score 19; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
 Db 21 CAAAAAAAAAAAAAAAAA 3

RESULT 49
 CN545723 26 bp mRNA linear EST 30-APR-2004
 LOCUS CN545723
 DEFINITION EST 17667 Ripe Grape Skin Triplex2 library vitifera cDNA
 clone B3CS00RL005C03 3', mRNA sequence.
 ACCESSION CN545723
 VERSION CN545723.1 GI:46910348
 SOURCE EST.
 ORGANISM Vitis vinifera
 Vitis vinifera
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; Vitaceae; Vitis.
 REFERENCE 1 (bases 1 to 26)
 Abbal,P., Agasse,A., Ageorges,A., Atanaseva,R., Barrieu,F.,
 Couture,C., Dedaldechamp,F., Delrot,S., Gliscent,D., Grimplet,J.,

TITLE Hamdi,S., Romieu,C. and Terrier,N.
 JOURNAL Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 Unpublished (2002)
 COMMENT Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Université de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourlaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: e.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES
 source
 1..26
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS00RL005C03"
 /dev_stage="ripening stage"
 /clone_lib="Ripe Grape Skin Triplex2 library"
 /note="Organ: Fruit skin; Vector: lambda Triplex2; Site 1:
 SfilA; Site 2: SfilB; Oriented library"

ORIGIN
 Query Match 0.7%; Score 19; DB 7; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
 Db 26 CAAAAAAAAAAAAAAAAA 8

RESULT 50
 CF299084 27 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--02-P02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--02-P02, mRNA
 sequence.
 ACCESSION CF299084
 VERSION CF299084.1 GI:33670845
 SOURCE EST.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 27)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..27
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--02-P02"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.7%; Score 19; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 23 CAAAAAAAAAAAAAAAAA 5

RESULT 51
CF310560/c 27 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--05-E14.B1 ABF3-overexpressing transgenic rice plasmid CDNA library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone ABF--05-E14, mRNA sequence.

ACCESSION CF310560.1 GI:33682321
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers
1..27

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--05-E14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid CDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 20 CAAAAAAAAAAAAAAAAA 2

RESULT 52
CF310745 27 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--05-J07.g1 ABF3-overexpressing transgenic rice plasmid CDNA library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone

ABF--05-J07, mRNA sequence.
CF310745
VERSION CF310745.1 GI:33682506
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers
1..27

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid CDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 5 CAAAAAAAAAAAAAAAAA 23

RESULT 53
CF311022/c 27 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--06-B07.g1 ABF3-overexpressing transgenic rice plasmid CDNA library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone ABF--06-B07, mRNA sequence.

ACCESSION CF311022.1 GI:33682783
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .27

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--06-B07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
CDNA library (ABP)"
/note="Vector: pCR4-TOPO, site 1: EcoRI; leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 54
LOCUS CN545777/c 27 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17721 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA
ACCESSION CN545777
VERSION CN545777.1 GI:46910402
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)
Abbal, P., Agasse, A., Ageorges, A., Atanaseva, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1. .27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL005G11"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

JOURNAL
COMMENT
TITLE
AUTHORS
REFERENCE
1 (bases 1 to 27)
Abbal, P., Agasse, A., Ageorges, A., Atanaseva, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1. .27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL005G11"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

ORIGIN

Query Match 0.7%; Score 19; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 27 CAAAAAAAAAAAAAAAAA 9

RESULT 55
LOCUS CN545880 27 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17824 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA
ACCESSION CN545880
VERSION CN545880.1 GI:46910505
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)
Abbal, P., Agasse, A., Ageorges, A., Atanaseva, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1. .27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL002H10"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

ORIGIN
Query Match 0.7%; Score 19; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 27 CAAAAAAAAAAAAAAAAA 9

RESULT 56
LOCUS N89936 27 bp mRNA linear EST 02-APR-1996
DEFINITION Zb32e12.s1 Soares fetal_lung_NbH19w Homo sapiens CDNA clone
IMAGE:302926 3' similar to gb:X59066 ATP SYNTHASE ALPHA CHAIN,
MITOCHONDRIAL PRECURSOR (HUMAN) ; mRNA sequence.
N89936
ACCESSION N89936.1 GI:1443263
VERSION N89936.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ORIGIN
Query Match 0.7%; Score 19; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 27)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maita, M.,
Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterson, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE
JOURNAL
COMMENT

The Maebur-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

FEATURES

source

Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: BT primer
High quality sequence stop: 8.

Location/Qualifiers

```
1..27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1247858"
/db_xref="taxon:9606"
/clone="IMAGE:302926"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal lung NDH19W"
/clone="Organ: lung; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-GTGTCACATCTGAAAGCGAGCGCGCAATTTTCTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Patricia Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NDH19W."
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ORIGIN

Query Match 0.7%; Score 19; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2661 CAAAAAAAAAAAAAAAAA 2679

Db 23 CAAAAAAAAAAAAAAAAA 5

RESULT 57
LOCUS

TA386G030 27 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 386G03, reverse sequence.

ACCESSION AL498287

VERSION AL498287.1 GI:11874009

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE
JOURNAL

Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 27)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrett, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

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1..27
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="386G03"
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ORIGIN

Query Match 0.7%; Score 19; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2661 CAAAAAAAAAAAAAAAAA 2679

Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 58
LOCUS

AL037026 28 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZps64H2264_r1 564 (synonym: hfb2) Homo sapiens cDNA clone
DKFZps64H2264, mRNA sequence.

ACCESSION AL037026

VERSION AL037026.1 GI:49681933

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

MIPS

Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany.

Location/Qualifiers

source

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1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZps64H2264"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="564 (synonym: hfb2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
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ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2661 CAAAAAAAAAAAAAAAAA 2679

Db 9 CAAAAAAAAAAAAAAAAA 27

RESULT 59

AL037270/c 28 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZP564E0970.s1.564 (synonym: hfbz2) Homo sapiens cDNA clone
DEFINITION DKFZP564E0970, mRNA sequence.
ACCESSION AL037270.1 GI:49681975
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Bloecker, H., Boecker, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Bloecker, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP564E0970"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="564 (synonym: hfbz2)"
/note="Vector: PAMPI, Site_1: NotI, Site_2: SalI"
ORIGIN
Query Match 0.7%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 20 CAAAAAAAAAAAAAAAAA 2
RESULT 60
AL037803/c 28 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZP564F027.s1.564 (synonym: hfbz2) Homo sapiens cDNA clone
DEFINITION DKFZP564F027, mRNA sequence.
ACCESSION AL037803
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Bloecker, H., Boecker, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Bloecker, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP564F027"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="564 (synonym: hfbz2)"
/note="Vector: PAMPI, Site_1: NotI, Site_2: SalI"
ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 19 CAAAAAAAAAAAAAAAAA 1
RESULT 61
AL039180/c 28 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZP566O204.r1.566 (synonym: hfk2) Homo sapiens cDNA clone
DEFINITION DKFZP566O204, mRNA sequence.
ACCESSION AL039180
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Bloecker, H., Boecker, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Bloecker, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566O204"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfk2)"
/note="Vector: PAMPI, Site_1: NotI, Site_2: SalI"
ORIGIN
Query Match 0.7%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 10 CAAAAAAAAAAAAAAAAA 28
RESULT 62
AL587582/c 28 bp mRNA linear EST 02-MAR-2001
LOCUS AL587582 BP Chicken Brain Library Gallus gallus cDNA clone
DEFINITION ROS059P03, mRNA sequence.
ACCESSION AL587582
VERSION EST.
KEYWORDS Gallus gallus (chicken)
SOURCE Gallus gallus
ORGANISM Gallus gallus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauiria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
AUTHORS Murray, F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Fraser Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK

Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCCGCCCTTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13P.

FEATURES

source

1..28
Location/Qualifiers
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059D03"
/issue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="vector: pSPORT1, Site 1: NotI, Site 2: SalI, Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3'; 3' adaptor sequence: 5'
GCCGCCCTTTT TTTT TTTT 3' Poly A RNA purchased from
Clontech (*6854-1)"

ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2661 CAAAAAAAAAAAAAAAAA 2679

Db 26 CAAAAAAAAAAAAAAAAA 8

RESULT 63
LOCUS BX554747 28 bp mRNA linear EST 10-OCT-2003
DEFINITION BX554747 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans CDNA clone Tse17c01_p1c, mRNA sequence.
ACCESSION BX554747
VERSION BX554747.1 GI:33378810
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 28)
Lehane, M.J., Akcey, S., Gibson, W., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Ronaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198

JOURNAL MEDLINE
PUBMED

COMMENT

Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.

FEATURES

source

1..28
Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse17c01_p1c"

/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T. Brucei"

ORIGIN

Query Match 0.7%; Score 19; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2661 CAAAAAAAAAAAAAAAAA 2679

Db 28 CAAAAAAAAAAAAAAAAA 10

RESULT 64
LOCUS CN545498 28 bp mRNA linear EST 30-APR-2004
DEFINITION CN545498 28 bp mRNA linear EST 30-APR-2004
clone B3CS00GL005G11 3', mRNA sequence.
ACCESSION CN545498
VERSION CN545498.1 GI:46910123
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 28)
Abbal, P., Agasse, A., Ageorges, A., Athanasova, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Gliscent, D., Grimplet, J.,
Hamdi, S., Komien, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES

source

1..28
Location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00GL005G11"
/dev_stage="green stage"
/clone_lib="Green Grape Skin Triplex2 library"
/note="Organ: Fruit skin; Vector: Lambda triplex2, Site 1:
5'ATA; Site 2: 5'ATB; Oriented library"

ORIGIN

Query Match 0.7%; Score 19; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2661 CAAAAAAAAAAAAAAAAA 2679

Db 28 CAAAAAAAAAAAAAAAAA 10

RESULT 65
LOCUS CN545659 28 bp mRNA linear EST 30-APR-2004
DEFINITION CN545659 28 bp mRNA linear EST 30-APR-2004
clone B3CS00RL004E11 3', mRNA sequence.


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ACCESSION  CN545659
VERSION     CN545659.1  GI:46910284
KEYWORDS
SOURCE      Vitis vinifera
ORGANISM    Eukaryota; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
            1 (bases 1 to 28)
REFERENCE   1 (bases 1 to 28)
AUTHORS     Abbel, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,
            Couture, C., Dedaldecamp, F., Delrot, S., Gilsant, D., Grimplet, J.,
            Hamdi, S., Romieu, C. and Terrier, N.
TITLE       Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
JOURNAL     Unpublished (2002)
COMMENT     Contract: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 61, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: 17.
FEATURES
source      Location/Qualifiers
            1..28
            /organism="Vitis vinifera"
            /mol_type="mRNA"
            /cultiVar="Cabernet Sauvignon"
            /db_xref="taxon:29760"
            /clone="B3CS00RL004E11"
            /dev_stage="ripening stage"
            /clone_lib="Ripe Grape Skin Triplex2 Library"
            /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
            SfiIA; Site_2: SfiIB; Oriented library"
ORIGIN
Query Match      0.7%; Score 19; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2661 CAAAAAAAAAAAAAAAAA 2679
Db 27 CAAAAAAAAAAAAAAAAA 9
RESULT 66
AZ481286/c 28 bp DNA linear GSS 04-OCT-2000
LOCUS      1M030124F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M030124 F, genomic survey sequence.
ACCESSION  AZ481286
VERSION    AZ481286.1  GI:10642351
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 28)
REFERENCE   1 (bases 1 to 28)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606

```

```

Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0303 row: 1 column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
FEATURES
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            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M030124"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PMD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PMD42 (GI|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
ORIGIN
Query Match      0.7%; Score 19; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2661 CAAAAAAAAAAAAAAAAA 2679
Db 28 CAAAAAAAAAAAAAAAAA 10
RESULT 67
AZ809971/c 28 bp DNA linear GSS 20-FEB-2001
LOCUS      2M0074C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0074C14 F, genomic survey sequence.
ACCESSION  AZ809971
VERSION    AZ809971.1  GI:12976769
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 28)
REFERENCE   1 (bases 1 to 28)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606

```


Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 1000 Std Error: 0.00
Plate: 0074 row: C column: 14
Seq primer: CTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 28.

FEATURES
source

1..28
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCM074C14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.7%; Score 19; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
|||
Db 28 CAAAAAAAAAAAAAAAAA 10

RESULT 68
AL038989 29 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZps566B184_r1.566 (synonym: hfkx2) Homo sapiens cDNA clone
DEFINITION DKFZps566B184, mRNA sequence.
ACCESSION AL038989
VERSION AL038989.1 GI:49682230
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 29)
REFERENCE Bloeker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Bioecker, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS

FEATURES

source
1..29
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZps566B184"

/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="XL1-2blue"
/clone_lib="566 (synonym: hfkx2)"
/note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
|||
Db 10 CAAAAAAAAAAAAAAAAA 28

RESULT 69
AL039052 29 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZps566F234_r1.566 (synonym: hfkx2) Homo sapiens cDNA clone
DEFINITION DKFZps566F234, mRNA sequence.
ACCESSION AL039052
VERSION AL039052.1 GI:49682239
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 29)
REFERENCE Bloeker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Bioecker, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers

FEATURES

source
1..29
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZps566F234"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="XL1-2blue"
/clone_lib="566 (synonym: hfkx2)"
/note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
|||
Db 10 CAAAAAAAAAAAAAAAAA 28

RESULT 70
AL048747 29 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZps566K043_r1.566 (synonym: hfkx2) Homo sapiens cDNA clone
DEFINITION DKFZps566K043, mRNA sequence.
ACCESSION AL048747
VERSION AL048747.1 GI:4727818
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 29)
REFERENCE Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehrer, et al.)

JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 FEATURES MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
 SOURCE Location/Qualifiers
 1. 29
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZPS66K043"
 /issue_type="Kidney"
 /dev_stage="fetal"
 /lab_host="X1-2blue"
 /clone_1ib="566 (synonym: hkd2)"
 /note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 0.7%; Score 19; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
 10 CAAAAAAAAAAAAAAAAA 28

RESULT 71
 B0590537 29 bp mRNA linear EST 06-DEC-2002
 LOCUS E012843-024-019-C03-T7 MP12-ADIS-024-storage root Beta vulgaris
 DEFINITION cDNA clone 024-019-C03 3-PRIME, mRNA sequence.
 ACCESSION B0590537
 VERSION B0590537.1 GI:26120120
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 29)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wzuck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelet,O.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 12472698
 Contact: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mp12-koeln.mpg.de
 Insert Length: 29 Std Error: 0.00
 Plate: 19 Row: C Column: 03
 Seq primer: T7; GTAATGACTCACTATAGGCGC.
 Location/Qualifiers
 1. 29
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:189579"
 /db_xref="taxon:161934"
 /clone="024-019-C03"
 /issue_type="storage root"
 /lab_host="EMDH10B"
 /clone_1ib="MP12-ADIS-024-storage root"
 /note="Vector: PCMVSPOR6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinzehnleber Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and

orientation:
 Spe-SalI-CCAGCGCTCCG-5prime-cDNA-polYA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 Project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

ORIGIN

Query Match 0.7%; Score 19; DB 5; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
 28 CAAAAAAAAAAAAAAAAA 10

RESULT 72
 BX551339/c 29 bp mRNA linear EST 10-OCT-2003
 LOCUS BX551339
 DEFINITION BX551339 Glossina morsitans morsitans adult infected gut Glossina
 morsitans morsitans cDNA clone Tse118a05_p1c, mRNA sequence.
 ACCESSION BX551339
 VERSION BX551339.1 GI:33375364
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 29)
 Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M.,
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina.
 morsitans morsitans and expression analysis of putative immune
 response genes
 Genome Biol. 4 (10), R63 (2003)
 22881942
 14519198
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5'
 end of the cDNA all p1c reads are from
 the 3' end.
 Location/Qualifiers
 1. 29
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse118a05_p1c"
 /issue_type="adult infected gut"
 /clone_1ib="Glossina morsitans morsitans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T. brucei"

ORIGIN

Query Match 0.7%; Score 19; DB 5; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
 29 CAAAAAAAAAAAAAAAAA 11

RESULT 73
BX553273/c
LOCUS
DEFINITION BX553273 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA Tse128d05_p1c, mRNA sequence.
ACCESSION BX553273
VERSION BX553273.1 GI:33377459
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 29)
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
FEATURES
source
1..29
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse128d05_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

ORIGIN
Query Match 0.7%; Score 19; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 29 CAAAAAAAAAAAAAAAAA 11

RESULT 74
BX55108/c
LOCUS
DEFINITION BX55108 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA Tse19e05_p1c, mRNA sequence.
ACCESSION BX55108
VERSION BX55108.1 GI:33379132
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 29)
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,

TITLE Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
FEATURES
source
1..29
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse19e05_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

ORIGIN
Query Match 0.7%; Score 19; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 29 CAAAAAAAAAAAAAAAAA 11

RESULT 75
BX55418/c
LOCUS
DEFINITION BX55418 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse20d06_p1c, mRNA sequence.
ACCESSION BX55418
VERSION BX55418.1 GI:33379412
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 29)
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES

source

Location/Qualifiers

1..29

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/note="country: Zimbabwe; EST from adult gut infected with T. brucei"

ORIGIN

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0.7%; Score 19; DB 5; Length 29;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679

Db 29 CAAAAAAAAAAAAAAAAA 11

Search completed: February 2, 2005, 23:31:50
Job time : 8232.78 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:07:10 / Search time 11376.2 Seconds
(without alignments)
11136.377 Million cell updates/sec

Title: US-10-048-046-1

Perfect score: 2679

Sequence: 1 aagaatcgcgcacgagcgcg.....acaaaaaaaaaaaaaaaaa 2679

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1393428

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
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6: gb_pat:*
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13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	0.8	21	6	AX825133 Sequence
C 2	20	0.7	21	6	AX825131 Sequence
C 3	20	0.7	21	6	AX825132 Sequence
C 4	20	0.7	21	6	AX825134 Sequence
C 5	20	0.7	21	6	AX825158 Sequence
C 6	20	0.7	25	6	AX825158 Sequence
C 7	20	0.7	25	6	AX825158 Sequence
C 8	20	0.7	30	6	AR051244 Sequence
C 9	20	0.7	30	6	AR127791 Sequence
C 10	20	0.7	30	6	AR127791 Sequence
C 11	19	0.7	30	6	AR139960 Sequence
C 12	19	0.7	20	6	AR140279 Sequence
C 13	19	0.7	20	6	AR140557 Sequence
C 14	19	0.7	21	6	AX825119 Sequence
C 15	19	0.7	21	6	AX825120 Sequence
C 16	19	0.7	21	6	AX825121 Sequence
C 17	19	0.7	21	6	AX825122 Sequence
C 18	19	0.7	21	6	AX825123 Sequence
C 19	19	0.7	21	6	AX825124 Sequence
C 19	19	0.7	21	6	AX825125 Sequence

C 20	19	0.7	21	6	AX825126 Sequence
C 21	19	0.7	21	6	AX825127 Sequence
C 22	19	0.7	21	6	AX825128 Sequence
C 23	19	0.7	21	6	AX825129 Sequence
C 24	19	0.7	21	6	AX825130 Sequence
C 25	19	0.7	21	6	AX825135 Sequence
C 26	19	0.7	21	6	AX825155 Sequence
C 27	19	0.7	21	6	AX825156 Sequence
C 28	19	0.7	21	6	AX825157 Sequence
C 29	19	0.7	21	6	AX825164 Sequence
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C 35	19	0.7	24	6	AX838365 Sequence
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C 38	19	0.7	25	6	AX338548 Sequence
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ALIGNMENTS

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RESULT 1
LOCUS AX825133/c 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 31 from Patent WO03072818.
ACCESSION AX825133
VERSION AX825133.1 GI:39750862
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

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REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 31 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
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DEFINITION Sequence 29 from Patent WO03072818.
ACCESSION AX825131
VERSION AX825131.1 GI:39750860
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 29 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
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ACCESSION AX825132
VERSION AX825132.1 GI:39750861
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ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 30 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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VERSION AX825134.1 GI:39750863
KEYWORDS
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artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 32 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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ACCESSION AX825158
VERSION AX825158.1 GI:39750887
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 56 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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ORIGIN

Query Match
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ACCESSION 129929
VERSION 129929.1 GI:1820720
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Pickup,D.J., Patel,D. and Antczak,J.B.
TITLE Site-specific RNA cleavage
JOURNAL Patent: US 5578468-A 42 26-NOV-1996;
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ORIGIN

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DEFINITION Sequence 12 from patent US 5830658.
ACCESSION AR051244
VERSION AR051244.1 GI:5974608
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
macromolecular structures
JOURNAL Patent: US 5830658-A 12 03-NOV-1998;
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ORIGIN

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DEFINITION Sequence 12 from patent US 6180777.
ACCESSION AR127791
VERSION AR127791.1 GI:14114386
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Horn,T.
TITLE Synthesis of branched nucleic acids
JOURNAL Patent: US 6180777-A 12 30-JAN-2001;
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ACCESSION 128373
VERSION 128373.1 GI:1819149
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
macromolecular structures
JOURNAL Patent: US 5571677-A 12 05-NOV-1996;
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DEFINITION AX825120
ACCESSION AX825120
VERSION AX825120.1 GI:39750849
KEYWORDS
SOURCE
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
METHOD for sorting single-stranded nucleic acids
PATENT: WO 03072818-A 18 04-SEP-2003;
Degussa Bioactives GmbH (DE)
LOCATION/Qualifiers

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ACCESSION AX825121
VERSION AX825121.1 GI:39750850
KEYWORDS
SOURCE
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
METHOD for sorting single-stranded nucleic acids
PATENT: WO 03072818-A 19 04-SEP-2003;
Degussa Bioactives GmbH (DE)
LOCATION/Qualifiers

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/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

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modified_base
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

modified_base
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/mod_base=OTHER

modified_base
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

modified_base
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

modified_base
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 16
AX825122/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 20 from Patent WO03072818.
DEFINITION AX825122
ACCESSION AX825122
VERSION AX825122.1 GI:39750851
KEYWORDS
SOURCE
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
METHOD for sorting single-stranded nucleic acids
PATENT: WO 03072818-A 20 04-SEP-2003;
Degussa Bioactives GmbH (DE)
LOCATION/Qualifiers

FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding
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/bound_moiety="Biotin"

modified_base
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/note="LNA-T (Locked Nucleic Acid) "
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modified_base
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

modified_base
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/mod_base=OTHER

modified_base
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/mod_base=OTHER

modified_base
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/mod_base=OTHER

/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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/mod_base=OTHER

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAAAAAA 2679
|||||
19 CAAAAAAAAAAAAAAAAAAAAA 1

Db 19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 17
AX825123/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 21 from Patent WO03072818.
DEFINITION AX825123
ACCESSION AX825123
VERSION AX825123.1 GI:39750852
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE

1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 21 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)

FEATURES

source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
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/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER 6
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER 12
modified_base 15
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER 18
modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAAAAAA 2679
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19 CAAAAAAAAAAAAAAAAAAAAA 1

Db 19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 18
AX825124/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 22 from Patent WO03072818.

DEFINITION Sequence 22 from Patent WO03072818.

ACCESSION AX825124
VERSION AX825124.1 GI:39750853
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE

1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 22 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)

FEATURES

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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
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/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
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modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER 12
modified_base 15
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER 18
modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAAAAAA 2679
|||||
19 CAAAAAAAAAAAAAAAAAAAAA 1

Db 19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 19
AX825125/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 23 from Patent WO03072818.
DEFINITION AX825125
ACCESSION AX825125
VERSION AX825125.1 GI:39750854
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE

1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 23 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)

FEATURES

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/db_xref="taxon:32630"
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Sequenz: Capture-Oligonukleotid"
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/bound_moiety="Biotin"

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modified_base 12 /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER
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ORIGIN

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Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1
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RESULT 20
AX825126/c AX825126 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825126
DEFINITION Sequence 24 from Patent WO03072818.
ACCESSION AX825126
VERSION AX825126.1 GI:39750855
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 24 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
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modified_base 6 /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
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ORIGIN

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modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
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modified_base 18 /mod_base=OTHER
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Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1
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RESULT 21
AX825127/c AX825127 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825127
DEFINITION Sequence 25 from Patent WO03072818.
ACCESSION AX825127
VERSION AX825127.1 GI:39750856
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 25 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
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modified_base 6 /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER
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ORIGIN

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Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1
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RESULT 22
AX825126/c AX825126 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825126
DEFINITION Sequence 26 from Patent WO03072818.
ACCESSION AX825126
VERSION AX825126.1 GI:39750857
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 26 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
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/bound_moiety="Biotin"
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modified_base 6 /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER
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AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 26 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
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/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/bound_molecy="Biotin"
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modified_base
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Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1
RESULT 23
AX825129/c AX825129 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 27 from Patent WO03072818.
ACCESSION AX825129
VERSION AX825129.1 GI:39750858
KEYWORDS
SOURCE .
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 27 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
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modified_base
21 /note="LNA-T (Locked Nucleic Acid) "
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Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1
RESULT 24
AX825130/c AX825130 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 28 from Patent WO03072818.
ACCESSION AX825130
VERSION AX825130.1 GI:39750859
KEYWORDS
SOURCE .
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 28 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
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Sequenz:Capture-Oligonukleotid"
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/bound_molecy="Biotin"
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6 /note="LNA-T (Locked Nucleic Acid) "
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Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1

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RESULT 25
LOCUS AX825155/c 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 53 from Patent WO03072818.
ACCESSION AX825155
VERSION AX825155.1 GI:39750884
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 53 04-SEP-2003,
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source location/Qualifiers
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Sequenz: Capture-Oligonukleotid"
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modified_base
21 /note="LNA-T (Locked Nucleic Acid)"
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ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2661 CAAAAAAAAAAAAAAAAAAAAA 2679
DB 20 CAAAAAAAAAAAAAAAAAAAAA 2
RESULT 26
LOCUS AX825156/c 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 54 from Patent WO03072818.
ACCESSION AX825156
VERSION AX825156.1 GI:39750885
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 54 04-SEP-2003,
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"

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/notes="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
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modified_base
21 /note="LNA-T (Locked Nucleic Acid)"
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ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2661 CAAAAAAAAAAAAAAAAAAAAA 2679
DB 20 CAAAAAAAAAAAAAAAAAAAAA 2
RESULT 27
LOCUS AX825157/c 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 55 from Patent WO03072818.
ACCESSION AX825157
VERSION AX825157.1 GI:39750886
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 55 04-SEP-2003,
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
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/db_xref="taxon:32630"
/notes="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
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modified_base
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modified_base
21 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
ORIGIN

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modified_base
18 /mod_base=OTHER
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
|||||
20 CAAAAAAAAAAAAAAAAA 2

RESULT 28
AX825164/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825164
DEFINITION Sequence 62 from Patent WO03072818.
ACCESSION AX825164
VERSION AX825164.1 GI:39750893
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 62 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
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/note="LNA-T (Locked Nucleic Acid)"
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ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
|||||
21 CAAAAAAAAAAAAAAAAA 3

RESULT 29
BD085544 22 bp RNA linear PAT 27-AUG-2002
LOCUS BD085544
DEFINITION Method of comparison and detection of RNA amount and DNA amount.
ACCESSION BD085544

VERSION BD085544.1 GI:22631154
KEYWORDS JP 2001333800-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 22)
AUTHORS Shimada, K.
TITLE Method of comparison and detection of RNA amount and DNA amount
JOURNAL Patent: JP 2001333800-A 1 04-DEC-2001;
UNITTECH CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2001333800-A/1
PD 04-DEC-2001
PF 30-MAY-2000 JP 2000160324
PI KAORI SHIMADA
PC C1201/68, C12N15/09, G01N33/50, C12N15/00
CC Method of comparison and detection of RNA amount and DNA amount

FEATURES
source FH Key location/Qualifiers
FT source 1. .22
/organism="Homo sapiens (human)".
1. .22
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
|||||
4 CAAAAAAAAAAAAAAAAA 22

RESULT 30
BD245230 23 bp DNA linear PAT 17-JUL-2003
LOCUS BD245230
DEFINITION Method of electrochemically detecting nucleic acid.
ACCESSION BD245230
VERSION BD245230.1 GI:33055000
KEYWORDS JP 2002532386-A/16.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 23)
AUTHORS Hartwich, G. and Heller, A.
TITLE Method of electrochemically detecting nucleic acid
JOURNAL Patent: JP 2002532386-A 16 02-OCT-2002;
FRIZ BIOCHEM GMBH
COMMENT OS Artificial Sequence
PN JP 2002532386-A/16
PD 02-OCT-2002
PF 19-NOV-1999 JP 2000583928
PR 23-NOV-1998 DE 198 53 957.6, 29-APR-1999 DE 199 21 940.0 PI
GERHARD HARTWICH, ADAM HELLER
PC C07H21/00, C07H21/02, C07H21/04, C12N15/09, C1201/68, G01N27/12, PC
G01N27/30,
PC G01N27/416, G01N27/48, G01N33/483, G01N33/50, G01N33/566, C12N15/00, PC
G01N27/46
CC Method of electrochemically detecting nucleic acid FH Key
location/Qualifiers
FT source 1. .23
/organism="Artificial Sequence".
1. .23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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Query Match      0.7%; Score 19; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2661 CAAAAAAAAAAAAAAAAAAAAA 2679
Db      5 CAAAAAAAAAAAAAAAAAAAAA 23

RESULT 31
BD196419/c      24 bp      DNA      linear      PAT 17-JUN-2003
LOCUS      Prostatic cancer gene.
DEFINITION      BD196419
ACCESSION      BD196419.1 GI:33006189
VERSION      JP 2002516657-A/8.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
TITLE      Prostatic cancer gene
JOURNAL      Patent: JP 2002516657-A 8 11-JUN-2002;
GENSET

COMMENT
OS      Homo sapiens (human)
PN      JP 2002516657-A/8
PD      11-JUN-2002
PF      22-DEC-1998 JP 2000525562
PR      22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
DANIEL COHEN,MARTA BLUMENFELD,IIVA CHUMAKOV,LYDIE BOUGUELERET PC
C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19
PC      C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
,C12N15/00,C12N5/00
PC      C12N5/00,C12N15/00
CC      primer oligonucleotide PGR32
FH      key      Location/Qualifiers
FT      misc binding 1..24.
            Location/Qualifiers
            1..24
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            /db_xref="taxon:9606"

ORIGIN
Query Match      0.7%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2661 CAAAAAAAAAAAAAAAAAAAAA 2679
Db      20 CAAAAAAAAAAAAAAAAAAAAA 2

RESULT 32
AR431312      24 bp      DNA      linear      PAT 18-DEC-2003
LOCUS      AR431312
DEFINITION      Sequence 6 from patent US 6651008.
ACCESSION      AR431312
VERSION      AR431312.1 GI:40193280
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Vaisberg,E.A., Adams,C.L., Sabry,U.H. and Crompton,A.M.
TITLE      Database system including computer code for predictive cellular
JOURNAL      bioinformatics
FEATURES      Patent: US 6651008-A 6 18-NOV-2003;
            Location/Qualifiers

ORIGIN

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source
1..24
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      0.7%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2660 AAAAAAAAAAAAAAAAAAAAAA 2678
Db      20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 33
AX817782      24 bp      DNA      linear      PAT 10-DEC-2003
LOCUS      AX817782
DEFINITION      Sequence 18 from Patent WO02067861.
ACCESSION      AX817782
VERSION      AX817782.1 GI:39722977
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
            artificial sequences.

TITLE      Oncolytic adenoviral vectors
JOURNAL      Patent: WO 02067861-A 18 06-SEP-2002;
FEATURES      Location/Qualifiers
            1..24
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Viral vector sequence"
            1..24
            /note="Fig. 1C. SV40 early Poly(A) site"
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ORIGIN
polyA_site

misc_feature
1..24
/note="Fig. 1C. SV40 early Poly(A) site"
3..24

ORIGIN
Query Match      0.7%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2661 CAAAAAAAAAAAAAAAAAAAAA 2679
Db      2 CAAAAAAAAAAAAAAAAAAAAA 20

RESULT 34
AX838369      24 bp      DNA      linear      PAT 15-DEC-2003
LOCUS      AX838369
DEFINITION      Sequence 8 from Patent WO02068627.
ACCESSION      AX838369
VERSION      AX838369.1 GI:39922050
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
            artificial sequences.

TITLE      Vector constructs
JOURNAL      Patent: WO 02068627-A 8 06-SEP-2002;
FEATURES      Location/Qualifiers
            1..24
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Viral vector sequence"
            1..24
            /note="Fig. 1C. SV40 early Poly(A) site"
            3..24

ORIGIN
polyA_site

misc_feature
1..24
/note="Fig. 1C. SV40 early Poly(A) site"
3..24

ORIGIN

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Query Match 0.7%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 2 CAAAAAAAAAAAAAAAAA 20

RESULT 35
BD097127/c 24 bp DNA linear PAT 27-AUG-2002
DEFINITION Support for immobilizing nucleotide and process for producing the same.
ACCESSION BD097127
VERSION BD097127.1 GI:22642701
KEYWORDS WO 0155365-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Tanga,M., Okamura,H., Takagi,K. and Takahashi,K.
TITLE Support for immobilizing nucleotide and process for producing the
JOURNAL Patent: WO 0155365-A 1 02-AUG-2001;
TOYO KOHAN CO LTD,MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,
KOJIRO TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0155365-A/1
PD 02-AUG-2001
PF 24-JAN-2001 WO 2001JP000443
PR 27-JAN-2000 JP 00P 019301
PI MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,KOJIRO PI
TAKAHASHI
PC C12N15/10,C07H21/04//G01N33/50,C1201/68
CC Support for immobilizing nucleotide and process for producing
the same
FT source 1..24
Key Location/Qualifiers
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
1..24
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 24 CAAAAAAAAAAAAAAAAA 6

RESULT 36
BD161931/c 24 bp DNA linear PAT 17-JAN-2003
LOCUS Method for carrying out thermal cycle of PCR using DNA-immobilized
DEFINITION substrate.
ACCESSION BD161931
VERSION BD161931.1 GI:27867689
KEYWORDS JP 2002191369-A/8.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Tanga,M., Okamura,H. and Takahashi,K.
TITLE Method for carrying out thermal cycle of PCR using DNA-immobilized
JOURNAL Patent: JP 2002191369-A 8 09-JUL-2002;
TOYO KOHAN CO LTD,KOJIRO TAKAHASHI
COMMENT OS Artificial Sequence

PN JP 2002191369-A/8
PD 09-JUL-2002
PF 27-DEC-2000 JP 2000399573
PI MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC Method for
carrying out thermal cycle of PCR using DNA- CC
immobilized
CC substrate
FT key Location/Qualifiers
FT source 1..24
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
1..24
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 24 CAAAAAAAAAAAAAAAAA 6

RESULT 37
AX338548 25 bp DNA linear PAT 09-JAN-2002
LOCUS Sequence 4 from Patent WO0188192.
DEFINITION AX338548
ACCESSION AX338548
VERSION AX338548.1 GI:18128948
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Nicolaides,N.C., Sasse,P.M., Grasso,L., Vogelstein,B. and
Kinzler,K.W.
TITLE A method for generating hypermutable organisms
JOURNAL Patent: WO 0188192-A 4 22-NOV-2001;
The Johns Hopkins University School of Medicine (US) ; Morphorek
Inc. (US) ; Nicolaides, Nicholas, C. (US) ; Sasse, Philip, M. (US) ;
Grasso, Luigi (US) ; Vogelstein, Bert (US)
FEATURES
source
1..25
Location/Qualifiers
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/db_xref="taxon:32630"
/note="Recombinant DNA"

ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 5 CAAAAAAAAAAAAAAAAA 23

RESULT 38
AX394507 25 bp DNA linear PAT 18-MAY-2002
LOCUS Sequence 52 from Patent WO0218638.
DEFINITION AX394507
ACCESSION AX394507
VERSION AX394507.1 GI:21065645
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
artificial sequences.

AUTHORS Risinger, C., Andersson, M.K., Lewander, T. and Olsson, E.
 TITLE Detection of cyp2d6 polymorphisms
 JOURNAL Patent: WO 0218638-A 52 07-MAR-2002;
 Gemini Genomics PLC (GB)
 FEATURES Location/Qualifiers
 SOURCE 1..25
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic oligonucleotide"
 ORIGIN
 Query Match 0.7%; Score 19; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2661 CAAAAAAAAAAAAAAAAA 2679
 DB 2 CAAAAAAAAAAAAAAAAA 20
 RESULT 39
 LOCUS AX394514 25 bp DNA linear PAT 18-MAY-2002
 DEFINITION Sequence 59 from Patent WO0218638.
 ACCESSION AX394514
 VERSION AX394514.1 GI:21065652
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Risinger, C., Andersson, M.K., Lewander, T. and Olsson, E.
 TITLE Detection of cyp2d6 polymorphisms
 JOURNAL Patent: WO 0218638-A 59 07-MAR-2002;
 Gemini Genomics PLC (GB)
 FEATURES Location/Qualifiers
 SOURCE 1..25
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic oligonucleotide"
 ORIGIN
 Query Match 0.7%; Score 19; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2661 CAAAAAAAAAAAAAAAAA 2679
 DB 24 CAAAAAAAAAAAAAAAAA 6
 RESULT 40
 LOCUS BD192375 26 bp DNA linear PAT 17-JUL-2003
 DEFINITION Reagents and methods useful for detecting diseases of the breast.
 ACCESSION BD192375
 VERSION BD192375.1 GI:33002114
 KEYWORDS JP 2002516576-A/14.
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 MODEL P.A.B., Cohen, M., Colpiter, T.L., Friedman, P.N., Gordon, J.,
 Grandos, E.N., Hodges, S.C., Klags, M.R., Kratochvil, J.D.,
 Russell, J.C., Scheffel, C.P., Stroupe, S.D. and Yu, H.
 Reagents and methods useful for detecting diseases of the breast
 Patent: JP 2002516576-A 14 04-JUN-2002;
 ABBOTT LABORATORIES
 JOURNAL ABOTT LABORATORIES
 TITLE Patent: JP 2002516576-A/14
 JOURNAL PD 04-JUN-2002

PF 19-JUN-1998 JP 199504891
 PR 20-JUN-1997 US 08/879354
 PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
 PI N FRIEDMAN,
 PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI
 KLAGS,
 PI JON D KRATOCHVIL, JOHN C RUSSELL, CHRISTI P SCHEFFEL, STEPHEN D
 PI STROUBE,
 PI HONG YU
 PC C12N15/12, C07K14/47, C12Q1/68, C12N15/85, C12N5/10, C07K16/18, PC
 G01N33/574
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers.
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 SOURCE 1..26
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 /db_xref="taxon:10095"
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 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2661 CAAAAAAAAAAAAAAAAA 2679
 DB 26 CAAAAAAAAAAAAAAAAA 8
 RESULT 41
 LOCUS I79496 26 bp DNA linear PAT 10-JUN-1998
 DEFINITION Sequence 3 from patent US 5707807.
 ACCESSION I79496
 VERSION I79496.1 GI:3207786
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Kato, K.
 TITLE Molecular indexing for expressed gene analysis
 JOURNAL Patent: US 5707807-A 3 13-JAN-1998;
 FEATURES Location/Qualifiers
 SOURCE 1..26
 /organism="unknown"
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 ORIGIN
 Query Match 0.7%; Score 19; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2661 CAAAAAAAAAAAAAAAAA 2679
 DB 26 CAAAAAAAAAAAAAAAAA 8
 RESULT 42
 LOCUS AX338547 26 bp DNA linear PAT 09-JAN-2002.
 DEFINITION Sequence 3 from Patent WO0188192.
 ACCESSION AX338547
 VERSION AX338547.1 GI:18128947
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Nicolaides, N.C., Sass, P.M., Grasso, L., Vogelstein, B. and
 Kinzler, K.W.

TITLE A method for generating hypermutable organisms
JOURNAL Patent: WO 0188192-A 3 22-NOV-2001;
The Johns Hopkins University School of Medicine (US) ; Morphotek
Inc. (US) ; Nicolaides, Nicholas, C. (US) ; Saas, Philip, W. (US) ;
Grasso, Luigi (US) ; Vogelstein, Bert (US)

FEATURES
source 1. .26
/organism="synthetic construct"
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ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
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5 CAAAAAAAAAAAAAAAAA 23

RESULT 43
BD097128 27 bp DNA linear PAT 27-AUG-2002
LOCUS Support for immobilizing nucleotide and process for producing the
DEFINITION same.

ACCESSION BD097128
VERSION BD097128.1 GI:22642702
KEYWORDS WO 0155365-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 27)
Tanga,M., Okamura,H., Takagi,K. and Takahashi,K.
Support for immobilizing nucleotide and process for producing the
Patent: WO 0155365-A 2 02-AUG-2001;
TOYO KOHAN CO LTD, MICHIFUMI TANGA, HIROSHI OKAMURA, KENICHI TAKAGI,
KOJIRO TAKAHASHI

REFERENCE 1 (bases 1 to 27)
Tanga,M., Okamura,H., Takagi,K. and Takahashi,K.
Support for immobilizing nucleotide and process for producing the
Patent: WO 0155365-A 2 02-AUG-2001;
TOYO KOHAN CO LTD, MICHIFUMI TANGA, HIROSHI OKAMURA, KENICHI TAKAGI,
KOJIRO TAKAHASHI

COMMENT OS Artificial Sequence
PN WO 0155365-A/2
PD 02-AUG-2001
PF 24-JAN-2001 WO 2001JP000443
PR 27-JAN-2000 JP 00P 019301
PI MICHIFUMI TANGA, HIROSHI OKAMURA, KENICHI TAKAGI, KOJIRO
TAKAHASHI

PC C12N15/10,C07H21/04//G01N33/50,C12Q1/68
CC Support for immobilizing nucleotide and process for producing
the same
C12N15/10,C07H21/04//G01N33/50,C12Q1/68
CC Support for immobilizing nucleotide and process for producing
the same
FH Key
FT source 1. .27
Location/Qualifiers
1. .27
/organism="Artificial Sequence".
Location/Qualifiers
1. .27
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
|||||
5 CAAAAAAAAAAAAAAAAA 23

RESULT 44
BD161932 27 bp DNA linear PAT 17-JAN-2003
LOCUS Method for carrying out thermal cycle of PCR using DNA-immobilized
DEFINITION substrate.

ACCESSION BD161932
VERSION BD161932.1 GI:27867690
KEYWORDS JP 2002191369-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 27)
Tanga,M., Okamura,H. and Takahashi,K.
Method for carrying out thermal cycle of PCR using DNA-immobilized
substrate
Patent: JP 2002191369-A 9 09-JUL-2002;
TOYO KOHAN CO LTD, KOJIRO TAKAHASHI

COMMENT OS Artificial Sequence
PN JP 2002191369-A/9
PD 09-JUL-2002
PF 27-DEC-2000 JP 2000399573
PI MICHIFUMI TANGA, HIROSHI OKAMURA, KOJIRO TAKAHASHI
PC C12N15/09,C12N15/09,C12Q1/68,C12N15/00 CC Method for
carrying out thermal cycle of PCR using DNA- CC
immobilized
CC substrate
FH Key
FT source 1. .24
Location/Qualifiers
1. .24
/organism="Artificial Sequence".
Location/Qualifiers
1. .27
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
|||||
5 CAAAAAAAAAAAAAAAAA 23

RESULT 45
AX391845 28 bp RNA linear PAT 23-MAR-2002
LOCUS Sequence 10 from Patent WO0216574.
DEFINITION AX391845
ACCESSION AX391845
VERSION AX391845.1 GI:19700427
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
Reimholz,R. and Ploeger,F.
Method for identifying peptides that can be specifically cleaved
and the use of peptide sequences of this type
Patent: WO 0216574-A 10 28-FEB-2002;
Xzillion GmbH & Co.KG (DE)

FEATURES

source 1. .28
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Puromycin-Linker-RNA-Tail"

ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
|||||
10 CAAAAAAAAAAAAAAAAA 28

RESULT 46
LOCUS AR438517 29 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7 from patent US 6664064.
ACCESSION AR438517
VERSION AR438517.1 GI:42663388
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dietmaier,W.
TITLE Method for melting curve analysis of repetitive PCR products
JOURNAL Patent: US 6664064-A 7 16-DEC-2003;
FEATURES location/Qualifiers
source 1..29
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 29;
Best Local Similarity 100.0%; Pred.No.1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 1 CAAAAAAAAAAAAAAAAA 19

RESULT 47
LOCUS AX430216 29 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 7 from Patent EP1207210.
ACCESSION AX430216
VERSION AX430216.1 GI:21655581
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Dietmaier,W.
TITLE Method for melting curve analysis of repetitive PCR products
JOURNAL Patent: EP 1207210-A 7 22-MAY-2002;
FEATURES Roche Diagnostics GmbH (DE) ; F. HOFMANN-LA ROCHE AG (CH)
location/Qualifiers
source 1..29
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 29;
Best Local Similarity 100.0%; Pred.No.1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 1 CAAAAAAAAAAAAAAAAA 19

RESULT 48
LOCUS BD165919 29 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for melting curve analysis of repetitive PCR products.
ACCESSION BD165919
VERSION BD165919.1 GI:27871731
KEYWORDS JP 2002191384-A/7.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 29)
AUTHORS Dietmaier,W.

TITLE Method for melting curve analysis of repetitive PCR products
JOURNAL Patent: JP 2002191384-A 7 09-JUL-2002;
COMMENT F HOFMANN LA ROCHE AG
OS Homo sapiens (human)
FN JP 2002191384-A/7
PD 09-JUL-2002
PF 13-NOV-2001 JP 2001348017
PR 15-NOV-2000 EP 00124897.0
PT WOLFGANG DIETMAIER
PC C12N15/09,C12Q1/68,C12N15/00
CC Method for melting curve analysis of repetitive PCR products
FH Key location/Qualifiers
FT source 1..29
/organism="Homo sapiens (human)"

FEATURES location/Qualifiers
source 1..29
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 29;
Best Local Similarity 100.0%; Pred.No.1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 1 CAAAAAAAAAAAAAAAAA 19

RESULT 49
LOCUS AX079108 30 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 6 from Patent WO0106226.
ACCESSION AX079108
VERSION AX079108.1 GI:13158682
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mueller,O.
TITLE Methods for determining the proliferation activity of cells
JOURNAL Patent: WO 0106226-A 6 25-JAN-2001;
FEATURES Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
location/Qualifiers
source 1..30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 30;
Best Local Similarity 100.0%; Pred.No.1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 6 CAAAAAAAAAAAAAAAAA 24

RESULT 50
LOCUS AX079109/c 30 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 7 from Patent WO0106226.
ACCESSION AX079109
VERSION AX079109.1 GI:13158683
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1

AUTHORS Mueller,O.
TITLE Methods for determining the proliferation activity of cells
JOURNAL Patent: WO 0106226-A 7 25-JAN-2001;
Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
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/db_xref="taxon:33630"
/note="Oligonucleotide"
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Query Match 0.7%; Score 19; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2661 CMAAAAAAAAAAAAAA 2679
Db 29 CMAAAAAAAAAAAAAA 11
RESULT 51
AR034896/c AR034896 18 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 12 from patent US 5869643.
ACCESSION AR034896
VERSION AR034896.1 GI:5950501
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chateletain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a
JOURNAL Patent: US 5869643-A 12 09-FEB-1999;
FEATURES location/Qualifiers
source 1. .18
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/mol_type="unassigned DNA"
ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 52
AR034899 AR034899 18 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 18 from patent US 5869643.
ACCESSION AR034899
VERSION AR034899.1 GI:5950504
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chateletain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a
JOURNAL Patent: US 5869643-A 18 09-FEB-1999;
FEATURES location/Qualifiers
source 1. .18
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/mol_type="unassigned DNA"
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Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 53
AR058305 AR058305 18 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 3 from patent US 5837820.
ACCESSION AR058305
VERSION AR058305.1 GI:5983882
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS De Rose,R., Douce,R., Duval,M., Job,C. and Job,D.
TITLE Seed specific biotinylated protein, SBPE5, from leguminous plants
JOURNAL Patent: US 5837820-A 3 17-NOV-1998;
FEATURES location/Qualifiers
source 1. .18
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/mol_type="unassigned DNA"
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Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 54
AR097579/c AR097579 18 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 9 from patent US 6071745.
ACCESSION AR097579
VERSION AR097579.1 GI:12806309
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.,Patsy., Wallace,R.Bruce., Coseman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to
preserve RNA and DNA contained in cells for use in molecular
biology experiments
JOURNAL Patent: US 6071745-A 9 06-JUN-2000;
FEATURES location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 55
AR106506 AR106506 18 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 30 from patent US 6107060.
ACCESSION AR106506

AUTHORS Mueller,O.
TITLE Methods for determining the proliferation activity of cells
JOURNAL Patent: WO 0106226-A 7 25-JAN-2001;
Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES
source 1. .30
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/mol_type="unassigned DNA"
/db_xref="taxon:33630"
/note="Oligonucleotide"
ORIGIN
Query Match 0.7%; Score 19; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2661 CMAAAAAAAAAAAAAA 2679
Db 29 CMAAAAAAAAAAAAAA 11
RESULT 51
AR034896/c AR034896 18 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 12 from patent US 5869643.
ACCESSION AR034896
VERSION AR034896.1 GI:5950501
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chateletain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a
JOURNAL Patent: US 5869643-A 12 09-FEB-1999;
FEATURES location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 52
AR034899 AR034899 18 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 18 from patent US 5869643.
ACCESSION AR034899
VERSION AR034899.1 GI:5950504
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chateletain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a
JOURNAL Patent: US 5869643-A 18 09-FEB-1999;
FEATURES location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 53
AR058305 AR058305 18 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 3 from patent US 5837820.
ACCESSION AR058305
VERSION AR058305.1 GI:5983882
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS De Rose,R., Douce,R., Duval,M., Job,C. and Job,D.
TITLE Seed specific biotinylated protein, SBPE5, from leguminous plants
JOURNAL Patent: US 5837820-A 3 17-NOV-1998;
FEATURES location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 54
AR097579/c AR097579 18 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 9 from patent US 6071745.
ACCESSION AR097579
VERSION AR097579.1 GI:12806309
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.,Patsy., Wallace,R.Bruce., Coseman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to
preserve RNA and DNA contained in cells for use in molecular
biology experiments
JOURNAL Patent: US 6071745-A 9 06-JUN-2000;
FEATURES location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 55
AR106506 AR106506 18 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 30 from patent US 6107060.
ACCESSION AR106506

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VERSION      AR106506.1  GI:12821036
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      1 (bases 1 to 18)
TITLE        Keeling, P. and Guan, H.
JOURNAL      Starch encapsulation
FEATURES     Patent: US 6107060-A 30 22-AUG-2000;
SOURCE       Location/Qualifiers
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            /mol_type="unassigned DNA"

ORIGIN
Query Match      0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2662 AAAAAAAAAAAAAAAAAA 2679
Db      1 AAAAAAAAAAAAAAAAAA 18

RESULT 56
BD222596/c 18 bp DNA linear PAT 17-JUL-2003
DEFINITION  Aminooxy-modified nucleoside compound and oligomer compound
ACCESSION  BD222596
VERSION    BD222596
KEYWORDS   BD222596.1 GI:33032366
SOURCE     JP 2002522447-A/14.
ORGANISM   synthetic construct
REFERENCE   1 (bases 1 to 18)
AUTHORS     Manoharan, M., Cook, P.D., Prakash, T.P. and Kawasaki, A.M.
TITLE       Aminooxy-modified nucleoside compound and oligomer compound
JOURNAL     Patent: JP 2002522447-A 14 23-JUL-2002;
COMMENT     ISIS PHARMACEUTICALS INC
            OS Artificial Sequence
            PN JP 2002522447-A/14
            PD 23-JUL-2002
            PF 09-AUG-1999 JP 2000563675
            PR 07-AUG-1998 US 09/130973
            PI MUTIRAH MANOHARAN, PHILIP DAN COOK, THAZHA P PRAKASH, ANDREW M
            PI KAWASAKI
            PC C07H19/167, C07H19/067, C07H19/10, C07H19/20, C07H21/02, C12N15/00,
            CC C12N15/00
            CC Description of Artificial Sequence: antisense sequence FH
            KEY Location/Qualifiers
            FT source 1..18
            /organism="Artificial Sequence".
            /location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

ORIGIN
Query Match      0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2662 AAAAAAAAAAAAAAAAAA 2679
Db      1 AAAAAAAAAAAAAAAAAA 18

RESULT 57
E28535 18 bp DNA linear PAT 18-JUN-2001
LOCUS    E28535

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DEFINITION  Method for labeling oligonucleotide and utilization thereof.
ACCESSION  E28535
VERSION    E28535.1 GI:13025387
KEYWORDS   JP 1999075880-A/2.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE   Unclassified.
AUTHORS      1 (bases 1 to 18)
TITLE        Kenichi, H., Hiroshi, Y. and Masahide, N.
JOURNAL      Method for labeling oligonucleotide and utilization thereof
FEATURES     Patent: JP 1999075880-A 2 23-MAR-1999;
SOURCE       CHEMO SERO THERAPEUT RES INST
            OS Unidentified
            PN JP 1999075880-A/2
            PD 23-MAR-1999
            PF 10-JUL-1998 JP 1998195719
            PR KENICHI HANAKI, HIROSHI YOSHIKURA, MASAHIDE NOZAKI PC
            PI C12N15/09, C12Q1/68, G01N33/58, C12N15/00
            CC Strandedness: Single;
            CC Topology: Linear;
            CC Key
            FT source 1..18
            /location/Qualifiers
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            /location/Qualifiers
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            /db_xref="taxon:32644"

ORIGIN
Query Match      0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2662 AAAAAAAAAAAAAAAAAA 2679.
Db      1 AAAAAAAAAAAAAAAAAA 18

RESULT 58
E28536/c 18 bp DNA linear PAT 18-JUN-2001
LOCUS    E28536
DEFINITION  Method for labeling oligonucleotide and utilization thereof.
ACCESSION  E28536
VERSION    E28536.1 GI:13025388
KEYWORDS   JP 1999075880-A/3.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE   Unclassified.
AUTHORS      1 (bases 1 to 18)
TITLE        Kenichi, H., Hiroshi, Y. and Masahide, N.
JOURNAL      Method for labeling oligonucleotide and utilization thereof
COMMENT     Patent: JP 1999075880-A 3 23-MAR-1999;
            CHEMO SERO THERAPEUT RES INST
            OS Unidentified
            PN JP 1999075880-A/3
            PD 23-MAR-1999
            PF 10-JUL-1998 JP 1998195719
            PR KENICHI HANAKI, HIROSHI YOSHIKURA, MASAHIDE NOZAKI PC
            PI C12N15/09, C12Q1/68, G01N33/58, C12N15/00
            CC Strandedness: Single;
            CC Topology: Linear;
            CC Key
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            /db_xref="taxon:32644"

ORIGIN

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Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 59
LOCUS I79509 18 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 16 from patent US 5707807.
ACCESSION I79509
VERSION I79509.1 GI:3207799
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 16 13-JAN-1998;
FEATURES Location/Qualifiers
1. 18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 60
LOCUS AR208426 18 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6383754.
ACCESSION AR208426
VERSION AR208426.1 GI:21509577
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaufman,J.C., Koch,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: US 6383754-A 6 07-MAY-2002;
FEATURES Location/Qualifiers
1. 18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2660 AAAAAAAAAAAAAAAAAA 2677
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 61
LOCUS AR215435 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 9 from patent US 6410321.
ACCESSION AR215435

VERSION AR215435.1 GI:23313691
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.P., Wallace,R.B., Cosman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to preserve RNA and DNA contained in cells for use in molecular biology experiments
JOURNAL Patent: US 6410321-A 9 25-JUN-2002;
FEATURES Location/Qualifiers
1. 18
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 62
LOCUS AR222464 18 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 24 from patent US 6429300.
ACCESSION AR222464
VERSION AR222464.1 GI:23329995
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 24 06-AUG-2002;
FEATURES Location/Qualifiers
1. 18
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 63
LOCUS AR412363 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6639062.
ACCESSION AR412363
VERSION AR412363.1 GI:40167473
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified nucleosidic compounds and oligomeric compounds prepared therefrom
JOURNAL Patent: US 6639062-A 14 28-OCT-2003;
FEATURES Location/Qualifiers
1. 18
/organism="unknown"

ORIGIN /mol_type="genomic DNA"

Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 64
LOCUS AR473365 18 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9 from patent US 6686460.
ACCESSION AR473365
VERSION AR473365.1 GI:42708816
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin, C.-I.P., Wallace, R.B., Coesman, V. and French, C.
TITLE Method and formulation for lyophilizing cultured human cells to preserve RNA and DNA contained in cells for use in molecular biology experiments
JOURNAL Patent: US 6686460-A 9 03-FEB-2004;
FEATURES Location/Qualifiers
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source /organism="unknown"
/mol_type="genomic DNA"

ORIGIN /mol_type="genomic DNA"

Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 65
LOCUS AR487019 18 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 6 from patent US 6706476.
ACCESSION AR487019
VERSION AR487019.1 GI:47251966
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Thirstrup, K., Warthoe, P. and Petersen, N.B.
TITLE Process for amplifying and labeling single stranded cDNA by 5' ligated adaptor mediated amplification
JOURNAL Patent: US 6706476-A 6 16-MAR-2004;
FEATURES Location/Qualifiers
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source /organism="unknown"
/mol_type="genomic DNA"

ORIGIN /mol_type="genomic DNA"

Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 66
LOCUS AR487020 18 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 7 from patent US 6706476.
ACCESSION AR487020
VERSION AR487020.1 GI:47251967
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Thirstrup, K., Warthoe, P. and Petersen, N.B.
TITLE Process for amplifying and labeling single stranded cDNA by 5' ligated adaptor mediated amplification
JOURNAL Patent: US 6706476-A 7 16-MAR-2004;
FEATURES Location/Qualifiers
1..18
source /organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 67
LOCUS AX004875 18 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 4 from Patent W0910527.
ACCESSION AX004875
VERSION AX004875.1 GI:9928275
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bayer, E. and Schewitz, J.
TITLE Method for isolating anionic organic substances from aqueous systems using cationic polymeric nanoparticles
JOURNAL Patent: WO 9910527-A 4 04-MAR-1999;
FEATURES Location/Qualifiers
1..18
source /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3' palmitoyl oligonucleotide"

ORIGIN

Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 68
LOCUS AX004879 18 bp RNA linear PAT 24-AUG-2000
DEFINITION Sequence 8 from Patent W0910527.
ACCESSION AX004879
VERSION AX004879.1 GI:9928279
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Bayer, E. and Schwelitz, J.
TITLE Method for isolating anionic organic substances from aqueous systems using cationic polymer nanoparticles
JOURNAL Patent: WO 9910527-A 8 04-MAR-1999;
SUBDEUTSCHE KALCKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="2' methyl-modified oligonucleotide"
modified_base 1..18
/mod_base=um
ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 69
LOCUS AX008117 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 2 from Patent WO9967378.
ACCESSION AX008117
VERSION AX008117.1 GI:9995742
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha, M.J., Parniak, M.A., Wilds, C., Arion, D., Noronha, A.M. and Borkow, G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL Patent: WO 9967378-A 2 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"
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Query Match 0.7%; Score 18; DB 6; Length 18;
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Db 18 AAAAAAAAAAAAAAAAAA 1

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DEFINITION Sequence 3 from Patent WO9967378.
ACCESSION AX008118
VERSION AX008118.1 GI:9995743
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha, M.J., Parniak, M.A., Wilds, C., Arion, D., Noronha, A.M. and

TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL Patent: WO 9967378-A 3 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
FEATURES Location/Qualifiers
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/note="Use as an oligomer"
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 71
LOCUS AX008122/c 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 7 from Patent WO9967378.
ACCESSION AX008122
VERSION AX008122.1 GI:9995747
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha, M.J., Parniak, M.A., Wilds, C., Arion, D., Noronha, A.M. and Borkow, G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL Patent: WO 9967378-A 7 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
FEATURES Location/Qualifiers
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Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 72
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DEFINITION Sequence 8 from Patent WO9967378.
ACCESSION AX008123
VERSION AX008123.1 GI:9995748
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha, M.J., Parniak, M.A., Wilds, C., Arion, D., Noronha, A.M. and Borkow, G.

TITLE
Antisense oligonucleotide constructs based on beta -arabino furanose
and its analogues
JOURNAL
Patent: WO 967378-A 8 29-DEC-1999;
DAMIA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
(CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
BORKOW GADI (IL)

FEATURES
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Location/Qualifiers
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RESULT 73
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DEFINITION Sequence 29 from Patent WO9732023.
ACCESSION AX028845
VERSION AX028845.1 GI:10189948
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brugliera, F., Holton, T. A. and Michael, M. Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: WO 9732023-A 29 04-SEP-1997;
FILORIGENE LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY
ALBERT (AU); MICHAEL MICHAEL ZENON (AU)

FEATURES
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1. 18
Location/Qualifiers
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/note="Oligonucleotide"

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Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2678
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RESULT 74
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LOCUS AX047271
DEFINITION Sequence 21 from Patent WO068422.
ACCESSION AX047271
VERSION AX047271.1 GI:11876551
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Muehleger, K., Angerer, B., Seela, F., Ankenbauer, W., Augustin, M.,
Gumbiowski, K., and Zulauf, M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 21 16-NOV-2000;

FEATURES
Roche Diagnostics GmbH (DE)
Location/Qualifiers
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ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
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QY 2662 AAAAAAAAAAAAAAAAAA 2679
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RESULT 75
AX047273/c 18 bp DNA linear PAT 15-DEC-2000
LOCUS AX047273
DEFINITION Sequence 23 from Patent WO068422.
ACCESSION AX047273
VERSION AX047273.1 GI:11876553
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Muehleger, K., Angerer, B., Seela, F., Ankenbauer, W., Augustin, M.,
Gumbiowski, K., and Zulauf, M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 23 16-NOV-2000;
Roche Diagnostics GmbH (DE)

FEATURES
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Location/Qualifiers
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/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

ORIGIN
Query Match 0.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
18 AAAAAAAAAAAAAAAAAA 1

Search completed: February 2, 2005, 20:25:55
Job time : 11379.2 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:40:25 ; Search time 1477.59 Seconds
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Title: US-10-048-046-1

Perfect score: 2679

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Gapop 60.0 , Gapext 60.0

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2	19	0.7	19	US-10-205-309-650	Sequence 650, App
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4	19	0.7	20	US-09-224-683-32	Sequence 32, Appl
5	19	0.7	20	US-10-671-395-433	Sequence 433, App
6	19	0.7	20	US-10-671-395-654	Sequence 654, App
7	19	0.7	20	US-10-175-608-32	Sequence 32, Appl
8	19	0.7	21	US-10-410-031-190	Sequence 190, App
9	19	0.7	24	US-09-901-484A-10	Sequence 10, Appl
10	19	0.7	24	US-09-853-526-10	Sequence 10, Appl
11	19	0.7	24	US-10-081-969-18	Sequence 18, Appl
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15	19	0.7	25	US-09-942-310-59	Sequence 59, Appl
16	19	0.7	25	US-10-002-536A-5	Sequence 5, Appl
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18	19	0.7	26	US-09-853-646-3	Sequence 3, Appl
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22	18	0.7	18	US-09-994-311-6	Sequence 6, Appl
23	18	0.7	18	US-09-776-479-913	Sequence 913, App
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30	18	0.7	18	US-10-208-357-24	Sequence 24, Appl
31	18	0.7	18	US-10-112-653-882	Sequence 882, App
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35	18	0.7	18	US-10-056-479A-15	Sequence 15, Appl
36	18	0.7	18	US-10-352-704-12	Sequence 12, Appl
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38	18	0.7	18	US-10-075-335-9	Sequence 9, Appl
39	18	0.7	18	US-10-292-088-144	Sequence 144, App
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54	18	0.7	18	US-10-674-159A-112	Sequence 112, App
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64	18	0.7	19	US-09-853-526-515	Sequence 515, App
65	18	0.7	19	US-09-970-971A-15	Sequence 15, Appl
66	18	0.7	19	US-09-970-971A-16	Sequence 16, Appl
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APP

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; Publication No US20030190635A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using
; TITLE OF INVENTION: Interfering RNA
; FILE REFERENCE: 900/033
; CURRENT APPLICATION NUMBER: US/10/205,309
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 325
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-205-309-325

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; Publication No. US20030190635A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using
; TITLE OF INVENTION: Interfering RNA
; FILE REFERENCE: 900/033
; CURRENT APPLICATION NUMBER: US/10/205,309
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 674
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; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-205-309-650

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 32, Application US/09005243
; Patent No. US20020018763A1
; GENERAL INFORMATION:
; APPLICANT: Zaebo, Kristina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

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STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/569,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-224-683-32

Query Match      0.7%; Score 19; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2661 CAAAAAAAAAAAAAAAAAAAAA 2679
Db      19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 5
US-10-671-395-433/c
Sequence 433, Application US/10671395
Publication No. US20040132063A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Glerser, James K.
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOAAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25

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RESULT 8
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: Publication NO. US20040010817A1
: GENERAL INFORMATION:
: APPLICANT: Shockley, Jay M.
: APPLICANT: Schmutz, Judy
: APPLICANT: Browne, John A.
: TITLE OF INVENTION: Plant Acyl-CoA Synthetase
: FILE REFERENCE: DOM-07654
: CURRENT APPLICATION NUMBER: US/10/410,031
: CURRENT FILING DATE: 2003-04-09
: NUMBER OF SEQ ID NOS: 191
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 190
: LENGTH: 21
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:

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OTHER INFORMATION: Synthetic
US-10-410-031-190

Query Match 0.7%; Score 19; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 CAAAAAAAAAAAAAAAAA 3

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US-09-901-484A-10/c
Sequence 10, Application US/09901484A
Parent No. US20020119460A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bouguetelret, Lydie
TITLE OF INVENTION: Prostate Cancer Gene
FILE REFERENCE: GEN-T11XC3D2
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 09/901,484A
PRIOR FILING DATE: 1997-12-22
PRIOR APPLICATION NUMBER: US 60/099,658
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 09/218,207
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 09/338,907
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: US 09/853,526
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 578
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 24
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(24)
OTHER INFORMATION: primer oligonucleotide PGR132
US-09-901-484A-10

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Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 20 CAAAAAAAAAAAAAAAAA 2

RESULT 10

US-09-853-526-10/c
Sequence 10, Application US/09853526
Patent No. US20020165345A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Ilya, Chumakov
APPLICANT: Bouguetelret, Lydie
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENSET.18C1PCP
CURRENT FILING DATE: US/09/853,526
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/338,907
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 08/996,306
PRIOR FILING DATE: 1997-12-22

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PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 09/218,207
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patent.pm
SEQ ID NO 10
LENGTH: 24
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..24
OTHER INFORMATION: primer oligonucleotide PGR132
US-09-853-526-10

Query Match 0.7%; Score 19; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 20 CAAAAAAAAAAAAAAAAA 2

RESULT 11

US-10-081-969-18
Sequence 18, Application US/10081969
Publication No. US20030104625A1
GENERAL INFORMATION:
APPLICANT: Cheng, Cheng
APPLICANT: Clarke, Lori
APPLICANT: Connolly, Sheila
APPLICANT: Emmet, David
APPLICANT: Forty-Schaudies, Suzanne
APPLICANT: Gorziglia, Mario
APPLICANT: Hallenbeck, Paul
APPLICANT: Hay, Carl
APPLICANT: Jakubczak, John
APPLICANT: Kaleko, Michael
APPLICANT: Phipps, Sandrina
APPLICANT: Police, Seshidhar
APPLICANT: Ryan, Patricia
APPLICANT: Steward, David
APPLICANT: Xie, Yuefeng
TITLE OF INVENTION: No. US20030104625A1 Oncolytic Adenoviral Vectors
FILE REFERENCE: 4-31704A/GTI
CURRENT APPLICATION NUMBER: US/10/081,969
CURRENT FILING DATE: 2002-02-32
PRIOR APPLICATION NUMBER: US 60/270,922
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/295,037
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/348,670
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Viral vector sequence
NAME/KEY: misc feature
LOCATION: (1)..(24)
OTHER INFORMATION: Fig. 1C. SV40 early Poly(A) site
NAME/KEY: polyA site
LOCATION: (3)..(24)
OTHER INFORMATION:
US-10-081-969-18

Query Match	0.7%;	Score 19;	DB 9;	Length 25;
Best Local Similarity	100.0%;	Pred. No. 1.7e+02;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	2661	CAAAAAAAAAAAAAAAAAA	2679
Db	24	CAAAAAAAAAAAAAAAAAA	6


```
RESULT 16
US-10-002-536A-5/c
; Sequence 5, Application US/10002536A
; Publication No. US20030108874A1
; GENERAL INFORMATION:
; APPLICANT: Kane, Michael D.
; APPLICANT: Nagel, Aaron C.
; APPLICANT: Dombkowski, Alan A.
; TITLE OF INVENTION: COMPOSITIONS AND SYSTEMS FOR IDENTIFYING AND COMPARING EXPRESSED
; FILE REFERENCE: 65446-87
; CURRENT APPLICATION NUMBER: US/10/002,536A
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This is a synthesized sequence.
US-10-002-536A-5

Query Match          0.7%; Score 19; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2661 CAAAAAAAAAAAAAAAAA 2679
Db      21 CAAAAAAAAAAAAAAAAA 3

RESULT 17
US-09-099-823-14/c
; Sequence 14, Application US/09099823
; Patent No. US20020018990A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: SCHEFFEL, CHRISTI
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; NUMBER OF INVENTIONS: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,823
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,354
; FILING DATE: 20-JUN-1997
```

```
ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6120, US, P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-099-823-14

Query Match          0.7%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2661 CAAAAAAAAAAAAAAAAA 2679
Db      26 CAAAAAAAAAAAAAAAAA 8

RESULT 18
US-09-853-646-3
; Sequence 3, Application US/09853646
; Patent No. US20020055106A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas
; APPLICANT: Saes, Philip
; APPLICANT: Grassio, Luigi
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: A METHOD FOR GENERATING HYPERMUTABLE
; FILE REFERENCE: 01107,00138
; CURRENT APPLICATION NUMBER: US/09/853,646
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/204,769
; PRIOR FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant DNA
US-09-853-646-3

Query Match          0.7%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2661 CAAAAAAAAAAAAAAAAA 2679
Db      5 CAAAAAAAAAAAAAAAAA 23

RESULT 19
US-10-182-434-2
; Sequence 2, Application US/10182434
; Publication No. US20030190633A1
; GENERAL INFORMATION:
; APPLICANT: TANGA, Michifumi
; APPLICANT: OKAMURA, Hitoshi
; APPLICANT: TAKAGI, Kenichi
; APPLICANT: TAKAHASHI, Kojiro
; TITLE OF INVENTION: SUPPORT FOR FIXING NUCLEOTIDE AND PROCESS FOR PRODUCING THE SAME
; FILE REFERENCE: TANGAS
; CURRENT APPLICATION NUMBER: US/10/182,434
```

```

; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: JP 2000-019301
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-182-434-2

Query Match
Best Local Similarity 100.0%; Score 19; DB 15; Length 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 5 CAAAAAAAAAAAAAAAAA 23

RESULT 20
US-09-809-545A-84/C
; Sequence 84, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS 017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligos corresponding to polylinker sequence.
US-09-809-545A-84

Query Match
Best Local Similarity 100.0%; Score 18; DB 9; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 21
US-09-888-326-837/C
; Sequence 837, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AMS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 837
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
```

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; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-837

Query Match
Best Local Similarity 100.0%; Score 18; DB 10; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 22
US-09-994-311-6/C
; Sequence 6, Application US/09994311
; Publication No. US20030082556A1
; GENERAL INFORMATION:
; APPLICANT: Kaufman, Joseph C.
; APPLICANT: Roth, Matthew E.
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Feng, Li
; APPLICANT: Latimer, Darin R.
; TITLE OF INVENTION: Binary Encoded Sequence Tags
; FILE REFERENCE: AGL 100
; CURRENT APPLICATION NUMBER: US/09/994,311
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/09/637,751
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-6

Query Match
Best Local Similarity 100.0%; Score 18; DB 10; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 AAAAAAAAAAAAAAAAAA 2677
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 23
US-09-776-479-913/C
; Sequence 913, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fournon, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 913
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
```

US-09-776-479-913

Query Match 0.7%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
18 AAAAAAAAAAAAAAAAAA 1

RESULT 24

US-09-776-479-939/c
; Sequence 939, Application US/09776479
; Publication No. US20030087848a1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 939
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-939

Query Match 0.7%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
18 AAAAAAAAAAAAAAAAAA 1

RESULT 25

US-09-370-541-14/c
; Sequence 14, Application US/09370541
; Publication No. US20030088079a1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Antinociceptive Modified Nucleosidic Compounds And Oligomeric
; FILE REFERENCE: IS13993
; CURRENT FILING DATE: 1999-08-09
; EARLIER FILING DATE: 1998-08-07
; EARLIER FILING DATE: 1998-08-07
; EARLIER FILING DATE: 1998-01-30
; EARLIER FILING DATE: 1997-02-14
; EARLIER FILING DATE: 1997-02-14
; EARLIER FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-370-541-14

Query Match 0.7%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
18 AAAAAAAAAAAAAAAAAA 1

RESULT 26

US-09-776-479-913/c
; Sequence 913, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 913
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-913

Query Match 0.7%; Score 18; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
18 AAAAAAAAAAAAAAAAAA 1

RESULT 27

US-09-776-479-939/c
; Sequence 939, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 939
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-939

Query Match 0.7%; Score 18; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 28

US-09-979-275A-7/c
; Sequence 7, Application US/09979275A
; Publication No. US20040110919A1
; GENERAL INFORMATION:
; APPLICANT: NAGAI, HIROSHI
; APPLICANT: KURODA, KYOKO
; APPLICANT: NAKAJIMA, TERUMI
; TITLE OF INVENTION: NOVEL PROTEINS HAVING HEMOLYTIC ACTIVITY AND GENES
; FILE REFERENCE: 037181.5061US
; CURRENT APPLICATION NUMBER: US/09/979,275A
; PRIOR FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: PCT/JPO1/02209
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: this sequence may encompass 12-18 nucleotides
US-09-979-275A-7

Query Match 0.7%; Score 18; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 29

US-10-125-295-9/c
; Sequence 9, Application US/10125295
; Publication No. US20020164572A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Ching-I Patsy
; Wallace, Robert Bruce
; Cosseman, Jeffrey
; French, Cynthia
; TITLE OF INVENTION: Myophibrization of Cultured Human Cells
; to Preserve RNA and DNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/125,295
FILING DATE: 17-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/545,225
FILING DATE: 07-Apr-2000
APPLICATION NUMBER: US 08/884,029
FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 02558B-059100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:

NAME/KEY: modified_base

LOCATION: 13..18
OTHER INFORMATION: /mod_base= OTHER
/note= "c at positions 13-18 may be present or absent"

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-125-295-9

Query Match 0.7%; Score 18; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 30

US-10-208-357-24
; Sequence 24, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
; APPLICANT: Kurtz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/10/208,357
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/619,103
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-24

Query Match 0.7%; Score 18; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 1 AAAAAAAAAAAAAAAAAA 18

```
RESULT 31
US-10-112-653-882/c
; Sequence 882, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(LAWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 882
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-882

Query Match      0.7%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 32
US-10-017-995-913/c
; Sequence 913, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 913
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-913

Query Match      0.7%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 33
US-10-017-995-939/c
; Sequence 939, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
```

```
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 939
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-939

Query Match      0.7%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 34
US-10-206-613-4/c
; Sequence 4, Application US/10206613
; Publication No. US20030104432A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Zhidong
; APPLICANT: Jablons, David
; APPLICANT: You, Liang
; APPLICANT: He, Biao
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-119510US
; CURRENT APPLICATION NUMBER: US/10/206,613
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 60/308,190
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligo dt-18
US-10-206-613-4

Query Match      0.7%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 35
US-10-056-479A-15/c
; Sequence 15, Application US/10056479A
; Publication No. US20030175678A1
; GENERAL INFORMATION:
; APPLICANT: Bowen, Benjamin A.
; APPLICANT: Deakin, Edward
; APPLICANT: Goldsmith, Neil
; APPLICANT: Haudenschild, Christian
; APPLICANT: Houck, David
; APPLICANT: McAlpine, James B.
; APPLICANT: Neilsen, Soren
; APPLICANT: Pazolet, Christopher
```

APPLICANT: Spencer, Marget E.
APPLICANT: Stafford, Angela
TITLE OF INVENTION: Methods for Identifying Genes Regulating
FILE OF INVENTION: Desired Cell Phenotypes
FILE REFERENCE: 50273/005002
CURRENT APPLICATION NUMBER: US/10/056,479A
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/263,807
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 15
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-056-479A-15

Query Match 0.7%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 36

US-10-352-704-12/C
Sequence 12, Application US/10352704
Publication No. US20030176690A1
GENERAL INFORMATION:

APPLICANT: Chatelain, Francois
Kumarev, Viktor

TITLE OF INVENTION: Process for Preparing Polynucleotides on
a Solid Support and Apparatus Permitting its
Implementation

NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/352,704
FILING DATE: 28-Jan-2003
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/358,556A
FILING DATE: 14-DEC-1994

APPLICATION NUMBER: FR 9315164
FILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:

NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

NAME/KEY: CDS
LOCATION: 1..18

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: CDS
LOCATION: 1..18
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-352-704-12

Query Match 0.7%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 37

US-10-352-704-18
Sequence 18, Application US/10352704
Publication No. US20030176690A1
GENERAL INFORMATION:

APPLICANT: Chatelain, Francois
Kumarev, Viktor

TITLE OF INVENTION: Process for Preparing Polynucleotides on
a Solid Support and Apparatus Permitting its
Implementation

NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/352,704
FILING DATE: 28-Jan-2003
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/358,556A
FILING DATE: 14-DEC-1994

APPLICATION NUMBER: FR 9315164
FILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:

NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: CDS
LOCATION: 1..18

NAME/KEY: CDS
LOCATION: 1..18

SEQUENCE DESCRIPTION: SEQ ID NO: 18;
US-10-352-704-18

Query Match 0.7%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 38

US-10-075-335-9/c
; Sequence 9, Application US/10075335
; Publication No. US20030186237A1
; GENERAL INFORMATION:
; APPLICANT: Ginsberg, Stephen
; APPLICANT: Che, Shaoli
; TITLE OF INVENTION: Methods and Compositions of Amplifying RNA
; FILE REFERENCE: HO-P02202US2
; CURRENT APPLICATION NUMBER: US/10/075,335
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/268,664
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/348,242
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/268,645
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/344,557
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/306,216
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/350,176
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-075-335-9

Query Match 0.7%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 39

US-10-292-088-144/c
; Sequence 144, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-Pf/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,990
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144

LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-292-088-144

Query Match 0.7%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 40

US-10-314-578-913/c
; Sequence 913, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 913
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-913

Query Match 0.7%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 41

US-10-314-578-939/c
; Sequence 939, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 939
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-314-578-939

Query Match 0.7%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 42
US-10-389-155-97/c

Sequence 97, Application US/10389155
Publication No. US20030229208A1
GENERAL INFORMATION:

APPLICANT: Queen, Cary L.

Co, Man Sung
Schneider, William P.
Landolfi, Nicholas F.
Coeligh, Kathleen L.
Sclick, Harold E.

TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/389,155

FILING DATE: 13-Mar-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/325,000

FILING DATE: 01-JUN-1999

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US 08/484,537

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 011823-002650US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: modified_base

LOCATION: 13..18

OTHER INFORMATION: /mod_base= OTHER

/note= "T at positions 13-18 may be

present or absent"

SEQUENCE DESCRIPTION: SEQ ID NO: 97:

US-10-389-155-97

Query Match 0.7%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 43

US-10-271-602B-84

Sequence 84, Application US/10271602B

Publication No. US20040002073A1

GENERAL INFORMATION:

APPLICANT: Alice Xiang Li

APPLICANT: Ghazala Hashmi

APPLICANT: Michael Seul

TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI

FILE REFERENCE: BY CONCURRENT INTERROGATION AND ENZYME-MEDIATED DETECTION

CURRENT APPLICATION NUMBER: US/10/271,602B

PRIOR FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 60/329,427

PRIOR FILING DATE: 2001-10-14

PRIOR APPLICATION NUMBER: 60/329,620

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 60/329,428

PRIOR FILING DATE: 2001-10-14

PRIOR APPLICATION NUMBER: 60/329,619

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 60/364,416

PRIOR FILING DATE: 2002-03-14

NUMBER OF SEQ ID NOS: 212

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 84

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Probe sequence derived from human genomic sequence

US-10-271-602B-84

Query Match 0.7%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 44

US-10-334-143-204/c

Sequence 204, Application US/10334143

Publication No. US20040009549A1

GENERAL INFORMATION:

APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH

APPLICANT: SUDARSANAM, SUCHA

TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL

FILE REFERENCE: 038602/1543

CURRENT APPLICATION NUMBER: US/10/334,143

PRIOR FILING DATE: 2002-12-31

PRIOR APPLICATION NUMBER: 60/343,169

PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentn Ver. 2.1
SEQ ID NO 204
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
FEATURE:
OTHER INFORMATION: this sequence may encompass 12-18 nucleotides in length
US-10-334-143-204

Query Match 0.7%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 45
US-10-389-417-97/c
Sequence 97, Application US/10389417
Publication No. US20040049014A1
GENERAL INFORMATION:
APPLICANT: Queen, Gary L.
Co, Man Sung
Schneider, William P.
Landolfi, Nicholas F.
Coeligh, Kathleen L.
Selick, Harold B.
TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,417
FILING DATE: 13-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 13..18
OTHER INFORMATION: /mod_base= OTHER
/note= "T at positions 13-18 may be present or absent"
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-389-417-97

Query Match 0.7%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 46
US-10-653-416-26/c
Sequence 26, Application US/10653416
Publication No. US20040110201A1
GENERAL INFORMATION:
APPLICANT: RASHTCHIAN, AYOUR
APPLICANT: SCHUSTER, DAVID M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CDNA SYNTHESIS
FILE REFERENCE: 38266-0011
CURRENT APPLICATION NUMBER: US/10/653,416
CURRENT FILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: 60/407,248
PRIOR FILING DATE: 2002-09-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentn Ver. 3.2
SEQ ID NO 26
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
FEATURE:
OTHER INFORMATION: this sequence may encompass 12-18 nucleotides according
US-10-653-416-26

Query Match 0.7%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 47
US-10-785-744-15/c
Sequence 15, Application US/10785744
Publication No. US20040133941A1
GENERAL INFORMATION:
APPLICANT: Bowen, Benjamin A.
APPLICANT: Deakin, Edward
APPLICANT: Goldsmith, Neil
APPLICANT: Haudenschild, Christian
APPLICANT: Houck, David
APPLICANT: McAlpine, James B.
APPLICANT: Nielsen, Soren
APPLICANT: Pazoles, Christopher

APPLICANT: Spencer, Marget E.
APPLICANT: Stafford, Angela
TITLE OF INVENTION: Methods for Identifying Genes Regulating
TITLE OF INVENTION: Desired Cell Phenotypes
FILE REFERENCE: 50273/005002
CURRENT APPLICATION NUMBER: US/10/785,744
CURRENT FILING DATE: 2004-02-23
PRIOR APPLICATION NUMBER: US/10/056,479
PRIOR FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/263,807
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-785-744-15

Query Match 0.7%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 48
US-10-735-592-1/c
Sequence 1, Application US/10735592
Publication No. US20040171571A1
GENERAL INFORMATION:
APPLICANT: Art. Krieg
APPLICANT: Joerg Volmer
TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
FILE REFERENCE: C1037.700380S01
CURRENT APPLICATION NUMBER: US/10/735,592
CURRENT FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Version 3.2
SEQ ID NO 1
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-1

Query Match 0.7%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 49
US-10-628-525-30
Sequence 30, Application US/10628525
Publication No. US20040185114A1
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
Guan, Hanning
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
CITY: Boulder

STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/628,525
FILING DATE: 28-Jul-2003
CLASSIFICATION: 800
PRIORITY DATA:
APPLICATION NUMBER: US/08/941,445
FILING DATE: 30-SEP-1997
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Not Relevant
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-628-525-30

Query Match 0.7%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 50
US-10-849-072-21
Sequence 21, Application US/10849072
Publication No. US20040214221A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH
TITLE OF INVENTION: High density labeling of DNA with modified or
TITLE OF INVENTION: "chromophore" carrying nucleotides and DNA polymerases
FILE REFERENCE: 4780/00/WO
CURRENT APPLICATION NUMBER: US/10/849,072
CURRENT FILING DATE: 2004-05-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: second
US-10-849-072-21

Query Match 0.7%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
1 AAAAAAAAAAAAAAAAAA 18

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 51
US-10-849-072-23/c
; Sequence 23, Application US/10849072
; Publication No. US20040214221A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: High density labeling of DNA with modified or
; TITLE OF INVENTION: "chromophore" carrying nucleotides and DNA polymerases
; FILE REFERENCE: 4780/00/MO
; CURRENT APPLICATION NUMBER: US/10/849,072
; PRIOR FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: second
US-10-849-072-23

Query Match 0.7%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 52
US-10-831-778-913/c
; Sequence 913, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; PRIOR FILING DATE: 2004-04-23
; CURRENT FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 913
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-913

Query Match 0.7%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 53
US-10-831-778-939/c
; Sequence 939, Application US/10831778
; Publication No. US20040235774A1

; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; PRIOR FILING DATE: 2004-04-23
; CURRENT FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 939
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-939

Query Match 0.7%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 54
US-10-674-159A-112/c
; Sequence 112, Application US/10674159A
; Publication No. US20040242518A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jianzhu
; APPLICANT: Ge, Qing
; APPLICANT: Eigen, Herman
; TITLE OF INVENTION: Influenza Therapeutic
; FILE REFERENCE: 0492611-0506
; CURRENT APPLICATION NUMBER: US/10/674,159A
; CURRENT FILING DATE: 2003-09-29
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 112
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mRNA
US-10-674-159A-112

Query Match 0.7%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 55
US-10-776-933-150/c
; Sequence 150, Application US/10776933
; Publication No. US20040241717A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THURIE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISENBACH, MARGIT
; TITLE OF INVENTION: OLIGONUCLEIC COMPOUNDS FOR THE MODULATION OF THIOREDOXIN
; TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: 58614(71432)
CURRENT APPLICATION NUMBER: US/10/776,933
CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/446,374
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 150
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: poly-T oligonucleotide
FEATURE:
OTHER INFORMATION: This sequence may encompass 12-18 nucleotides
OTHER INFORMATION: according to the specification as filed
US-10-776-933-150

Query Match 0.7%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 56
US-10-776-917-141/c
Sequence 141, Application US/10776917
Publication No. US20040248840A1
GENERAL INFORMATION:
APPLICANT: HANSEN, BO
APPLICANT: THREU, CHARLOTTE ALBAEK
APPLICANT: WESTERGAARD, MAJKEN
APPLICANT: PETERSEN, KATILDE DUMONG
APPLICANT: WISSENBACH, MARBIT
TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF RAS EXPRESSION
FILE REFERENCE: 58609(71432)
CURRENT APPLICATION NUMBER: US/10/776,917
CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/446,363
PRIOR FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: DK 2003-01539
PRIOR FILING DATE: 2003-10-20
NUMBER OF SEQ ID NOS: 201
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 141
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: poly-T oligonucleotide
FEATURE:
OTHER INFORMATION: this sequence may encompass 12-18 nucleotides according to the
OTHER INFORMATION: specification as filed
US-10-776-917-141

Query Match 0.7%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 57
US-10-766-096-9/c
Sequence 9, Application US/10766096
Publication No. US20040265786A1
GENERAL INFORMATION:

APPLICANT: Lin, Ching-I Patsy
Wallace, Robert Bruce
Cosman, Jeffrey
French, Cynthia
TITLE OF INVENTION: Lyophilization of Cultured Human Cells
to Preserve RNA and DNA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/766,096
FILING DATE: 27-Jan-2004
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/884,029
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 02558B-059100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 13..18
OTHER INFORMATION: /mod_base= OTHER
/note= "t at positions 13-18 may be
present or absent."
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-766-096-9

Query Match 0.7%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 58
US-10-872-984-6/c
Sequence 6, Application US/10872984
Publication No. US20040265888A1
GENERAL INFORMATION:
APPLICANT: Kaufman, Joseph C.
APPLICANT: Roth, Matthew E.
APPLICANT: Lizardi, Paul M.
APPLICANT: Feng, Li
APPLICANT: Latimer, Darin R.
TITLE OF INVENTION: Binary Encoded Sequence Tags
FILE REFERENCE: AGI 100
CURRENT APPLICATION NUMBER: US/10/872,984
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/09/994,311

```
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/09/637,751
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-872-984-6

Query Match          0.7%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2660 AAAAAAAAAAAAAAAAAA 2677
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 59
US-10-638-141-10/c
; Sequence 10, Application US/10638141
; Publication No. US2005003364A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; APPLICANT: Kapoun, Ann Marie
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS.013A
; CURRENT APPLICATION NUMBER: US/10/638,141
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US/09/665,728
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/156,277
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-638-141-10

Query Match          0.7%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2662 AAAAAAAAAAAAAAAAAA 2679
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 60
US-09-917-138-1/c
; Sequence 1, Application US/09917138
; Patent No. US20020031776A1
; GENERAL INFORMATION:
; APPLICANT: TULLIS, Richard
; APPLICANT: STEIFEL, Jerome
; TITLE OF INVENTION: ENZYMATIC LABELLING AND DETECTION OF DNA
; FILE REFERENCE: 24730-2207B
; CURRENT APPLICATION NUMBER: US/09/917,138
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 09/580,358
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/136,545
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 7
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: Biotinylation at the 5' end
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Combined DNA/RNA
US-09-917-138-1

Query Match          0.7%; Score 18; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 61
US-09-917-138-2
; Sequence 2, Application US/09917138
; Patent No. US20020031776A1
; GENERAL INFORMATION:
; APPLICANT: TULLIS, Richard
; APPLICANT: STEIFEL, Jerome
; TITLE OF INVENTION: ENZYMATIC LABELLING AND DETECTION OF DNA
; FILE REFERENCE: 24730-2207B
; CURRENT APPLICATION NUMBER: US/09/917,138
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 09/580,358
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/136,545
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Combined DNA/RNA
US-09-917-138-2

Query Match          0.7%; Score 18; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2662 AAAAAAAAAAAAAAAAAA 2679
Db      1 AAAAAAAAAAAAAAAAAA 18

RESULT 62
US-09-371-307-85/c
; Sequence 85, Application US/09371307A
; Patent No. US20020053095A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
```

```
APPLICANT: Rao, Sudabathula
APPLICANT: Ream, Joel E.
APPLICANT: Logusch, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOBT:216
CURRENT APPLICATION NUMBER: US/09/371.307A
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 85
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-371-307-85
```

```
Query Match          0.7%; Score 18; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      18 AAAAAAAAAAAAAAAAAA 1
```

```
RESULT 63
US-09-901-484A-515/c
Sequence 515, Application US/09901484A
Patent No. US20020119460A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Prostate Cancer Gene
FILE REFERENCE: GEN-T11XC3D2
CURRENT APPLICATION NUMBER: US/09/901.484A
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 08/996,306
PRIOR FILING DATE: 1997-12-22
PRIOR APPLICATION NUMBER: US 60/099,658
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 09/218,207
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 09/338,907
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: US 09/853,526
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patentin version 3.1
SEQ ID NO 515
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(19)
OTHER INFORMATION: potential microsequencing oligo for 4-4-187.mis2
US-09-901-484A-515
```

```
Query Match          0.7%; Score 18; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2
```

```
RESULT 64
US-09-853-526-515/c
Sequence 515, Application US/09853526
```

```
Patent No. US20020165345A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Ilya, Chumakov
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENSET.18CP1CP
CURRENT APPLICATION NUMBER: US/09/853,526
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/338,907
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 08/996,306
PRIOR FILING DATE: 1997-12-22
PRIOR APPLICATION NUMBER: 60/099,658
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 09/218,207
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 515
LENGTH: 19
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..15
OTHER INFORMATION: potential microsequencing oligo for 4-4-187.mis2
US-09-853-526-515
```

```
Query Match          0.7%; Score 18; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2
```

```
RESULT 65
US-09-970-971A-15/c
Sequence 15, Application US/09970971A
Publication No. US20030096979A1
GENERAL INFORMATION:
APPLICANT: Mohan, Venkatraman
APPLICANT: Cook, Phillip Dan
APPLICANT: Kawasaki, Andrew M.
TITLE OF INVENTION: Oligonucleotides Having DNA Form and B-DNA Form Conformational
FILE REFERENCE: ISIS4789
CURRENT APPLICATION NUMBER: US/09/970,971A
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. US20030096979A1el Sequence
NAME/KEY: misc_feature
LOCATION: (16)..(19)
OTHER INFORMATION: 3'-O-MOE
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(19)
OTHER INFORMATION: P=O
US-09-970-971A-15
```

```
Query Match          0.7%; Score 18; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 2662 AAAAAAAAAAAAAAAAAA 2679
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 66

US-09-970-971A-16/C
; Sequence 16, Application US/09970971A
; Publication No. US20030096979A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Mohan, Venktraman
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Kawasaki, Andrew M.
; TITLE OF INVENTION: Oligonucleotides Having DNA Form and B-DNA Form Conformational
; FILE REFERENCE: ISIS4789
; CURRENT APPLICATION NUMBER: US/09/970,971A
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030096979A1el Sequence
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 3'-O-MOE
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: P=O
US-09-970-971A-16

Query Match 0.7%; Score 18; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 67

US-09-970-971A-26/C
; Sequence 26, Application US/09970971A
; Publication No. US20030096979A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Mohan, Venktraman
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Kawasaki, Andrew M.
; TITLE OF INVENTION: Oligonucleotides Having DNA Form and B-DNA Form Conformational
; FILE REFERENCE: ISIS4789
; CURRENT APPLICATION NUMBER: US/09/970,971A
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030096979A1el Sequence
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 2'-modified T
US-09-970-971A-26

Query Match 0.7%; Score 18; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 68

US-09-996-292A-54/C
; Sequence 54, Application US/0996292A
; Publication No. US20030158403A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Maier, Martin A.
; APPLICANT: Prakash, Thazha P.
; APPLICANT: Rajeev, Kallanthottathil Gopalan
; TITLE OF INVENTION: Nuclease Resistant Chimeric Oligonucleotides
; FILE REFERENCE: ISIS-4804
; CURRENT APPLICATION NUMBER: US/09/996,292A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: N= phenoxazine
US-09-996-292A-54

Query Match 0.7%; Score 18; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 69

US-09-996-292A-55/C
; Sequence 55, Application US/0996292A
; Publication No. US20030158403A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Maier, Martin A.
; APPLICANT: Prakash, Thazha P.
; APPLICANT: Rajeev, Kallanthottathil Gopalan
; TITLE OF INVENTION: Nuclease Resistant Chimeric Oligonucleotides
; FILE REFERENCE: ISIS-4804
; CURRENT APPLICATION NUMBER: US/09/996,292A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: N= G-clamp modification
US-09-996-292A-55

Query Match 0.7%; Score 18; DB 10; Length 19;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 70

US-10-096-221-3
; Sequence 3, Application US/10096221
; Publication No. US20020164628A1
; GENERAL INFORMATION:
; APPLICANT: Kurn, Nutch
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; FILE REFERENCE: 49269200700
; CURRENT APPLICATION NUMBER: US/10/096,221
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US 60/274,236
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: misc.feature
; LOCATION: 1
; OTHER INFORMATION: n = A,T,C or G
US-10-096-221-3

Query Match 0.7%; Score 18; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
Db 2 AAAAAAAAAAAAAAAAAA 19

RESULT 71

US-10-208-357-25
; Sequence 25, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
; APPLICANT: Kurtz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/10/208,357
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/619,103
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-25

Query Match 0.7%; Score 18; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 72

US-10-123-597-1/c
; Sequence 1, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc.feature
; LOCATION: (15)-(18)
; OTHER INFORMATION: 5-methyl-2'-aminoxyethoxy
US-10-123-597-1

Query Match 0.7%; Score 18; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 73

US-10-123-597-2/c
; Sequence 2, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc.feature
; LOCATION: (15)-(18)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-10-123-597-2

Query Match 0.7%; Score 18; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 74

US-10-123-597-3/C
; Sequence 3, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-methoxyethoxy
US-10-123-597-3

Query Match 0.7%; Score 18; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 75

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; Sequence 4, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)

OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-10-123-597-4

Query Match 0.7%; Score 18; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

Search completed: February 3, 2005, 00:11:19
Job time : 1480.59 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:25:00 ; Search time 256.971 Seconds
(without alignment)
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Title: US-10-048-046-1

Perfect score: 2679

Sequence: 1 aagattcgcgcagcagccg.....acaaaaaaaaaaaaaaaa 2679

Scoring table:

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Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size: 0

Total number of hits satisfying chosen parameters: 682300

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	0.7	30	1 US-08-455-627-12	Sequence 12, Appl
3	20	0.7	30	2 US-08-689-856-12	Sequence 12, Appl
4	20	0.7	30	3 US-08-787-321-12	Sequence 12, Appl
5	19	0.7	20	3 US-08-482-918-32	Sequence 32, Appl
6	19	0.7	20	3 US-09-224-681-32	Sequence 32, Appl
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14	19	0.7	24	4 US-09-721-154-6	Sequence 6, Appl
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99	18	0.7	19	4 US-09-227-782-12	Sequence 12, Appl
100	18	0.7	19	4 US-09-227-782-14	Sequence 14, Appl

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C 116 18 0.7 19 4 US-10-123-587-1 Sequence 1, Appl
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C 128 18 0.7 19 4 US-09-349-033A-1 Sequence 1, Appl
C 129 18 0.7 19 4 US-09-435-806-6 Sequence 6, Appl
C 130 18 0.7 19 4 US-09-435-806-7 Sequence 7, Appl
C 131 18 0.7 19 4 US-10-121-135-5 Sequence 5, Appl
C 132 18 0.7 19 4 US-10-121-135-26 Sequence 26, Appl
C 133 18 0.7 19 4 US-09-371-307-85 Sequence 85, Appl
C 134 18 0.7 19 4 US-10-098-816-15 Sequence 15, Appl
C 135 18 0.7 19 4 US-10-098-816-16 Sequence 16, Appl
C 136 18 0.7 19 4 US-10-098-816-17 Sequence 17, Appl
C 137 18 0.7 19 4 US-10-098-816-18 Sequence 18, Appl
C 138 18 0.7 19 4 US-10-098-816-26 Sequence 26, Appl
C 139 18 0.7 20 1 US-08-146-504-16 Sequence 16, Appl
C 140 18 0.7 20 2 US-08-379-593-5 Sequence 5, Appl
C 141 18 0.7 20 2 US-08-975-976-16 Sequence 16, Appl
C 142 18 0.7 20 2 US-08-997-080-83 Sequence 83, Appl
C 143 18 0.7 20 2 US-08-997-362-83 Sequence 83, Appl
C 144 18 0.7 20 2 US-08-965-780-1 Sequence 1, Appl
C 145 18 0.7 20 3 US-08-873-970-83 Sequence 83, Appl
C 146 18 0.7 20 3 US-08-765-340-96 Sequence 96, Appl
C 147 18 0.7 20 3 US-09-095-855-83 Sequence 83, Appl
C 148 18 0.7 20 3 US-09-407-675-1 Sequence 1, Appl
C 149 18 0.7 20 3 US-08-482-918-33 Sequence 33, Appl
C 150 18 0.7 20 3 US-08-482-918-34 Sequence 34, Appl
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ALIGNMENTS

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RESULT 1
US-08-113-646A-42
; Sequence 42, Application US/08113646A
; Patent No. 5578468
; GENERAL INFORMATION:
; APPLICANT: PICKUP, David J.
; APPLICANT: PATEL, Dhaval Kumar
; APPLICANT: ANTICZAK, James B.
; TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHIVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/113,646A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/084,406
FILING DATE: 10-AUG-1987
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-20
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-113-646A-42
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Query Match 0.7%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2660 AAAAAAAAAAAAAAAAAA 2679
Db 5 AAAAAAAAAAAAAAAAAA 24
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RESULT 2
US-08-455-627-12
; Sequence 12, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergej M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 nucleotides
; TYPE: nucleic acid
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-455-627-12

Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 AAAAAAAAAAAAAAAAAA 2679
|||||
DB 4 AAAAAAAAAAAAAAAAAA 23

RESULT 3
US-08-689-856-12
Sequence 12, Application US/08689856
Patent No. 5830658
GENERAL INFORMATION:

APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward LLP
STREET: Five Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,856
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/455,627
FILING DATE: 31-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: LYNX-003/01 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-689-856-12

Query Match 0.7%; Score 20; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 AAAAAAAAAAAAAAAAAA 2679
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DB 4 AAAAAAAAAAAAAAAAAA 23

RESULT 4
US-08-787-321-12
Sequence 12, Application US/08787321A
Patent No. 6180777
GENERAL INFORMATION:
APPLICANT: Horn, Thomas

TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
FILE REFERENCE: (1300)-1199,002
CURRENT APPLICATION NUMBER: US/08/787,321A
CURRENT FILING DATE: 1997-01-03
EARLIER APPLICATION NUMBER: US PROV 60/009,918
EARLIER FILING DATE: 1996-01-12
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-08-787-321-12

Query Match 0.7%; Score 20; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 AAAAAAAAAAAAAAAAAA 2679
|||||
DB 4 AAAAAAAAAAAAAAAAAA 23

RESULT 5
US-08-482-918-32/C
Sequence 32, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:

APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-918-32

Query Match 0.7%; Score 19; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2,3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2661 CAAAAAAAAAAAAAAAAA 2679
|||
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 6

US-09-224-681-32/c
Sequence 32, Application US/09224681
Patent No. 6207454

GENERAL INFORMATION:

APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448

TELEX:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-09-224-681-32

Query Match 0.7%; Score 19; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2661 CAAAAAAAAAAAAAAAAA 2679
|||
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 7

US-08-336-728A-32/c
Sequence 32, Application US/08336728A
Patent No. 6207802

GENERAL INFORMATION:

APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448

TELEX:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-336-728A-32

Query Match 0.7%; Score 19; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 8

US-09-635-251-32/c
; Sequence 32, Application US/09635251
; Patent No. 6759315
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristina M.
; Bosseiman, Robert A.
; Suggs, Sidney V.
; Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/635,251
; APPLICATION NUMBER: 07-Aug-2000
; FILING DATE: 07-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,182
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: 08/172,329
; FILING DATE: 21-DEC-1993
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; APPLICATION NUMBER: 07/684,535
; FILING DATE: 04-OCT-1991
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32957A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-635-251-32

Query Match 0.7%; Score 19; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 19 CAAAAAAAAAAAAAAAAA 1

Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 9

PCT-US94-05407-7
; Sequence 7, Application PC/TUS9405407
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05407
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/061,694
; FILING DATE: 13-MAY-1993
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
PCT-US94-05407-7

Query Match 0.7%; Score 19; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 5 CAAAAAAAAAAAAAAAAA 23

RESULT 10

PCT-US94-05407-8/c
; Sequence 8, Application PC/TUS9405407
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05407
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/061,694
; FILING DATE: 13-MAY-1993
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
PCT-US94-05407-8

Query Match 0.7%; Score 19; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 19 CAAAAAAAAAAAAAAAAA 1

RESULT 11

US-08-996-306-10/c
Sequence 10, Application US/0896306
Patent No. 5945522
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Prostate cancer gene
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,306
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Israelson, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: GENSET.018A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PGRT32
LOCATION: complement 5198..5221
OTHER INFORMATION: Location relative to seqID3
US-08-996-306-10

Query Match 0.7%; Score 19; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 20 CAAAAAAAAAAAAAAAAA 2

RESULT 12

US-09-338-907-10/c
Sequence 10, Application US/09338907
Patent No. 6265546
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Ilya, Chumakov
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENSET.18CPICP
CURRENT APPLICATION NUMBER: US/09/338,907
CURRENT FILING DATE: 1999-06-23
EARLIER APPLICATION NUMBER: 08/996,306
EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: 60/099,658
EARLIER FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: 09/218,207
EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patent.pm
SEQ ID NO 10
LENGTH: 24
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..24
OTHER INFORMATION: primer oligonucleotide PGRT32
US-09-338-907-10

Query Match 0.7%; Score 19; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679
DB 20 CAAAAAAAAAAAAAAAAA 2

RESULT 13

US-09-218-207-10/c
Sequence 10, Application US/09218207
Patent No. 6346381
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Prostate cancer gene
FILE REFERENCE: GENSET.018CPI
CURRENT APPLICATION NUMBER: US/09/218,207
CURRENT FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: 08/996,306
EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: 60/099,658
EARLIER FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patent.pm
SEQ ID NO 10
LENGTH: 24
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..24
OTHER INFORMATION: primer oligonucleotide PGRT32
US-09-218-207-10

Query Match 0.7%; Score 19; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2661 CAAAAAAAAAAAAAAAAA 2679

Db 20 CAAAAAAAAAAAAAAAAA 2

RESULT 14
US-09-721-154-6/c
Sequence 6, Application US/09721154
Patent No. 6651008

GENERAL INFORMATION:
APPLICANT: Vaisberg, Eugeni
APPLICANT: Adams, Cynthia
APPLICANT: Sady, James
APPLICANT: Crompton, Anne
TITLE OF INVENTION: Database system including computer code
FILE REFERENCE: CYLOP007C2
CURRENT APPLICATION NUMBER: US/09/721,154
CURRENT FILING DATE: 2002-06-14
PRIORITY APPLICATION NUMBER: 09/311,996
PRIORITY FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Pseudo-sequence

US-09-721-154-6

Query Match 0.7%; Score 19; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2660 AAAAAAAAAAAAAAAAAA 2678
Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 15
US-08-621-914A-3/c
Sequence 3, Application US/08621914A
Patent No. 5707807

GENERAL INFORMATION:
APPLICANT: KATO, KIKUYA
TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,914A
FILING DATE: 26-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAWRENCE III, STANTON T.
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-107-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: other nucleic acid
US-08-621-914A-3

Query Match 0.7%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 26 CAAAAAAAAAAAAAAAAA 8

RESULT 16
US-10-003-998A-7
Sequence 7, Application US/10003998A
Patent No. 6664064

GENERAL INFORMATION:
APPLICANT: Roche Diagnostic GmbH
TITLE OF INVENTION: Method for melting curve analysis of repetitive PCR
FILE REFERENCE: 5438/00/EP
CURRENT APPLICATION NUMBER: US/10/003,998A
CURRENT FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 29
TYPE: DNA
ORGANISM: Homo sapiens
US-10-003-998A-7

Query Match 0.7%; Score 19; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2661 CAAAAAAAAAAAAAAAAA 2679
Db 1 CAAAAAAAAAAAAAAAAA 19

RESULT 17
US-09-724-028A-18/c
Sequence 18, Application US/09724028A
Patent No. 6777180

GENERAL INFORMATION:
APPLICANT: Fisher, Paul B.
TITLE OF INVENTION: METHOD FOR FULL-LENGTH cDNA CLONING
FILE REFERENCE: A34701 (070050,1728)
CURRENT APPLICATION NUMBER: US/09/724,028A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer PCTAR3
US-09-724-028A-18

Query Match 0.7%; Score 19; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2660 AAAAAAAAAAAAAAAAAA 2678
Db 1 CAAAAAAAAAAAAAAAAA 19

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 18

US-08-621-914A-16/C
Sequence 16, Application US/08621914A

Patent No. 5707807

GENERAL INFORMATION:

APPLICANT: KATO, KIKUYA

TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE

TITLE OF INVENTION: ANALYSIS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS

STREET: 1155 AVENUE OF THE AMERICAS

CITY: NEW YORK

STATE: NY

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,914A

FILING DATE: 26-MAR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: LAWRENCE III, STANTON T.

REGISTRATION NUMBER: 25,736

REFERENCE/DOCKET NUMBER: 7005-107-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: other nucleic acid

US-08-621-914A-16

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.1e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2662 AAAAAAAAAAAAAAAAAA 2679

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 19

US-08-346-429-3

Sequence 3, Application US/08346429

Patent No. 5837820

GENERAL INFORMATION:

APPLICANT: Derose, Richard

APPLICANT: Douce, Roland

APPLICANT: Duval, Manuel

APPLICANT: Job, Claudette

APPLICANT: Job, Dominique

TITLE OF INVENTION: PROTEIN CAPABLE OF BEING BIOTINYLATED WHICH CAN

TITLE OF INVENTION: BE USED FOR DETERMINING THE GERMINATION STAGE OF

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: USA

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/346,429

FILING DATE: 29-NOV-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Digilio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 9507

TELECOMMUNICATION INFORMATION:

TELEPHONE: 516-742-4343

TELEFAX: 516-742-4343

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-346-429-3

Query Match 0.7%; Score 18; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.1e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2662 AAAAAAAAAAAAAAAAAA 2679

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 20

US-08-358-556A-12/C

Sequence 12, Application US/08358556A

Patent No. 5869643

GENERAL INFORMATION:

APPLICANT: Chatelain, Francois

APPLICANT: Kumarev, Viktor

TITLE OF INVENTION: Process for Preparing Polynucleotides on its

TITLE OF INVENTION: Implementation

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jacobson, Price, Holman & Stern

STREET: 400 Seventh St. N.W.

CITY: Washington D.C.

COUNTRY: U.S.A.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,556A

FILING DATE: 14-DEC-1994

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 9315164

FILING DATE: 16-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Player, William E.

REGISTRATION NUMBER: 31,409

REFERENCE/DOCKET NUMBER: 10577/P58418

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-6666

TELEFAX: (202) 393-5350

```
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: CDS
LOCATION: 1..18
US-08-358-556A-12

Query Match      0.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 21
US-08-358-556A-18
Sequence 18, Application US/08358556A
Patent No. 5869643
GENERAL INFORMATION:
APPLICANT: Chatelain, Francois
TITLE OF INVENTION: Process for Preparing Polynucleotides on
a Solid Support and Apparatus Permitting its
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,556A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9315164
FILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/PS8418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
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NAME/KEY: CDS
LOCATION: 1..18
US-08-358-556A-18

Query Match      0.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 22
US-08-469-852A-4/C
Sequence 4, Application US/08469852A
Patent No. 5874213
GENERAL INFORMATION:
APPLICANT: Cummins, Lendell L.
APPLICANT: Freier, Susan M.
APPLICANT: Griffey, Richard
APPLICANT: Stivates, Susan G.
TITLE OF INVENTION: Capillary Electrophoretic Detection of
Nucleic Acids
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5874213rls LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Nordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,852A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,509
FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-2015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-852A-4

Query Match      0.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 23
US-08-295-509B-4/C
Sequence 4, Application US/08295509B
Patent No. 6045995
GENERAL INFORMATION:
```

APPLICANT: Cummins, Lendell L.
APPLICANT: Grefer, Susan M.
APPLICANT: Griffey, Richard
APPLICANT: Sivarata, Susan G.
TITLE OF INVENTION: Capillary Electrophoretic Detection of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz and No. 6045995r1s
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,509B
FILING DATE: 24-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-1395
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-295-509B-4

Query Match 0.7%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 24
US-08-884-029-9/c
Sequence 9, Application US/08884029
Patent No. 6071745
GENERAL INFORMATION:
APPLICANT: Lin, Ching-I Paray
APPLICANT: Wallace, Robert Bruce
APPLICANT: Coesman, Jeffrey
APPLICANT: French, Cynthia
TITLE OF INVENTION: Lyophilization of Cultured Human Cells
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,029

FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 02558B-059100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 13..18
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note="t at positions 13-18 may be
US-08-884-029-9

Query Match 0.7%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 25
US-08-941-445A-30
Sequence 30, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanning
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Greenlee, Winner and Sullivan, P. C.
STREET: 5370 Manhattan Circle
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: not relevant
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
US-08-941-445A-30

Query Match 0.7%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 26
US-09-637-751A-6/C

Sequence 6, Application US/09637751A
Patent No. 6383754
GENERAL INFORMATION:
APPLICANT: Kaufman, Joseph C.
APPLICANT: Roth, Matthew E.
APPLICANT: Lizardi, Paul M.
APPLICANT: Feng, Li
APPLICANT: Lacimer, Darin R.
TITLE OF INVENTION: Binary Encoded Sequence Tags
Patent No. 6383754
FILE REFERENCE: AGL 100
CURRENT APPLICATION NUMBER: US/09/637,751A
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-637-751A-6

Query Match 0.7%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2660 AAAAAAAAAAAAAAAAAA 2677
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 27
US-09-545-325-9/C
Sequence 9, Application US/09545325
Patent No. 6410321
GENERAL INFORMATION:
APPLICANT: Lin, Ching-I Patsy
Wallace, Robert Bruce
Cosman, Jeffrey
French, Cynthia
TITLE OF INVENTION: Lyophilization of Cultured Human Cells
to Preserve RNA and DNA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/545,225
FILING DATE: 07-Apr-2000
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/884,029
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 02558B-059100US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

FEATURE:
NAME/KEY: modified_base
LOCATION: 13..18
OTHER INFORMATION: /mod_base= OTHER
/note= "t at positions 13-18 may be present or absent"
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-545-325-9

Query Match 0.7%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 28
US-09-619-103-24
Sequence 24, Application US/09619103
Patent No. 6429300
GENERAL INFORMATION:
APPLICANT: Kurz, Markus
APPLICANT: Lonse, Peter
APPLICANT: Wagner, Richard
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: 50036/031002
CURRENT APPLICATION NUMBER: US/09/619,103
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/145,834
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-24

Query Match 0.7%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 29
US-09-370-541-14/C

Sequence 14, Application US/09370541
Patent No. 6639062
GENERAL INFORMATION:
APPLICANT: Manoharan, Muchiah
APPLICANT: Cook, Phillip Dan
APPLICANT: Prakash, Thazha P
APPLICANT: Kawasaki, Andrew M
TITLE OF INVENTION: Antisense-Modified Nucleoside Compounds and Oligomeric
FILE REFERENCE: 15183993
CURRENT APPLICATION NUMBER: US/09/370,541
EARLIER FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: 09/130,973
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 09/016,520
EARLIER FILING DATE: 1998-01-30
EARLIER APPLICATION NUMBER: 60/037,143
EARLIER FILING DATE: 1997-02-14
EARLIER APPLICATION NUMBER: 09/344,260
EARLIER FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 14
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-370-541-14

Query Match
Best Local Similarity 100.0%; Score 18; DB 4; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 30
US-10-125-295-9/c
Sequence 9, Application US/10125295
Patent No. 6686460
GENERAL INFORMATION:
APPLICANT: Lin, Ching-I Patsy
Wallace, Robert Bruce
Cosman, Jeffrey
French, Cynthia
TITLE OF INVENTION: Lyophilization of Cultured Human Cells
to Preserve RNA and DNA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
City: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 17-Apr-2002
APPLICATION NUMBER: US/10/125,295
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/545,225
FILING DATE: 07-Apr-2000
APPLICATION NUMBER: US 08/884,029
FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 02558B-059100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 13..18
OTHER INFORMATION: /mod_base= OTHER
/note= "at positions 13-18 may be
present or absent"
US-10-125-295-9

Query Match
Best Local Similarity 100.0%; Score 18; DB 4; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 31
US-09-803-263-6
Sequence 6, Application US/09803263
Patent No. 6706476
GENERAL INFORMATION:
APPLICANT: Thirstrup, Kenneth
TITLE OF INVENTION: A Process for Amplifying and Labeling Single Stranded cDNA by 5'
FILE REFERENCE: 674513-2003.1
CURRENT APPLICATION NUMBER: US/09/803,263
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 6
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Poly-a tail
US-09-803-263-6

Query Match
Best Local Similarity 100.0%; Score 18; DB 4; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 32
US-09-803-263-7/c
Sequence 7, Application US/09803263
Patent No. 6706476
GENERAL INFORMATION:
APPLICANT: Thirstrup, Kenneth
TITLE OF INVENTION: A Process for Amplifying and Labeling Single Stranded cDNA by 5'
FILE REFERENCE: 674513-2003.1
CURRENT APPLICATION NUMBER: US/09/803,263
CURRENT FILING DATE: 2001-03-09

NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Complement of poly-a tail
US-09-803-263-7

Query Match 0.7%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 33
US-09-994-311-6/c
Sequence 6, Application US/09994311
Patent No. 6773886

GENERAL INFORMATION:
APPLICANT: Kaufman, Joseph C.
APPLICANT: Roth, Matthew E.
APPLICANT: Lizardi, Paul M.
APPLICANT: Peng, Li
APPLICANT: Latimer, Darin R.
TITLE OF INVENTION: Binary Encoded Sequence Tags
Patent No. 6773886

FILE REFERENCE: AGI 100
CURRENT APPLICATION NUMBER: US/09/994.311
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US/09/637.751
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6

LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-6

Query Match 0.7%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2660 AAAAAAAAAAAAAAAAAA 2677
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 34
US-09-142-108C-29/c
Sequence 29, Application US/09142108C
Patent No. 6774285

GENERAL INFORMATION:
APPLICANT: Bruggiera, Filippa
APPLICANT: Holton, Timothy A.
APPLICANT: Michael, Michael Z.
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 11658
CURRENT APPLICATION NUMBER: US/09/142.108C
CURRENT FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: PMS386
PRIOR FILING DATE: 1996-03-01
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29

LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
US-09-142-108C-29

Query Match 0.7%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2661 CAAAAAAAAAAAAAAAAA 2678
Db 18 CAAAAAAAAAAAAAAAAA 1

RESULT 35
PCT-US94-05407-4/c
Sequence 4, Application PC/TUS9405407
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05407
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/061,694
FILING DATE: 13-MAY-1993

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
PCT-US94-05407-4

Query Match 0.7%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 36
US-08-756-728A-1/c
Sequence 1, Application US/08756728A
Patent No. 5821354

GENERAL INFORMATION:
APPLICANT: Lelietc, Guy
APPLICANT: Martel, Remi
TITLE OF INVENTION: RADIOLABELLED DNA OLIGONUCLEOTIDE, METHOD
OF PREPARATION AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th floor
CITY: Hackensack
STATE: New Jersey

COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,728A
FILING DATE: 26-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT- INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1398-1-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-943-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PRIMER"
HYPOTHETICAL: NO
US-08-756-728A-1

Query Match 0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 37
US-08-469-852A-2/c
Sequence 2, Application US/08469852A
Patent No. 5874213
GENERAL INFORMATION:
APPLICANT: Cummins, Lendell L.
APPLICANT: Freier, Susan M.
APPLICANT: Griffey, Richard
APPLICANT: Srivatsa, Susan G.
TITLE OF INVENTION: Capillary Electrophoretic Detection of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5874213r18 LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,852A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,509
FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325

REFERENCE/DOCKET NUMBER: ISIS-2015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-852A-2

Query Match 0.7%; Score 18; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 38
US-08-271-882B-16/c
Sequence 16, Application US/08271882B
Patent No. 6017696
GENERAL INFORMATION:
APPLICANT: Michael J. Heller
APPLICANT: Eugene Tu
APPLICANT: Glen A. Evans
APPLICANT: Ronald G. Sosnowski
TITLE OF INVENTION: SELF-ADDRESSABLE
TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND
TITLE OF INVENTION: DEVICES FOR
TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,882B
FILING DATE: July 7, 1994
CLASSIFICATION:
APPLICATION NUMBER: 08/146,504
FILING DATE: No. 6017696 September 1, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, David B.
REGISTRATION NUMBER: 31,125
REFERENCE/DOCKET NUMBER: 207/263
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: nucleic
TYPE: acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-271-882B-16

Query Match 0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 39
US-08-295-509B-2/c
Sequence 2, Application US/08295509B
Patent No. 6045995

GENERAL INFORMATION:
APPLICANT: Cummins, Lendell L.
APPLICANT: Freiler, Susan M.
APPLICANT: Grifley, Richard
APPLICANT: Sivalba, Susan G.
TITLE OF INVENTION: Capillary Electrophoretic Detection of
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz and No. 6045995r1s
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295.509B
FILING DATE: 24-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: 1SIS-1395
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-295-509B-2

Query Match 0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 40
US-08-881-784-18/c
Sequence 18, Application US/08881784
Patent No. 6083731

GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B.
APPLICANT: Lupien, Shari L.
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE PRODUCTION OF LIMONENE HYDROXYLASES
NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
ADDRESS: PLLC
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881.784
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: MSUR19777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 224-0718
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..19
OTHER INFORMATION: /product= "Primer 3.B (Table 1)"
US-08-881-784-18

Query Match 0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2662 AAAAAAAAAAAAAAAAAA 2679
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 41
US-09-234-237-1/c
Sequence 1, Application US/09234237
Patent No. 6127124

GENERAL INFORMATION:
APPLICANT: Leeds, Janet M.
APPLICANT: Cummins, Lendell L.
TITLE OF INVENTION: Fluorescence Based Nuclease Assay
FILE REFERENCE: 1SIS3308
CURRENT APPLICATION NUMBER: US/09/234,237
CURRENT FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 1
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6127124el
US-09-234-237-1

Query Match 0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2662 AAAAAAAAAAAAAAAAAA 2679

Db 19 |||||
AAAAAAAAAAAAAAAAAAAA 2

RESULT 42

US-09-016-520-20/c
Sequence 20, Application US/09016520A
Patent No. 6127533
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/016,520A
CURRENT FILING DATE: 1998-01-30
EARLIER APPLICATION NUMBER: 60/037,143
EARLIER FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)..(18)
OTHER INFORMATION: 5-methyl-2'-aminoxyethoxy
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-016-520-20

Query Match 0.7% Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 43

US-09-016-520-21/c
Sequence 21, Application US/09016520A
Patent No. 6127533
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/016,520A
CURRENT FILING DATE: 1998-01-30
EARLIER APPLICATION NUMBER: 60/037,143
EARLIER FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)..(18)
OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-016-520-21

Query Match 0.7% Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 44

US-09-016-520-22/c
Sequence 22, Application US/09016520A
Patent No. 6127533
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/016,520A
CURRENT FILING DATE: 1998-01-30
EARLIER APPLICATION NUMBER: 60/037,143
EARLIER FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)..(18)
OTHER INFORMATION: 2'-methoxyethoxy
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-016-520-22

Query Match 0.7% Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 45

US-09-016-520-23/c
Sequence 23, Application US/09016520A
Patent No. 6127533
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/016,520A
CURRENT FILING DATE: 1998-01-30
EARLIER APPLICATION NUMBER: 60/037,143
EARLIER FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)..(19)
OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-016-520-23

Query Match 0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 46

US-09-016-520-24/C
; Sequence 24, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; EARLIER FILING DATE: 1998-01-30
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-methoxyethoxy
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-016-520-24

Query Match 0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 47

US-09-016-520-25/C
; Sequence 25, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-O-propyl
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-016-520-25.

Query Match 0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 48

US-09-016-520-26/C
; Sequence 26, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-016-520-26

Query Match 0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 49

US-09-016-520-27/C
; Sequence 27, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature

```
LOCATION: (18)
OTHER INFORMATION: 5-methyl-2'-methoxyethoxy
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Sequence
US-09-016-520-27
```

```
Query Match      0.7% Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2662 AAAAAAAAAAAAAAAAAA 2679
DB      19 AAAAAAAAAAAAAAAAAA 2
```

RESULT 50

```
US-09-016-520-31/c
Sequence 31, Application US/09016520A
Patent No. 6127533
```

```
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/016,520A
CURRENT FILING DATE: 1998-01-30
EARLIER APPLICATION NUMBER: 60/037,143
EARLIER FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
NAME/KEY: misc feature
LOCATION: (15)-(18)
OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-016-520-31
```

```
Query Match      0.7% Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2662 AAAAAAAAAAAAAAAAAA 2679
DB      19 AAAAAAAAAAAAAAAAAA 2
```

RESULT 51

```
US-09-016-520-33/c
Sequence 33, Application US/09016520A
Patent No. 6127533
```

```
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/016,520A
CURRENT FILING DATE: 1998-01-30
EARLIER APPLICATION NUMBER: 60/037,143
EARLIER FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 19
TYPE: DNA
```

```
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (16)-(19)
OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-016-520-33
```

```
Query Match      0.7% Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2662 AAAAAAAAAAAAAAAAAA 2679
DB      19 AAAAAAAAAAAAAAAAAA 2
```

RESULT 52

```
US-09-016-520-34/c
Sequence 34, Application US/09016520A
Patent No. 6127533
```

```
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/016,520A
CURRENT FILING DATE: 1998-01-30
EARLIER APPLICATION NUMBER: 60/037,143
EARLIER FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
NAME/KEY: misc feature
LOCATION: (16)-(19)
OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-016-520-34
```

```
Query Match      0.7% Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2662 AAAAAAAAAAAAAAAAAA 2679
DB      19 AAAAAAAAAAAAAAAAAA 2
```

RESULT 53

```
US-09-016-520-44/c
Sequence 44, Application US/09016520A
Patent No. 6127533
```

```
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/016,520A
CURRENT FILING DATE: 1998-01-30
EARLIER APPLICATION NUMBER: 60/037,143
EARLIER FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 44
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; OTHER INFORMATION: Sequence
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-methyleneaminoxyethoxy
US-09-016-520-44

Query Match          0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 54
US-09-378-568-4/c
; Sequence 4, Application US/09378568
; Patent No. 6147200
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Fraser, Allister S
; APPLICANT: Prakash, Thazha P
; TITLE OF INVENTION: 2'-O-acetamido Modified Monomers and Oligomers
; FILE REFERENCE: IS1S4071
; CURRENT APPLICATION NUMBER: US/09/378,568
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: Sequence
US-09-378-568-4

Query Match          0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 55
US-09-130-973-20/c
; Sequence 20, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: IS1S2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 20
```

```
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5 methyl, 2'-aminoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1
US-09-130-973-20

Query Match          0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 56
US-09-130-973-21/c
; Sequence 21, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: IS1S2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 21
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5 methyl, 2'-dimethylaminoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1
US-09-130-973-21

Query Match          0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 57
US-09-130-973-22/c
; Sequence 22, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: IS1S2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentln Ver. 2.1
```

```
/ SEQ ID NO 22
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (15)..(18)
/ OTHER INFORMATION: 2'-O-methoxyethyl (MOE)
/ OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1
/ OTHER INFORMATION: Sequence
US-09-130-973-22
```

```
Query Match          0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2
```

RESULT 58

```
US-09-130-973-23/c
/ Sequence 23, Application US/09130973
/ Patent No. 6172209
/ GENERAL INFORMATION:
/ APPLICANT: Manoharan, Muthiah
/ APPLICANT: Cook, Phillip Dan
/ APPLICANT: Prakash, Thazha P
/ APPLICANT: Kawasaki, Andrew M
/ TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
/ FILE REFERENCE: ISIS2955
/ CURRENT APPLICATION NUMBER: US/09/130,973
/ CURRENT FILING DATE: 1998-08-07
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 23
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (16)..(19)
/ OTHER INFORMATION: 2'-O-dimethylaminoxyethyl
/ OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1
/ OTHER INFORMATION: Sequence
US-09-130-973-23
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Query Match          0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2
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RESULT 59

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US-09-130-973-24/c
/ Sequence 24, Application US/09130973
/ Patent No. 6172209
/ GENERAL INFORMATION:
/ APPLICANT: Manoharan, Muthiah
/ APPLICANT: Cook, Phillip Dan
/ APPLICANT: Prakash, Thazha P
/ APPLICANT: Kawasaki, Andrew M
/ TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
/ FILE REFERENCE: ISIS2955
/ CURRENT APPLICATION NUMBER: US/09/130,973
/ CURRENT FILING DATE: 1998-08-07
/ NUMBER OF SEQ ID NOS: 58
```

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/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (16)..(19)
/ OTHER INFORMATION: 2'-O-methoxyethyl
/ OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1
/ OTHER INFORMATION: Sequence
US-09-130-973-24
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```
Query Match          0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2
```

RESULT 60

```
US-09-130-973-25/c
/ Sequence 25, Application US/09130973
/ Patent No. 6172209
/ GENERAL INFORMATION:
/ APPLICANT: Manoharan, Muthiah
/ APPLICANT: Cook, Phillip Dan
/ APPLICANT: Prakash, Thazha P
/ APPLICANT: Kawasaki, Andrew M
/ TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
/ FILE REFERENCE: ISIS2955
/ CURRENT APPLICATION NUMBER: US/09/130,973
/ CURRENT FILING DATE: 1998-08-07
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 25
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (16)..(19)
/ OTHER INFORMATION: 2'-O-propyl
/ OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1
/ OTHER INFORMATION: Sequence
US-09-130-973-25
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Query Match          0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2
```

RESULT 61

```
US-09-130-973-26/c
/ Sequence 26, Application US/09130973
/ Patent No. 6172209
/ GENERAL INFORMATION:
/ APPLICANT: Manoharan, Muthiah
/ APPLICANT: Cook, Phillip Dan
/ APPLICANT: Prakash, Thazha P
/ APPLICANT: Kawasaki, Andrew M
/ TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
/ FILE REFERENCE: ISIS2955
/ CURRENT APPLICATION NUMBER: US/09/130,973
/ CURRENT FILING DATE: 1998-08-07
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; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)
; OTHER INFORMATION: 5 methyl, 2'-dimethylaminoxyethyl
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-26
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```

Query Match      0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2
```

```

RESULT 62
US-09-130-973-27/c
; Sequence 27, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)
; OTHER INFORMATION: 5 methyl, 2'-O-methoxyethyl
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-27
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```

Query Match      0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2
```

```

RESULT 63
US-09-130-973-31/c
; Sequence 31, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
```

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; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)-(18)
; OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-31
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Query Match      0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2
```

```

RESULT 64
US-09-130-973-33/c
; Sequence 33, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)-(19)
; OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-33
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Query Match      0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2
```

```

RESULT 65
US-09-130-973-34/c
; Sequence 34, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: ISIS2955
```

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; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T'-2'-DMOEt)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1
; OTHER INFORMATION: Sequence
; US-09-130-973-34

Query Match      0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 66
; US-09-130-973-44/c
; Sequence 44, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: 1S182955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 44
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-O-methyleneiminoxyethyl thymidine
; OTHER INFORMATION: Sequence
; US-09-130-973-44

Query Match      0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 67
; US-09-292-768-18/c
; Sequence 18, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; TITLE OF INVENTION: LIMONENE HYDROXYLASES
; FILE REFERENCE: wsur13463
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; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer 3.B
; NAME/KEY: misc feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: Oligonucleotide primer that primes the polyA tail
; OTHER INFORMATION: on cDNA molecules
; US-09-292-768-18

Query Match      0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 68
; US-09-477-902-20/c
; Sequence 20, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: 1S182824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5-methyl-2'-aminoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; US-09-477-902-20

Query Match      0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2662 AAAAAAAAAAAAAAAAAA 2679
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 69
; US-09-477-902-21/c
; Sequence 21, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
```


APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/477,902
CURRENT FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 09/016,520
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/037,143
PRIOR FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)..(18)
OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-477-902-21

Query Match 0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679

Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 70
US-09-477-902-22/c
Sequence 22, Application US/09477902
Patent No. 6194598
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/477,902
CURRENT FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 09/016,520
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/037,143
PRIOR FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
TYPE: DNA
LENGTH: 19
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)..(18)
OTHER INFORMATION: 2'-methoxyethoxy
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Sequence
US-09-477-902-22

Query Match 0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679

Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 71

US-09-477-902-23/c
Sequence 23, Application US/09477902
Patent No. 6194598
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/477,902
CURRENT FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 09/016,520
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/037,143
PRIOR FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)..(19)
OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-477-902-23

Query Match 0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679

Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 72
US-09-477-902-24/c
Sequence 24, Application US/09477902
Patent No. 6194598
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/477,902
CURRENT FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 09/016,520
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/037,143
PRIOR FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
TYPE: DNA
LENGTH: 19
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)..(19)
OTHER INFORMATION: 5-methyl-2'-methoxyethoxy
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Sequence
US-09-477-902-24

Query Match 0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2662 AAAAAAAAAAAAAAAAAA 2679

```
Db      19  |||||
AAAAAAAAAAAAAAAAAAAA 2

RESULT 73
US-09-477-902-25/c
; Sequence 25, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-O-propyl
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-477-902-25

Query Match      0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2662 AAAAAAAAAAAAAAAAAAAAAA 2679
|||||
AAAAAAAAAAAAAAAAAAAA 2

RESULT 74
US-09-477-902-26/c
; Sequence 26, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-477-902-26
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```
Query Match      0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2662 AAAAAAAAAAAAAAAAAAAAAA 2679
|||||
AAAAAAAAAAAAAAAAAAAA 2

RESULT 75
US-09-477-902-27/c
; Sequence 27, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)
; OTHER INFORMATION: 5-methyl-2'-methoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-477-902-27

Query Match      0.7%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2662 AAAAAAAAAAAAAAAAAAAAAA 2679
|||||
AAAAAAAAAAAAAAAAAAAA 2

Db      19  |||||
AAAAAAAAAAAAAAAAAAAA 2
```

Search completed: February 2, 2005, 23:37:45
Job time : 257.971 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:07:30 ; Search time 979.597 Seconds
(without alignments)
11866.381 Million cell updates/sec

Title: US-10-048-046-1_COPY_81_399

Perfect score: 319
Sequence: 1 gtgatacccgatgagcggc.....tacagactgggagatcacc 319

Scoring table:

ORIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 1821985598 residues

Word size: 0

Total number of hits satisfying chosen parameters: 46458

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

Database:

EST:
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	12	3.8	14	5	BQ593541 S013408-0
3	12	3.8	18	1	A1042533 OY0603.x
4	12	3.8	19	8	A2662892 1M0542D15
5	12	3.8	20	6	CF317946 HD--07-N0
6	12	3.8	23	8	A2450598 1M0249H23
7	12	3.8	24	6	CF291636 14R00T--0
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9	12	3.8	25	8	A2374695 1M0127108
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11	12	3.8	27	6	CF339613 RCL1--05-
12	12	3.8	27	9	CF680176 PR10128A
13	12	3.8	28	8	A2458545 1M0262B15
14	12	3.8	29	6	CF327746 NACL--02-
15	12	3.8	30	2	BE904656 601498767
16	12	3.8	30	6	BH662998 SALK_0929
17	12	3.4	20	6	CF339443 RCL1--04-
18	12	3.4	20	8	A2595239 1M0407B18
19	12	3.4	21	8	A2355162 1M0094A24
20	12	3.4	21	9	AG202462 Pan_trog1
21	12	3.4	22	8	A2360666 1M0104F04
22	12	3.4	22	8	A2787102 2M0033B03
23	12	3.4	24	7	L32031 HMMXP10C7B
24	12	3.4	24	8	A2387872 1M0147021

25	11	3.4	25	1	AA911748
26	11	3.4	26	8	AZ309743
27	11	3.4	26	8	A2792942
28	11	3.4	26	8	BH863411
29	11	3.4	26	8	BZ384018
30	11	3.4	27	9	TA45F03P
31	11	3.4	28	1	A1766710
32	11	3.4	28	8	AZ958079
33	11	3.4	29	8	AZ805819
34	11	3.4	29	9	TA128C02P
35	11	3.4	29	9	TA217F07Q
36	11	3.4	30	8	AZ654405
37	11	3.4	30	8	BZ763848
38	11	3.4	30	9	AG200629
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40	10	3.1	19	1	A1696833
41	10	3.1	19	8	AZ589109
42	10	3.1	19	8	AZ989459
43	10	3.1	19	8	AZ994873
44	10	3.1	19	8	CF281215
45	10	3.1	20	6	CF325351
46	10	3.1	20	8	AZ307610
47	10	3.1	20	8	AZ311347
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51	10	3.1	20	9	AJ591197
52	10	3.1	20	9	CL680205
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54	10	3.1	21	7	D11772
55	10	3.1	21	8	AZ405406
56	10	3.1	21	8	AZ583481
57	10	3.1	21	8	AZ607204
58	10	3.1	21	8	AZ658074
59	10	3.1	22	2	BE979698
60	10	3.1	22	6	CF309993
61	10	3.1	22	8	AZ798615
62	10	3.1	22	8	AZ812224
63	10	3.1	22	9	TA114F05P
64	10	3.1	23	6	CF298913
65	10	3.1	23	8	AZ324328
66	10	3.1	23	8	AZ345542
67	10	3.1	23	8	AZ761953
68	10	3.1	23	8	AZ952138
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71	10	3.1	23	9	AG202522
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75	10	3.1	24	8	AZ648378
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81	10	3.1	25	8	AZ303953
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83	10	3.1	25	9	TA308E06P
84	10	3.1	25	9	TA329H09Q
85	10	3.1	25	1	AJ678364
86	10	3.1	26	5	BP083294
87	10	3.1	26	8	AZ413337
88	10	3.1	26	8	AZ660695
89	10	3.1	26	8	AZ663250
90	10	3.1	26	8	AZ949204
91	10	3.1	26	8	BH903520
92	10	3.1	26	8	BH903523
93	10	3.1	26	8	BH903525
94	10	3.1	27	8	AZ813093
95	10	3.1	27	8	AZ830946
96	10	3.1	27	8	BH792336
97	10	3.1	27	9	TA326B02P

AA911748	0115911.5
AZ309743	1M0015N05
A2792942	2M0045N21
BH863411	SALK_0938
BZ384018	SALK_1349
TA45F03P	A1453965 T. brucei
A1766710	u156b01.x
AZ958079	2M0225O10
AZ805819	2M0067K19
TA128C02P	AL464340 T. brucei
TA217F07Q	AL479008 T. brucei
AZ654405	AZ654405 1M0528K06
BZ763848	SALK_1226
AG200629	Pan_trog1
CL438015	PS1661-N
A1696833	wc74609.x
AZ589109	1M0397D22
AZ989459	2M0272M17
AZ994873	2M0280D02
CF281215	14E7L--08
CF325351	UMT1--03-
AZ307610	1M0009G15
AZ311347	1M0026C16
AZ366451	1M0115N07
AZ436192	1M0233K14
AZ492125	1M0326I05
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CL680205	PRI0128A
AJ666336	AJ666336 AJ666336
D11772	HMMH01E05
AZ405406	1M0174P08
AZ583481	1M0378K06
AZ607204	1M0429H03
AZ658074	1M0534G12
BE979698	602288551
CF309993	ABF--04-G
AZ798615	2M0035F19
AZ812224	2M0078G13
AJ678364	AJ678364 T. brucei
TA114F05P	7LEAF--02
CF298913	CF298913
AZ324328	1M0046B16
AZ345542	1M0080A14
AZ761953	1M0556K06
AZ952138	2M0216C19
TA125F10Q	AL463486 T. brucei
AG198216	AG198216 Pan_trog1
AG202522	2M00070001
BM400127	5009-0-66
AZ362057	1M0107E05
AZ492799	1M0327B10
AZ648378	1M0517D24
AZ658569	1M0535I19
AZ807619	2M0070001
AG201478	Pan_trog1
A1638719	tc24e01.x
A1679469	cu74c11.x
AZ303953	1M0003N18
AZ364139	1M0110A14
TA308E06P	AL490757 T. brucei
TA329H09Q	AL492434 T. brucei
AJ678364	AJ678364
BP083294	BP083294
AZ413337	1M0197J13
AZ660695	1M0538K22
AZ663250	1M0542J16
AZ949204	2M0212M04
BH903520	SALK_1028
BH903523	SALK_1028
BH903525	SALK_1028
AZ813093	2M0080C08
AZ830946	2M0110N24
BH792336	SALK_0634
AL492719	T. brucei

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C 101	10	3.1	28	7	W54502	mc01b04.t1
C 102	10	3.1	28	8	AQ026271	1(3)L6241
C 103	10	3.1	28	8	AZ307173	1M0008003
C 104	10	3.1	28	8	AZ491585	AZ491585
C 105	10	3.1	28	8	AZ503891	1M0345216
C 106	10	3.1	28	8	BH907764	1M0345216
C 107	10	3.1	28	8	TA264B01P	TA264B01P
C 108	10	3.1	28	9	TA203385	TA203385
C 109	10	3.1	29	8	AZ364006	AZ364006
C 110	10	3.1	29	8	AZ476559	1M010F02
C 111	10	3.1	29	8	AZ595520	1M0295C02
C 112	10	3.1	29	8	AZ619807	1M0408M09
C 113	10	3.1	29	8	AZ651823	1M0450N11
C 114	10	3.1	29	8	AZ801848	2M0060A03
C 115	10	3.1	29	8	AZ841479	2M0139A01
C 116	10	3.1	29	8	BH846915	SAUK_0110
C 117	10	3.1	29	9	TA102E020	TA102E020
C 118	10	3.1	29	9	TA108H010	TA108H010
C 119	10	3.1	29	9	TA262C120	TA262C120
C 120	10	3.1	29	9	TA262H05Q	TA262H05Q
C 121	10	3.1	30	4	BE539470	601060134
C 122	10	3.1	30	4	BE539470	601060134
C 123	10	3.1	30	6	CP324474	CP324474
C 124	10	3.1	30	6	AZ317450	HDN--06-X
C 125	10	3.1	30	8	AZ343274	HDN--06-X
C 126	10	3.1	30	8	AZ396226	1M0036A07
C 127	10	3.1	30	8	AZ471850	1M0076C04
C 128	10	3.1	30	8	AZ582204	1M0160N09
C 129	10	3.1	30	8	AZ582204	1M0374N19
C 130	10	3.1	30	8	AZ774809	2M0040005
C 131	10	3.1	30	8	AZ821583	2M0094I23
C 132	10	3.1	30	9	BH902925	SAUK_1015
C 133	10	3.1	30	9	TA255B11P	TA255B11P
C 134	9	2.8	11	9	AJ600625	Arabi10ps
C 135	9	2.8	14	1	AJ659358	AJ659358
C 136	9	2.8	15	1	AJ666289	AJ666289
C 137	9	2.8	16	1	AJ666289	AJ666289
C 138	9	2.8	16	1	AA968729	01E9H11.8
C 139	9	2.8	16	4	AJ676705	AJ676705
C 140	9	2.8	17	4	BG926060	HMC23-1-E
C 141	9	2.8	17	7	AM247673	2820207.5
C 142	9	2.8	18	5	CF921142	gmrbRw3-
C 143	9	2.8	18	5	BQ586393	S014468-0
C 144	9	2.8	19	1	AJ590807	Arabi10ps
C 145	9	2.8	19	1	AJ476315	1A15C09.X
C 146	9	2.8	19	1	AJ647104	AJ647104
C 147	9	2.8	19	5	BX552609	BX552609
C 148	9	2.8	19	8	AZ410166	1M0182J17
C 149	9	2.8	19	8	AZ411188	1M0232004
C 150	9	2.8	19	8	AZ450047	1M0248A08
					AZ458806	1M0263012

ALIGNMENTS

RESULT 1
AZ411813 24 bp DNA linear GSS 03-OCT-2000
LOCUS
DEFINITION
INV0185H03F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0185H03 F, genomic survey sequence.
ACCESSION
AZ411813
VERSION
AZ411813.1 GI:10535826
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duvall, B., Hamil, C., Telam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

JOURNAL

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

EMAIL: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0185 row: H column: 03
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0185H03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1/4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 4.4%; Score 14; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 CACGTCTCTCTGAG 111
Db 2 CACGTCTCTCTGAG 15

RESULT 2
BQ593541 14 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION
S013408-024-026-P02-SP6 MP1Z-RDIS-024-developing root Beta vulgaris
cDNA clone 024-026-P02 5-PRIME, mRNA sequence.
ACCESSION
BQ593541
VERSION
BQ593541.1 GI:26123124
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris

REFERENCE
AUTHORS
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amarantaceae; Beta.
Herwig, R., Schultz, B., Weishaar, B., Hennig, S., Steinfath, M.,

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radloff, U.
Construction of a 'uniGene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
MEDLINE
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 26 row: F column: 02
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
Location/Qualifiers
1..14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:193314"
/db_xref="taxon:161934"
/clone="024-026-P02"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_1lb="MP1Z-ADIS-024-developing root"
/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzielbener Saatnucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: sequencing granted in the context of the GABI-Best project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.tzpd.de>

ORIGIN
Query Match 3.8%; Score 12; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 173 CTGCTCTCTGA 184
|||||||
1 CTGCTCTCTGA 12

RESULT 3
A1042533 18 bp mRNA linear EST 30-JUN-1998
A1042533
LOCUS
DEFINITION
oy06e03.x1 Soares senescent fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:1665052 3' similar to TR-015662 O15662
TRANSCRIPTION-RELATED PROTEIN ; mRNA sequence.
ACCESSION
A1042533
VERSION
A1042533.1 GI:3281727
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 18)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapdb-remail.nih.gov
This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.lbl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40m3 fwd. ET from Amerham

High quality sequence stop: 1.
Location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1665052"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/clone_1lb="Soares senescent fibroblasts NBHSF"
/note="Vector: pT73D (Pharmacia) with a modified polylinker V type; phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGGCCGCAATTTTATTTTATTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 3.8%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 225 TGACACTGGAAG 236
|||||||
5 TGACACTGGAAG 16

RESULT 4
A2662892/c 19 bp DNA linear GSS 14-DEC-2000
A2662892/c
LOCUS
DEFINITION
1M0542D15F Mouse 10kb plasmid UNGC1M library Mus musculus genomic clone UNGC1M0542D15 F, genomic survey sequence.
ACCESSION
A2662892
VERSION
A2662892.1 GI:11800038
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
REFERENCE
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: D column: 15
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNG1M0542D15"
/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.8%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 AGCACCGTGA 253

Db 13 AGCACCGTGA 2

RESULT 5

CF317946/c

LOCUS

DEFINITION HD--07-N06.g1 OSHDAC1-overexpressing transgenic rice plasmid cdNA

HD--07-N06, mRNA sequence.

ACCESSION

CF317946

VERSION

CF317946.1

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

REFERENCE

1 (bases 1 to 20)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nam B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Yonsei University

Yongin, Kyonggi, Korea

Tel.: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..20

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HD-07-N06"

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/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone.lib="OSHDA1-overexpressing transgenic rice plasmid

cdNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 3.8%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGC 50

Db 14 CGCGCGCGCGC 3

RESULT 6

AZ450598

LOCUS

DEFINITION IM0249H23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic

clone UUGCIM0249H23 F, genomic survey sequence.

ACCESSION

AZ450598

VERSION

AZ450598.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0249 row: H column: 23

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

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/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone.lib="Mouse 10kb plasmid UUGCIM library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 3.8%; Score 12; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 GGAGCGGAGT 122
|||||
Db 3 GGAGCGGAGT 14

RESULT 7

CP291636/c 24 bp mRNA linear EST 14-AUG-2003
LOCUS CP291636
DEFINITION 14ROOT--02-C09.g1 Rice root plasmid cDNA library (14ROOT) *Oryza sativa* (japonica cultivar-group) cDNA clone 14ROOT--02-C09, mRNA sequence.

ACCESSION CP291636
VERSION CP291636.1 GI:33660669
KEYWORDS EST.
SOURCE *Oryza sativa* (japonica cultivar-group)
ORGANISM *Oryza sativa* (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzae; Oryza.
1 (bases 1 to 24)
KIM,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., KIM,J.K., Kim,Y.-K., and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@jdo.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1. .24
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/culti_var="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-C09"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match 3.8%; Score 12; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 CGCGCGCGCGCG 50
|||||
Db 24 CGCGCGCGCGCG 13

RESULT 8
AZ346816 24 bp DNA linear GSS 29-SEP-2000
LOCUS AZ346816
DEFINITION 1M0082816F Mouse 10kb plasmid UUGCM library Mus musculus genomic
clone UUGCM0082816 F, genomic survey sequence.
ACCESSION AZ346816
VERSION AZ346816.1 GI:10426053
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingay,A., von
Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

TITLE

JOURNAL

COMMENT
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: B column: 16
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCM0082816"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1[473114]gb[AF129672.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 3.8%; Score 12; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 151 CCTTCCTCC 162
|||||
Db 9 CCTTCCTCC 20

RESULT 9
AZ374695 25 bp DNA linear GSS 02-OCT-2000
LOCUS AZ374695
DEFINITION 1M0127108R Mouse 10kb plasmid UUGCM library Mus musculus genomic
clone UUGCM0127108 R, genomic survey sequence.
ACCESSION AZ374695
VERSION AZ374695.1 GI:10488395
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0127 row: 1 column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0127108"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.8%; Score 12; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 GGCGCGGAGGAG 88
|||||
Db 12 GGCGCGGAGGAG 23

RESULT 10
AZ793814/c 25 bp DNA linear GSS 16-FEB-2001
LOCUS AZ793814
DEFINITION 2M0047J3JF Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0047J3J F, genomic survey sequence.
ACCESSION AZ793814
VERSION AZ793814.1 GI:12939150
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0047 row: J column: 13
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0047J13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.8%; Score 12; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 GGAGGAGGCGCA 93
|||||
Db 24 GGAGGAGGCGCA 13

RESULT 11
CF339613 27 bp mRNA linear EST 18-AUG-2003
LOCUS CF339613
DEFINITION RC11--05-g12 g1 Regenerated callus lambda phage cDNA library (RC11)
Oryza sativa (Japponica cultivar-group) cDNA clone RC11--05-g12,
mRNA sequence.
ACCESSION CF339613
VERSION CF339613.1 GI:33827599
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Song, S. I., Kim, J. K., Kim, Y. K., and Nahm, B. H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1-05-G12"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

Query Match 3.8%; Score 12; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCCGCCGCCGC 50
15 CGCCGCCGCCGC 26

RESULT 12
CL680176 27 bp DNA linear GSS 09-JUL-2004
LOCUS PRI0128a.D10.2 - PRI0128a.BR (27) Mixed stage fosmid library of P.
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL680176
VERSION CL680176.1 GI:50187006
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Nemadiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Strinivasan, J., Otto, G. W., Kahlow, U., Geisler, R., and Sommer, R. V.
TITLE Append: an Acedb database for the nematode satel[li]te organism
JOURNAL Pristionchus pacificus
COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: raf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7

Class: fosmid ends.
Location/Qualifiers
1. .27
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pBf10s-5 Fosmid vector"

ORIGIN
Query Match 3.8%; Score 12; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 TTAACAAGCTGA 273
1 TTAACAAGCTGA 12

RESULT 13
A2458545 28 bp DNA linear GSS 04-OCT-2000
LOCUS A2458545/c 1M0262B15R Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION clone UUCGM0262B15 R, genomic survey sequence.
ACCESSION A2458545
VERSION A2458545.1 GI:10616670
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rolly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0262 row: B column: 15
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0262B15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGM library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrolitically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.8%; Score 12; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 CGCGCCGCGCCG 54
DB 25 CGCGCCGCGCCG 14

RESULT 14
CF327746/c 29 bp mRNA linear EST 18-AUG-2003
LOCUS NAFL--02-F18.g1 Rice callus plasmid cDNA library (NAFL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NAFL--02-F18, mRNA
sequence.

ACCESSION CF327746 GI:33803742
VERSION CF327746.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
TITLE
AUTHORS
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

Source

1. .29
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NAFL-02-F18"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NAFL)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match 3.8%; Score 12; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCCGCGCCG 50
DB 13 CGCGCCGCGCCG 2

RESULT 15

BE904656/c 30 bp mRNA linear EST 20-OCT-2000
LOCUS BE904656
DEFINITION 601498767F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900665 5',
mRNA sequence.

ACCESSION BE904656
VERSION BE904656.1 GI:10397135
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>
1 (bases 1 to 30)
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHM9700 row: e column: 18
High quality sequence scop: 30.
Location/Qualifiers

FEATURES

source

1. .30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3900665"
/issue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: qligo dt.
Average insert size 1.1 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 3.8%; Score 12; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCCGCGCCG 50
DB 14 CGCGCCGCGCCG 3

RESULT 16
BH862998 30 bp DNA linear GSS 05-AUG-2002
LOCUS BH862998/c
DEFINITION SALK 092934 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_092934, genomic survey sequence.

ACCESSION BH862998
VERSION BH862998.1 GI:22098324
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 30)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
CONTACT: Joseph R. Ecker
The Salk Institute for Biological Studies

TITLE Arabidopsis Genome
JOURNAL
AUTHORS
COMMENT

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckers@sal.k.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At5g67610.

Class: TDNA tagged.

Location/Qualifiers

FEATURES

Source

1. 30
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_092934"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 3.8%; Score 12; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 266 AACCTGAAGCTT 277
|||||
Db 17 AACCTGAAGCTT 6

RESULT 17
CF339443 20 bp mRNA linear EST 18-AUG-2003
LOCUS CF339443/c
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-003,
mRNA sequence.

ACCESSION CF339443

VERSION CF339443.1 GI:33827271
KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Song, S. I., Kim, Y. K., Kim, Y. K., and Nahm, B. H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B. H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 350 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

TITLE

JOURNAL

COMMENT

FEATURES

Source

1. 20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--04-003"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E. coli SOLR"
/clone_idb="Regenerated callus lambda phage cDNA library
(RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SacI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

ORIGIN

end with SetI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

Query Match 3.4%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 GCCGCCGCCGC 50
|||||
Db 20 GCCGCCGCCGC 10

RESULT 18
A2595239 20 bp DNA linear GSS 13-DEC-2000
LOCUS A2595239/c
DEFINITION 1M0407B18R Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCGM0407B18 R, genomic survey sequence.

ACCESSION A2595239 GI:11717429
VERSION A2595239.1
KEYWORDS GSS.

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0407 row: B column: 18
Seq primer: CACACAGAAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

Source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0407B18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_idb="Mouse 10kb plasmid UGCGM library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G1[4732114]gb[AP29072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to

adapored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      3.4% Score 11; DB 8; Length 21;
Best Local Similarity 100.0%; Prod. No. 1.9e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      153 TTTTCCTTCCCC 163
          |||||
Db       4 TTTTCCTTCCCC 14

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RESULT 20					
AG202462/c					
LOCUS	AG202462	21 bp	DNA	1 linear	GSS 06-MAR-2004
DEFINITION	Pan troglodytes DNA, clone: RP43-085O14.T7, genomic survey sequence.				

ACCESSION	AG202462
VERSION	AG202462.1
KEYWORDS	GSS
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes

REFERENCE
AUTHORS

1 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J.,

TITLE	Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
REFERENCE	BAC end sequences of library RP-43
JOURNAL	Unpublished
AUTHORS	2 (bases 1 to 21)
PART	Part H. Kim Y. Kim S. Han Y. Woo T. Park Y. Eum C. T.

TITLE Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
JOURNAL Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute

Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail: redstone@mail.kriib.re.kr, URL: <http://phs.grc.kriib.re.kr/>,
Tel: +82-42-880-7100, Fax: +82-42-880-7101)

COMMENT
15:10:02-42-880-1181, fax:82-42-860-4409)
Clones are derived from the chimerae BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance

of clone tracking errors.
PRIMERS
Sequencing: T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcORI

FEATURES

Location/Qualifiers

R.Site 1 : EcORI

R.Site 2 : EcORI.

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Source
1. .21
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/mol_type="genomic DNA"
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/clone="RP43-085014.T7"
/db_xref="taxon:9598"
/ncbi_taxonomy="genomic DNA"

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/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC lib.rv"

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ORIGIN	Query Match
1	34% Score 11 PD 0 Percent of

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      Query Match      5.73%  score 11;  DB 9;  length 21;
      Best Local Similarity 100.0%;  Pred. No. 1.9e+06;
      Matches 11;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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QY 301 ACAGACTGGGG 311

Db 21 ACAGACTGGGG 11

RESULT 21
A2360666

LOCUS	AZ360666	22 bp	DNA	linear	GENE	02-OCT-2000
DEFINITION	IM0104F04F Mouse 10kb plasmid UUC1M library Mus musculus genomic					

ACCESSION clone UNGC1M0104F04 F, genomic survey sequence.
 A2360666
 VERSION A2360666.1 GI:10474366
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 TITLE unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0104 row: F column: 04
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 FEATURES
 source location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UNG1M0104F04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UNGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gb]|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ACCESSION clone UNGC2M0033B03 F, genomic survey sequence.
 A2787102
 VERSION A2787102.1 GI:12925528
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 TITLE unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0033 row: B column: 03
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 FEATURES
 source location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UNG2M0033B03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UNGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gb]|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.4%; Score 11; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 202 AGTGATGAAA 212
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 Db 3 AGTGATGAAA 13

RESULT 22
 A2787102 22 bp DNA linear GSS 16-FEB-2001
 LOCUS
 DEFINITION ZM0033B03F Mouse 10kb plasmid UNGC1M library Mus musculus genomic

ORIGIN

Query Match 3.4%; Score 11; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 187 TCACTGTAGAA 197
 |||||
 Db 18 TCACTGTAGAA 8

RESULT 23
 I32031 24 bp mRNA linear EST 02-AUG-1995
 LOCUS
 DEFINITION H0MKP10C7B Human placenta Homo sapiens cDNA X22BBB, mRNA

sequence.
 accession 132031.1 GI:927073
 version 132031.1
 keywords EST.
 source Homo sapiens (human)
 organism Homo sapiens
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 authors 1 (bases 1 to 24)
 Lee, C.-C., Yazdani, A., Wehnert, M., Bailey, J., Couch, L., Xiong, M., Cooilbaugh, M.I., Chinnault, C.A., Baldini, A., Lindsay, E.A., Zhao, Z.-Y., and Caskey, C.T.H.
 title Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries
 journal Hum. Mol. Genet. 4, 1373-1380 (1995)
 medline 96090257
 pubmed 7581376
 comment Contact: Caskey, C.T.H.
 features Location/Qualifiers
 source 1..24
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /map="Xq12-q13.1"
 /clone="XP2E88"
 /clone_lib="Human placenta"
 /note="Arrayed cDNAs and cosmid libraries from human placental tissue"

Query Match 3.4%; Score 11; DB 7; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 TCAGGTGCGGT 225
 |||||
 5 TCAGGTGCGGT 15

RESULT 24
 locus AZ387872 24 bp DNA linear GSS 02-OCT-2000
 definition 1M0147021R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0147021 R, genomic survey sequence.
 accession AZ387872
 version AZ387872.1 GI:10501580
 keywords GSS.
 source Mus musculus (house mouse)
 organism Mus musculus
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 authors 1 (bases 1 to 24)
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duvall, B., Hamil, C., Jellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D. Weiser, R.
 title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 journal Unpublished (2000)
 comment Contact: Robert B. Weiser
 university of Utah Genome Center
 rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 tel: 801 585 5606
 fax: 801 585 7177
 email: ddunn@genetics.utah.edu
 insert length: 10000 Std Error: 0.00
 plate: 0147 row: 0 column: 21
 seq primer: CACACAGAAACAGCTATGACC
 class: plasmid ends
 high quality sequence stop: 24.
 location/Qualifiers

FEATURES

source 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0147021"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 3.4%; Score 11; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 CTTTCCTTCCC 162
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 13 CTTTCCTTCCC 23

RESULT 25
 locus AA911748 25 bp mRNA linear EST 24-AUG-1998
 definition o115g11.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1476644 3' similar to TR:Q99628 Q99628 STAR BINDING PROTEIN 1 ;, mRNA sequence.
 accession AA911748
 version AA911748.1 GI:3051112
 keywords EST.
 source Homo sapiens (human)
 organism Homo sapiens
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 authors 1 (bases 1 to 25)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 title National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 journal Unpublished (1997)
 comment Contact: Robert Strausberg, Ph.D.
 email: cga@b-remail.nih.gov
 tissue procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.
 cdna library preparation: M. Bento Soares, Ph.D.
 dna sequencing by: Washington University Genome Sequencing Center
 clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILMIL at: www.bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 insert length: 704 Std Error: 0.00
 seq primer: -40m13 fwd. ET from Amersham
 high quality sequence stop: 1.
 location/Qualifiers

FEATURES

SOURCE

1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1476644"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC4"
/note="Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 3.4%; Score 11; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 186 ATCACTGTAGA 196
|||||
Db 3 ATCACTGTAGA 13

RESULT 26

A2309743

LOCUS 26 bp DNA linear GSS 29-SEP-2000
DEFINITION clone UUGC1M0016N05 F, genomic survey sequence.
ACCESSION A2309743
VERSION A2309743.1 GI:10351041
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: N column: 05
Seq primer: CATTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

SOURCE

1..26
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0016N05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gblAF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells, and selected for ampicillin resistance."

ORIGIN

Query Match 3.4%; Score 11; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 152 CTTTCCTTCCC 162
|||||
Db 4 CTTTCCTTCCC 14

RESULT 27

A2792942

LOCUS 26 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M004S21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M004S21 R, genomic survey sequence.
ACCESSION A2792942
VERSION A2792942.1 GI:12937583
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: N column: 21
Seq primer: CACACAGGAAACACGATGACG
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

SOURCE

1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M004S21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD4 (g1/4732114[gb]/AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.4%; Score 11; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 GAGTGGACCAT 129
|||||
5 GAGTGGACCAT 15

RESULT 28

BH863411/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BH863411 26 bp DNA linear GSS 05-AUG-2002
SALK_093836 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_093836, genomic survey sequence.
BH863411 GI:22099002
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 26)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

FEATURES

source

Class: TDNA tagged.
Location/Qualifiers
1..26
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_093836"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 3.4%; Score 11; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 CTGTAGATTG 200
|||||
13 CTGTAGATTG 3

RESULT 29

BZ384018/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BZ384018 26 bp DNA linear GSS 26-NOV-2002
SALK_134931.24.10 x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_134931.24.10.x, genomic
survey sequence.
BZ384018 GI:25480886
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 26)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At5g35220.
Class: TDNA tagged.
Location/Qualifiers
1..26
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_134931.24.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

FEATURES

source

Class: TDNA tagged.
Location/Qualifiers
1..26
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_134931.24.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 3.4%; Score 11; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 154 TTCCTTCCCA 164
|||||
24 TTCCTTCCCA 14

RESULT 30

TA45F03P

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

TA45F03P 27 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 45f03, forward sequence,
genomic survey sequence.
TA453965
TA453965.1 GI:11856142
GSS.

SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 27)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb) . The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999) .
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1..27
 /organism="Trypanosoma brucei"
 /mol_type="Genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="45f03"
 ORIGIN
 Query Match 3.4%; Score 11; DB 9; Length 27;
 Best Local Similarity 100.0%; Pred. NO. 1.9e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 305 ACTGGGATGT 315
 |||||
 |||||
 Db 10 ACTGGGATGT 20
 RESULT 31 28 bp mRNA linear EST 02-JUL-1999
 A1786710 uc56b01.x1 Sugano mouse 1yter.mla Mus musculus cDNA clone
 LOCUS IMAGE:1922913, similar to SW:THM_RAT_P13437 3-KETOACYL-COA
 DEFINITION THIOLASE MITOCHONDRIAL ;, mRNA sequence.
 A1786710
 A1786710.1 GI:5334426
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Steptoe, M., Theisling, B., Allen, M., Bowers, Y.,
 Peterson, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R.,
 Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterston, R. and Wilson, R.
 The Mashu-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Marra M/Mashu-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.jnl.gov) for further information.
 MGI:980205

```

FEATURES
    source
        Trace considered overall poor quality
        Possible reversed clone: similarity on wrong strand
        Seq primer: custom primer used
        High quality sequence stop: 1.
        location/Qualifiers
            1..28
                /organism="Mus musculus"
                /mol_type="RNA"
                /strain="C57BL"
                /db_xref="taxon:10090"
                /clone="IMAGE:1923913"
                /sex="female"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_id="Sugano mouse liver mlia"
                /note="Organ: liver; Vector: pME185-FL3; Site 1: DraIII
                (CAGCTGTG); Site 2: DraII (CACCATGTG); 1st strand cDNA
                was primed with an oligo(dT) primer
                [ATGTGGCCTTTTCTTTTCTTTT]; double-stranded cDNA was
                ligated to a DraIII adaptor (TGTGGCCTACTG), digested
                and cloned into distinct DraIII sites of the pME185-FL3
                vector (5' site CAGCTGTG, 3' site CACCATGTG). XhoI should
                be used to isolate the cDNA insert. Site selection was
                performed to exclude fragments <1.5kb. Library
                constructed by Dr. Sumio Sugano (University of Tokyo
                Institute of Medical Science). Custom primers for
                sequencing: 5' end primer CTTGTGCTTAAGCTGCG and 3' end
                primer CGACTCTCAGCTCAGCACA."

ORIGIN
    Query Match      3.4%; Score 11; DB 1; Length 28;
    Beat Local Similarity 100.0%; Pred. No. 1.9e+06;
    Matches 11, Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      230 CTGGAAGATAC 240
Db      28 CTGGAAGATAC 18

RESULT 32
A2958079/c
LOCUS      A2958079      28 bp      DNA      linear      GSS 27-APR-2001
DEFINITION 2M0225010F Mouse 10kb plasmid U06C2M library Mus musculus genomic
clone U06C2M0225010 F, genomic survey sequence.
ACCESSION  A2958079
VERSION    A2958079.1 GI:13829306
KEYWORDS
SOURCE
ORGANISM  Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid insets
Unpublished (2000)
REFERENCE
PUBLISHED
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0225 row: 0 column: 10
Seq primer: CGTTGTAAGACAGCCACAT
Class: plasmid ends
High quality sequence stop: 28.
location/Qualifiers

```

source

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1. 28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M025010"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG2M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

Query Match 3.4%; Score 11; DB 8; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 TGGGAGATGCA 317
 |||||
 Db 18 TGGGAGATGCA 8

RESULT 33
 LOCUS AZ805819 29 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0067K19F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 clone UUCG2M0067K19 F, genomic survey sequence.
 ACCESSION AZ805819
 VERSION AZ805819.1 GI:12966630
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 29)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Jilam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0067 row: K column: 19
 Seq primer: CGTTCTAAACGACGGCACT
 Class: plasmid ends
 High quality sequence stop: 29.
 Location/Qualifiers

source

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1. 29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0067K19"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

Query Match 3.4%; Score 11; DB 8; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 CCGGAGAGAGG 89
 |||||
 Db 7 CCGGAGAGAGG 17

RESULT 34
 LOCUS TA128C02P/C 29 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 128C02, forward sequence.
 ACCESSION AL464340
 VERSION AL464340.1 GI:11834603
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 1 (bases 1 to 29)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.B., Rajandream, M.A. and Barrall, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrall@sanger.ac.uk and nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers

FEATURES

FEATURES

```
source
1..29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="128C02"

ORIGIN
Query Match 3.4%; Score 11; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 32 AAGCAGTGGCC 42
|||||
14 AAGCAGTGGCC 4

RESULT 35
TA217F070/c 29 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 217F07, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL479008
VERSION AL479008.1 GI:11844887
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 29)
Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,
Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,
Welville S.E., Rajandream M.A. and Barrell B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1..29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="217F07"

FEATURES
source
1..29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="217F07"

ORIGIN
Query Match 3.4%; Score 11; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 159 TCCCCAGCAAT 169
|||||
24 TCCCCAGCAAT 14

RESULT 36
A2654405/c 30 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0528K06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0528K06 R, genomic survey sequence.
```

```
ACCESSION A2654405
VERSION A2654405.1 GI:11791551
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
1 (bases 1 to 30)
Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamil C.,
Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T.,
Reilly M., Rose M., Rose R., Stokes R., Tingey A., von
Niederhausern A. and Wright D. Weis R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0528 row: K column: 06
Seq primer: CACACAGAAACACTATGACC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0528K06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_id="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1473214[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 3.4%; Score 11; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 240 CCAGCACCAGT 250
|||||
18 CCAGCACCAGT 8

RESULT 37
B2763848 30 bp DNA linear GSS 13-MAR-2003
LOCUS SALK_122613_25_20 x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_122613.25.20.x, genomic
```

survey sequence.

ACCESSION B2763848
 VERSION B2763848.1 GI:289356401
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 30)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 CONTACT: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1..30
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone_1fb="SALK_122613.25.20.x"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 3.4%; Score 11; DB 8; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 ACCTTCTCTC 160
 |||||
 Db 18 ACCTTCTCTC 28

RESULT 38
 AG200629 30 bp DNA linear GSS 06-MAR-2004
 LOCUS Pan troglodytes DNA, clone: RP43-082L13.TU, genomic survey
 DEFINITION
 AG200629
 AG200629.1 GI:45232804
 GSS.
 Pan troglodytes (chimpanzee)
 SOURCE Pan troglodytes
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 1
 Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
 Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
 BAC end sequences of library RP-43
 Unpublished
 2 (bases 1 to 30)
 Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
 Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
 Direct Submission
 Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of

BioScience and Biotechnology (KRIBB), Genome Research Center (GRC);
 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
 (E-mail: redstone@mail.krrib.re.kr, URL: <http://pms-grc.krrib.re.kr/>,
 Tel: 82-42-866-7181, Fax: 82-42-860-4409)
 Clones are derived from the chimpanzee BAC library RP-43. This BAC
 end was generated during the RAD process and may have higher chance
 of clone tracking errors.
 PRIMERS
 Sequencing: T7
 LIBRARY
 Vector : pBACe3.6
 R Site 1 : EcoRI
 R Site 2 : EcoRI
 Location/Qualifiers
 1..30
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-082L13.TU"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_1fb="RP-43 Chimpanzee Male BAC library"

ORIGIN

Query Match 3.4%; Score 11; DB 9; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 CCTTCTCTTC 161
 |||||
 Db 3 CCTTCTCTTC 13

RESULT 39
 CL438015 10 bp DNA linear GSS 18-MAR-2004
 LOCUS PST661-NR.Seg MICE1 Mus musculus genomic clone PST661-NR.Seg
 DEFINITION
 CL438015
 CL438015.1 GI:45574155
 GSS.
 Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 10)
 Hicks,G.G.
 www.Escellis.ca
 Unpublished (2002)
 CONTACT: Hicks GG
 Mammalian Functional Genomics Centre
 Manitoba Institute of Cell Biology, University of Manitoba
 ON5029, 675 McDermott Ave, Winnipeg, MB R3E 0V9, Canada
 Tel: 204 787 2133
 Fax: 204 787 2190
 Email: hicks@ggc.umanitoba.ca
 U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
 sequence information and target gene cloning can be generated. ES
 cell line harboring insertion mutation of target gene is available.
 Sequence analysis available from
http://140.193.242.7/eeadb/public_search.php?PST=PST661-NR.Se
 q
 Class: Gene Trap.
 Location/Qualifiers
 1..10
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="129 sv"
 /db_xref="taxon:10090"
 /clone="PST661-NR.Seg"
 /sex="Male"
 /cell_type="Embryonic stem cell"
 /cell_line="D3H (J1 subclone)"

FEATURES
 source

```

/clone_11b="MICB1"
/notes="Vector: U3NesSV1"

ORIGIN
Query Match      3.1%; Score 10; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      105 TCCTGAGGAA 114
      |||||
      1 TCGTAGAGAA 10

RESULT 40
A1696833      19 bp mRNA linear EST 17-DEC-1999
LOCUS      wc74e09.x1 NCI CGAP Paul Homo sapiens cDNA clone IMAGE:2324392 3'
DEFINITION similar to TR:001942 001942 EXTENSIN ; contains element TAR1
A1696833      repetitive element ; , mRNA sequence.
ACCESSION A1696833.1 GI:4984733
VERSION A1696833.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Unpublished (1997)
Email: cgapdb-remail.nlm.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbtrp/image/image.html

FEATURES
Source
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2324392"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_11b="NCI CGAP Paul"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1; SalI,
Site 2: NotI; Cloned unidirectionally. Primer: oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN
Query Match      3.1%; Score 10; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CGGAGGAGGG 90
      |||||
      2 CGGAGGAGGG 11

RESULT 41
A2589109      19 bp DNA linear GSS 13-DEC-2000
LOCUS      1M0397D22R Mouse 10kb plasmid U3NesSV1 library Mus musculus genomic
DEFINITION clone U3NesSV1M0397D22 R, genomic survey sequence.
ACCESSION A2589109

```

```

VERSION A2589109.1 GI:11711299
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0397 row: D column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U3NesSV1M0397D22"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, Ti-resistant, F-."
/clone_11b="Mouse 10kb plasmid U3NesSV1 library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g114732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      3.1%; Score 10; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      188 CACTGTAGAA 197
      |||||
      18 CACTGTAGAA 9

RESULT 42
A2989459      19 bp DNA linear GSS 27-APR-2001
LOCUS      2M0272M17R Mouse 10kb plasmid U3NesSV1 library Mus musculus genomic
DEFINITION clone U3NesSV1M0272M17 R, genomic survey sequence.
ACCESSION A2989459

```

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

AZ989459.1 GI:13860686
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0272 row: M column: 17
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0272M17"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 3.1%; Score 10; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 GTGATTACCA 266
 |||||
 Db 7 GTGATTACCA 16

RESULT 43
 AZ994873 19 bp DNA 1linear GSS 27-APR-2001
 LOCUS 2M0280D02R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 DEFINITION clone UUGC2M0280D02 R, genomic survey sequence.
 ACCESSION AZ994873

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

AZ994873.1 GI:13866100
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0280 row: D column: 02
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0280D02"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 3.1%; Score 10; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 TCAGGTACAG 224
 |||||
 Db 14 TCAGGTACAG 5

RESULT 44
 CF281215 20 bp mRNA 1linear EST 14-AUG-2003
 LOCUS 14BTL--08-C23.g1 Rice etiolated leaf plasmid cDNA library (14BTL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14BTL--08-C23, mRNA sequence.

ACCESSION CF281215
 VERSION CF281215.1 GI:33658602
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eubartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 Source
 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT1--03-A01"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI, mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

ORIGIN
 Query Match 3.1%; Score 10; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 TCGCCGCCGC 47
 |||||
 10 TCGCCGCCGC 1

Db 10 TCGCCGCCGC 1

RESULT 45
 CF25351/c
 LOCUS JMT1--03-A01.g1 AtJMT-overexpressing transgenic rice lambda phage
 DEFINITION cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA
 clone JMT1--03-A01, mRNA sequence.
 ACCESSION CF25351
 VERSION CF25351.1 GI:33798984
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eubartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 Source

source
 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT1--03-A01"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="AtJMT-overexpressing transgenic rice lambda
 phage cDNA library (JMT1)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site. mRNA was
 prepared from Arabidopsis Jaominate Carboxyl
 methyltransferase overexpression line."

ORIGIN
 Query Match 3.1%; Score 10; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 213 AATCAGGTCA 222
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 10 AATCAGGTCA 1

Db 10 AATCAGGTCA 1

RESULT 46
 AZ307610/c
 LOCUS AZ307610
 DEFINITION 20 bp DNA linear GSS 29-SEP-2000
 clone UUCGM0009G15 R, genomic survey sequence.
 ACCESSION AZ307610
 VERSION AZ307610.1 GI:10346782
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0009 row: G column: 15
 Seq primer: CACACAGCAACACCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM0009G15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCGM library"
 /note="Vector: pMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource

FEATURES
 Source

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 183 GAGATCACTG 192
Db 20 GAGATCACTG 11

RESULT 47

AZ311347/c 20 bp DNA linear GSS 29-SEP-2000
LOCUS 1M026C16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0026C16 R, genomic survey sequence.
ACCESSION AZ311347
VERSION AZ311347.1 GI:10354220
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: C column: 16
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0026C16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 212 AAATCAGTC 221
Db 12 AAATCAGTC 3

RESULT 48

AZ366451 20 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0115N07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0115N07 R, genomic survey sequence.
ACCESSION AZ366451
VERSION AZ366451.1 GI:10480151
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0115 row: N column: 07
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0115N07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 108 TGAGGAGCG 117
|||||
4 TGAGGAGCG 13

RESULT 49
LOCUS A2436192 20 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0233K14R Mouse 10kb plasmid UGCM1 library Mus musculus genomic
ACCESSION A2436192
VERSION A2436192.1 GI:10560205
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 023 row: K column: 14
Seq primer: CACACAGCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

1. .20
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0233K14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM1 library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 219 GTCAGGTGAC 228
|||||
5 GTCAGGTGAC 14

RESULT 50
LOCUS A2492125 20 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0326L05F Mouse 10kb plasmid UGCM1 library Mus musculus genomic
ACCESSION A2492125
VERSION A2492125.1 GI:10664534
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0326 row: L column: 05
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.

TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

1. .20
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0326L05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM1 library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 TTCTCTTCCC 162
|||||
Db 20 TTCTCTTCCC 11

RESULT 51

LOCUS AU591197 20 bp DNA linear GSS 15-JUN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 581B09, genomic survey sequence.

ACCESSION AJ591197.1 GI:37940821
VERSION GSS; left border; T-DNA flanking sequence.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepoint, L., Caboche, M., and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)

TITLE

JOURNAL
MEDLINE
PUBMED 22363535

REFERENCE 2 (bases 1 to 20)
AUTHORS Balzerque, S.
TITLE Direct Submision
JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue

COMMENT

Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.intobio.gen.fr>).
Location/Qualifiers

FEATURES

source 1..20
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="WassailleWet1ja"
/db_xref="taxon:3702"
/clone="581B09"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

misc_feature 1..20
/note="T-DNA flanking sequence
left border"

ORIGIN

Query Match 3.1%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 TTTCAGACT 307
|||||
Db 3 TTTCAGACT 12

RESULT 52

LOCUS CL680205/c 20 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0128a_H08.2 - PRI0128a.BR (20) Mixed stage fosmid library of *P. pacificus* var. *Californica* *Pristionchus pacificus* genomic, genomic survey sequence.

ACCESSION CL680205 GI:50187035
VERSION GSS.
KEYWORDS *Pristionchus pacificus*
SOURCE *Pristionchus pacificus*
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; *Pristionchus*.

REFERENCE

AUTHORS Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R., and Sommer, R.J.
TITLE 1 (bases 1 to 20)
JOURNAL AppDB: an Acids database for the nematode satellite organism *Pristionchus pacificus*
Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 0049707601371
Fax: 0049707601498
Email: raif.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers

FEATURES

source 1..20
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="Californica"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of *P. pacificus* var. *Californica*"
/note="Vector: pGP1fos-5 Fosmid vector"

ORIGIN

Query Match 3.1%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCGAGAGAG 30
|||||
Db 16 CCGAGAGAG 7

RESULT 53

LOCUS AU666336 21 bp mRNA linear EST 28-JUN-2004
DEFINITION AU666336 CSEGRAN09 Sus scrofa cDNA clone CO000033_N17, mRNA sequence.

ACCESSION AU666336 GI:49350787
VERSION AU666336.1
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 21)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector: pBluescriptII(KS+). R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
SOURCE

1. 21
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C000003.N17"
/tissue_type="placenta"
/clone_lib="CSEQRAN03"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

ORIGIN

Query Match 3.1%; Score 10; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 100 CGTCCTCCTG 109
|||||
Db 1 CGTCCTCCTG 10

RESULT 54
D11772/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

D11772 21 bp mRNA linear EST 02-DEC-1992
HMMH01B05 Liver HepG2 cell line. Homo sapiens cDNA clone hm01e05,
mRNA sequence.
D11772
D11772.1 GI:2155054
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 21)
Okubo, K., Horii, N., Matoba, R., Niiyama, T., Fukushima, A., Kojima, Y.
and Matsubara, K.
Large scale cDNA sequencing for analysis of quantitative and
qualitative aspects of gene expression
Nat. Genet. 2, 173-179 (1992)
94258199
1345164

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Kousaku Okubo, Naohiro Horii, Ryo Matoba, Toshiyuki Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
Institute for Molecular and Cellular Biology
Osaka University
1-3 Yamada-oka, Suita, Osaka 565, Japan.
location/Qualifiers
1. 21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:D058318E"
/db_xref="taxon:9606"
/clone="hm01e05"
/lab_host="E.coli1"

FEATURES
SOURCE

1. 21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:D058318E"
/db_xref="taxon:9606"
/clone="hm01e05"
/lab_host="E.coli1"

/clone_lib="Liver HepG2 cell line."
/note="3'-directed regional cDNA library. Cleaved by MboI
and transformed into E.coli1."

ORIGIN
Query Match 3.1%; Score 10; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 179 TCTGAGATC 188
|||||
Db 10 TCTGAGATC 1

RESULT 55
A2405406/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

A2405406 21 bp DNA linear GSS 03-OCT-2000
1M0174P08F Mouse 10kb plasmid UNGCM1 library Mus musculus genomic
clone UNGCM0174P08 F, genomic survey sequence.
A2405406
A2405406.1 GI:10529419
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0174 row: P column: 08
Seq primer: CGTTGTAACGACGGCCACT
Class: plasmid ends
High quality sequence stop: 21.
location/Qualifiers
1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNGCM0174P08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UNGCM1 library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was agarose from a derivative
of pMD42 (GI14732114[gb]/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 CAGCAATAAA 172
|||
12 CAGCAATAAA 3

RESULT 56

AZ583481/c 21 bp DNA linear GSS 13-DEC-2000
LOCUS AZ583481 Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0378K06 F, genomic survey sequence.

ACCESSION

AZ583481
VERSION AZ583481.1 GI:11703406

KEYWORDS

GSS.
Mus musculus (house mouse)

SOURCE

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiser, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE

Unpublished (2000)

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiser
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0378 row: K column: 06
Seq primer: CGTGTGAACGACGCGCCACT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21

FEATURES

Source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0378K06"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to

adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 ACCTTCCTT 159
|||
15 ACCTTCCTT 6

RESULT 57

AZ607204 21 bp DNA linear GSS 13-DEC-2000
LOCUS AZ607204 Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0429H03 R, genomic survey sequence.

ACCESSION

AZ607204
VERSION AZ607204.1 GI:11729394

KEYWORDS

GSS.
Mus musculus (house mouse)

SOURCE

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiser, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE

Unpublished (2000)

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiser
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: H column: 03
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21

FEATURES

Source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0429H03"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to

adaptoed vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 TAACTGCTC 178
|||||
1 TAACTGCTC 10

Db 1 TAACTGCTC 10

RESULT 58

AZ658074 21 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0534G12R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0534G12 R, genomic survey sequence.
ACCESSION AZ658074
VERSION AZ658074.1 GI:11795220
KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Isiam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0534 row: G column: 12

Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source

1..21
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0534G12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptoed DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[g14732114]p19072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptoed mouse DNA was annealed to

adaptoed vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 259 GATTACACAG 268
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2 GATTACACAG 11

Db 2 GATTACACAG 11

RESULT 59

BF979698/c 22 bp mRNA linear EST 23-JAN-2001
LOCUS 60228855.F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4374157 5',
DEFINITION mRNA sequence.
ACCESSION BF979698
VERSION BF979698.2 GI:12388195
KEYWORDS EST.

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 22)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jan 17, 2001 this sequence version replaced gi:12346913.

Contact: Robert Strausberg, Ph.D.
Email: cgapds-rt@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10037 row: F column: 14

High quality sequence stop: 22.

FEATURES
source

1..22
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4374157"
/lab_host="DH10B"
/clone_lib="NIH MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(GTCGAG); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.2 kb and normalized to KOT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NHGRI/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Query Match 3.1%; Score 10; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 CGCGCGCGCC 48
|||||
14 CGCGCGCGCC 5

Db 14 CGCGCGCGCC 5

RESULT 60

CF309993
 LOCUS 22 bp mRNA linear EST 15-AUG-2003
 DEFINITION ABF-04-G18.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF-04-G18, mRNA sequence.
 ACCESSION CF309993
 VERSION CF309993.1 GI:33681754
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 22)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 FEATURES
 source
 1..22
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF-04-G18"
 /rissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E. coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

ORIGIN
 Query Match 3.1%; Score 10; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 40 GCCGCCGCCG 49
 |||||
 7 GCCGCCGCCG 16
 |||||
 RESULT 61
 LOCUS A2788615 22 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0035F19R Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UUGC2M0035F19 R, genomic survey sequence.
 ACCESSION A2788615
 VERSION A2788615.1 GI:12928595
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 TITLE
 JOURNAL

COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0035 row: F column: 19
 Seq primer: CACACGGAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.
 FEATURES
 source
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0035F19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (91|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 3.1%; Score 10; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 306 CTGGGGATGT 315
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 11 CTGGGGATGT 20
 |||||
 RESULT 62
 LOCUS A2812224 22 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0078G13R Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UUGC2M0078G13 R, genomic survey sequence.
 ACCESSION A2812224
 VERSION A2812224.1 GI:12981261
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 TITLE
 JOURNAL

COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0078 Row: G Column: 13
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES
 source
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="MUSC2M0078G13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UNGCM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 3.1%; Score 10; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 255 CAGTGATTAA 264
 |||||
 22 CAGTGATTAA 13

Db

RESULT 63
 LOCUS TA114F05P 22 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 114F05, forward sequence,
 genomic survey sequence.
 ACCESSION AL462607
 VERSION AL462607.1 GI:11832412
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 22)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrill, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrill@sanger.ac.uk and

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT
 nh1@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrill, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
 source
 1..23
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="114f05"

ORIGIN
 Query Match 3.1%; Score 10; DB 9; Length 22;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 85 GAGGGCGGAG 94
 |||||
 14 GAGGGCGGAG 5

Db

RESULT 64
 LOCUS CF298913/c 23 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--02-K05.91 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--02-K05, mRNA
 sequence.
 ACCESSION CF298913
 VERSION CF298913.1 GI:33670674
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriactoidae; Oryzaceae; Oryza.
 1 (bases 1 to 23)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source
 1..23
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Naekdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--02-K05"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E. coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

ORIGIN

Query Match 3.1%; Score 10; DB 6; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 AGCACGCTG 251
 |||||
 21 AGCACGCTG 12

RESULT 65

AZ324328/c

LOCUS 23 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0046B16F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGIM0046B16 F, genomic survey sequence.

ACCESSION

AZ324328

VERSION 1
 KEYWORDS GI:10379937

SOURCE

ORGANISM Mus musculus (house mouse)
 Mus musculus

REFERENCE 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0046 row: B column: 16
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

1.23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0046B16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g1|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCC 48
 |||||
 16 CGCGCGCGCC 7

RESULT 66

AZ345542/c

LOCUS 23 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0080A14F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGIM0080A14 F, genomic survey sequence.

ACCESSION

AZ345542

VERSION 1
 KEYWORDS GI:10424779

SOURCE

ORGANISM Mus musculus (house mouse)
 Mus musculus

REFERENCE 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: A column: 14
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

1.23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0080A14"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g1|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 GAGGAGGCG 92
|||
10 GAGGAGGCG 1

RESULT 67
A2761953/c 23 bp DNA linear GSS 16-FEB-2001

LOCUS 1M0556K06R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0556K06 R, genomic survey sequence.

ACCESSION A2761953
VERSION A2761953.1 GI:12871452
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0556 row: K column: 06
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
SOURCE 1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0556K06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1, a copy-number
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 CTGGAGATCA 189
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19 CTGGAGATCA 10

RESULT 68
A2952138/c 23 bp DNA linear GSS 27-APR-2001

LOCUS 2M0216C19R Mouse 10kb plasmid UGCG2M library Mus musculus genomic
DEFINITION clone UGCG2M0216C19 R, genomic survey sequence.

ACCESSION A2952138
VERSION A2952138.1 GI:13823365
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0216 row: C column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0216C19"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1, a copy-number
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 3.1%; Score 10; DB 8; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GTTGTAAAGA 284
 |||||
 23 GTTGTAAAGA 14

RESULT 69
 TAI25F10Q/c 23 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 125f10, reverse sequence,
 DEFINITION
 ACCSSION AL463486.1 GI:11833996
 VERSION
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
 AUTHORS Hall, N., Bowman, S., Iennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 JOURNAL project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GYtat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/
 Location/Qualifiers
 1..23
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="125f10"

FEATURES
 source

ORIGIN
 Query Match 3.1%; Score 10; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 TCCCCAGCAA 168
 |||||
 20 TCCCCAGCAA 11

RESULT 70
 AG198216/c 23 bp DNA linear GSS 06-MAR-2004
 LOCUS Pan troyglodytes DNA, clone: RP43-078005.TU, genomic survey
 DEFINITION
 ACCSSION AG198216
 VERSION AG198216.1 GI:45230392
 KEYWORDS GSS.
 SOURCE Pan troyglodytes (chimpanzee)
 ORGANISM Pan troyglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE
 1

AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
 Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 TITLE BAC end sequences of Library RP-43
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 23)
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
 Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 TITLE Direct Submission
 JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
 Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
 52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
 (E-mail:redstone@mail.kribb.re.kr. URL:http://phs.grc.kribb.re.kr/,
 Tel:82-42-866-7181, Fax:82-42-860-4409)
 Clones are derived from the chimpanzee BAC library RP-43 This BAC
 end was generated during the R&D process and may have higher chance
 of clone tracking errors.
 PRIMERS
 Sequencing: TU
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
 Location/Qualifiers
 1..23
 /organism="Pan troyglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-078005.TU"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
 Query Match 3.1%; Score 10; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 AAGGTTGTTA 281
 |||||
 22 AAGGTTGTTA 13

RESULT 71
 AG202522 23 bp DNA linear GSS 06-MAR-2004
 LOCUS Pan troyglodytes DNA, clone: RP43-086A14.TU, genomic survey
 DEFINITION
 ACCSSION AG202522
 VERSION AG202522.1 GI:45234697
 KEYWORDS GSS.
 SOURCE Pan troyglodytes (chimpanzee)
 ORGANISM Pan troyglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE
 1
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
 Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 TITLE BAC end sequences of Library RP-43
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 23)
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
 Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 TITLE Direct Submission
 JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
 Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
 52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
 (E-mail:redstone@mail.kribb.re.kr. URL:http://phs.grc.kribb.re.kr/,
 Tel:82-42-866-7181, Fax:82-42-860-4409)
 Clones are derived from the chimpanzee BAC library RP-43 This BAC
 end was generated during the R&D process and may have higher chance
 of clone tracking errors.
 PRIMERS
 Sequencing: TU

LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1..23

FEATURES
source
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-086A14.TU"
/sex="male"
/cell_type="lymphocytes"
/clone_11b="RP-43 Chimpanzee Male BAC library"

ORIGIN
Query Match 3.1%; Score 10; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 AACGCGCT 179
|||||||
Db 1 AACGCGCT 10

RESULT 72
LOCUS BM400127 24 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-66-G02.c.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM400127
VERSION BM400127.1 GI:18200180
KEYWORDS EST
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 24)
Turkewitz A.P., Karer K.M., Jahn C., Ortae E., Kirk K.E.,
Frankel J. and Klobutcher J.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
Location/Qualifiers

1..24
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_11b="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match 3.1%; Score 10; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 262 TAACAGCTG 271
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Db 1 TAACAGCTG 10

RESULT 73
LOCUS AZ362057/c 24 bp DNA linear GSS 02-OCT-2000

DEFINITION IM0107E05F Mouse 10kb plasmid UGCM library Mus musculus genomic
clone UGCM0107E05 F, genomic survey sequence.
ACCESSION AZ362057
VERSION AZ362057.1 GI:10475757
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 24)
Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamil C.,
Islam H., Longacre S., Mahmood M., Meenen E., Pedersen T.,
Rellly M., Rose M., Rose R., Stokes R., Tingey A., von
Niederhausen A. and Wright D., Weiss R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

TITLE
JOURNAL
COMMENT
Insert Length: 10000 Std Error: 0.00
Plate: 0107 row: E column: 05
Seq primer: CGTGTGAACGACGCCACAG
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
source
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/sex="male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid UGCM library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil4732114[gb]/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 3.1%; Score 10; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 280 TAAGAGCAG 289
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Db 11 TAAGAGCAG 2

RESULT 74
LOCUS AZ492799 24 bp DNA linear GSS 05-OCT-2000

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DEFINITION      1M0327B10F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
                  clone UGCG1M0327B10 F, genomic survey sequence.
ACCESSION       A2492799
VERSION         A2492799.1  GI:10665858
KEYWORDS        GSS.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE       1 (bases 1 to 24)
AUTHORS         Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                  Niederhausern,A. and Wright,D.,Weiss,R.
                  Mouse whole genome scaffolding with paired end reads from 10kb
                  plasmid inserts
JOURNAL         Unpublished (2000)
COMMENT         Contact: Robert B. Weiss
                  University of Utah Genome Center
                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                  84112, USA
                  Tel: 801 585 5606
                  Fax: 801 585 7177
                  Email: ddunn@genetics.utah.edu
                  Insert Length: 10000 Std Error: 0.00
                  Plates: 0327 row: B column: 10
                  Seq primer: CGTTGTAAACGACGCCAGT
                  Class: plasmid ends
                  High quality sequence stop: 24.
FEATURES        Location/Qualifiers
Source          1..24
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UGCG1M0327B10"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_1lb="Mouse 10kb plasmid UGCG1M library"
                /note="Vector: PMD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pMD42 (g14732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
ORIGIN
Query Match      3.1%; Score 10; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY              240 CCAGCACCAG 249
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                |||||
Db              15 CCAGCACCAG 24

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DEFINITION      1M0517D24F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
                  clone UGCG1M0517D24 F, genomic survey sequence.
ACCESSION       A2648378
VERSION         A2648378.1  GI:11780785
KEYWORDS        GSS.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE       1 (bases 1 to 24)
AUTHORS         Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                  Niederhausern,A. and Wright,D.,Weiss,R.
                  Mouse whole genome scaffolding with paired end reads from 10kb
                  plasmid inserts
JOURNAL         Unpublished (2000)
COMMENT         Contact: Robert B. Weiss
                  University of Utah Genome Center
                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                  84112, USA
                  Tel: 801 585 5606
                  Fax: 801 585 7177
                  Email: ddunn@genetics.utah.edu
                  Insert Length: 10000 Std Error: 0.00
                  Plates: 0517 row: D column: 24
                  Seq primer: CGTTGTAAACGACGCCAGT
                  Class: plasmid ends
                  High quality sequence stop: 24.
FEATURES        Location/Qualifiers
Source          1..24
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UGCG1M0517D24"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_1lb="Mouse 10kb plasmid UGCG1M library"
                /note="Vector: PMD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pMD42 (g14732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
ORIGIN
Query Match      3.1%; Score 10; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY              232 GGAGATAC 241
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                |||||
Db              19 GGAGATAC 10

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Search completed: February 2, 2005, 23:31:58
 Job time : 987.597 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:06:25 ; Search time 149.916 Seconds
(without alignments)
11170.029 Million cell updates/sec

Title: US-10-048-046-1_COPY_81_399

Perfect score: 1 gtgaatcccatgagcgcgc.....tacagactgggagatgcatc 319

Sequence: 1 gtgaatcccatgagcgcgc.....tacagactgggagatgcatc 319

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 0

Total number of hits satisfying chosen parameters: 336436

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

Database :

N_Geneseq 23Sep04:*
1: Geneseq1990s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2000s:*
5: Geneseq2000s:*
6: Geneseq2000s:*
7: Geneseq2000s:*
8: Geneseq2000s:*
9: Geneseq2000s:*
10: Geneseq2000s:*
11: Geneseq2000s:*
12: Geneseq2000s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	6.3	28 5	AAF30355 Human che
2	16	5.0	20 2	AAV09174 Phosphoro
3	15	4.7	18 2	AAx63292 Delta-9-d
4	15	4.7	18 2	AAx63294 Delta-9-d
5	15	4.7	25 9	ACI37850 Human mic
6	15	4.7	27 6	AAI42088 Human glu
7	15	4.7	28 10	ADCS5392 Human pur
8	14	4.4	17 8	ACD65641 HCV minus
9	14	4.4	17 8	ACD57028 HCV minus
10	14	4.4	17 8	ACD65642 HCV minus
11	14	4.4	17 10	ADIS2305 Human tum
12	14	4.4	17 12	AD187191 HCV DNAzy
13	14	4.4	17 12	AD182872 HCV DNAzy
14	14	4.4	18 12	ADMS94802 Hepatitis
15	14	4.4	18 12	ADMS94802 Hepatitis
16	14	4.4	19 10	ADMS94802 Hepatitis
17	14	4.4	19 10	ADMS94802 Hepatitis
18	14	4.4	19 10	ADMS94802 Hepatitis
19	14	4.4	19 10	ADMS94802 Hepatitis
20	14	4.4	19 10	ADMS94802 Hepatitis
21	14	4.4	19 10	ADMS94802 Hepatitis

22	14	4.4	19 10	ADFS2686 Hepatitis
23	14	4.4	19 10	ADFS2703 Hepatitis
24	14	4.4	19 10	ADFS2726 Hepatitis
25	14	4.4	19 10	ADFS2030 Hepatitis
26	14	4.4	19 10	ADFS1994 Hepatitis
27	14	4.4	19 10	ADFS2685 Hepatitis
28	14	4.4	19 10	ADFS2698 Hepatitis
29	14	4.4	19 10	ADFS2007 Hepatitis
30	14	4.4	19 10	ADFS1990 Hepatitis
31	14	4.4	19 10	ADFS2690 Hepatitis
32	14	4.4	19 10	ADFS2002 Hepatitis
33	14	4.4	19 10	ADFS1989 Hepatitis
34	14	4.4	19 12	ADP05478 Hepatitis
35	14	4.4	20 2	AAV09175 Phosphoro
36	14	4.4	20 2	AAV3253 PCR prime
37	14	4.4	20 4	AAV67142 Human E2F
38	14	4.4	20 6	ABT08551 Human nov
39	14	4.4	20 12	ADJ34405 Human sec
40	14	4.4	20 12	ADP09916 Human NOV
41	14	4.4	22 6	AAI41635 Human col
42	14	4.4	22 10	ADH93941 Human gen
43	14	4.4	24 12	ADK98335 Primer of
44	14	4.4	25 2	AAQ34273 Upstream
45	14	4.4	25 9	ACK00756 Human mic
46	14	4.4	25 9	ACK00130 Human mic
47	14	4.4	25 9	ACK00130 Human mic
48	14	4.4	25 12	ADP15727 Renal cel
49	14	4.4	26 10	ABQ80298 Primer Te
50	14	4.4	30 6	ABX67739 Novel Hel
51	14	4.4	30 6	ABX67739 Novel Hel
52	14	4.4	30 10	ADFS9508 HIV-1 Rev
53	13	4.1	13 5	ABC69919 Oligonuc
54	13	4.1	13 5	ABF95242 Oligonuc
55	13	4.1	13 5	ABF95243 Oligonuc
56	13	4.1	13 5	ABC69918 Oligonuc
57	13	4.1	14 3	AAA26133 Oestrogen
58	13	4.1	14 6	ABN33308 HLA-DQB1
59	13	4.1	15 3	AAZ62579 Substrate
60	13	4.1	15 6	ABX00430 Hepatitis
61	13	4.1	16 2	AAQ26476 Probe DB6
62	13	4.1	16 6	AAQ26453 Probe DB6
63	13	4.1	16 6	ABL31182 Human HLA
64	13	4.1	17 6	ABV78964 Human HTP
65	13	4.1	17 6	ABV78965 Human HTP
66	13	4.1	17 6	ABV78968 Human HTP
67	13	4.1	17 6	ABV78967 Human HTP
68	13	4.1	17 6	ABV78966 Human HTP
69	13	4.1	17 6	ABK19313 Human ERG
70	13	4.1	17 6	ABK19314 Human ERG
71	13	4.1	17 6	ABK19315 Human ERG
72	13	4.1	17 6	ABV89388 Human POS
73	13	4.1	17 6	ABV89391 Human POS
74	13	4.1	17 6	ABV89392 Human POS
75	13	4.1	17 6	ABV89390 Human POS
76	13	4.1	17 8	ABV89389 Human POS
77	13	4.1	17 8	ACA09013 NFKB sub-
78	13	4.1	17 8	ACA09013 NFKB sub-
79	13	4.1	17 8	ACA09012 NFKB sub-
80	13	4.1	17 8	ACA09012 NFKB sub-
81	13	4.1	17 12	AD182871 HCV DNAzy
82	13	4.1	18 2	AAV61703 Hepatitis
83	13	4.1	18 2	AAV30545 HLA DOBI
84	13	4.1	18 6	ABL42991 Human chr
85	13	4.1	18 6	ABL30595 Human HLA
86	13	4.1	18 6	ABL30696 Human HLA
87	13	4.1	18 6	ABL30805 Human HLA
88	13	4.1	18 10	ADP69478 3' anchor
89	13	4.1	19 6	ABK28933 Cyclin DI
90	13	4.1	19 9	ACH03515 Human lat
91	13	4.1	19 10	ADDD00366 HCV codin
92	13	4.1	19 10	ADFS3778 Human VEG
93	13	4.1	19 10	ADFS6205 Human VEG
94	13	4.1	19 10	ADFS2709 Hepatitis

C 95	13	4.1	19	10	ADF51756	Adf51756 Hepatitis
C 96	13	4.1	19	10	ADF52013	Adf52013 Hepatitis
C 97	13	4.1	19	10	ADF52452	Adf52452 Hepatitis
C 98	13	4.1	20	2	AAQ21051	Aaq21051 Primer 4-
C 99	13	4.1	20	2	AAT89745	Aat89745 Oligonuc
C 100	13	4.1	20	2	AAZ07024	Aaz07024 Apolipop
C 101	13	4.1	20	6	ABL42978	AbL42978 Human chr
C 102	13	4.1	20	6	ABI92933	AbI92933 Capture o
C 103	13	4.1	20	8	ABT15791	Abt15791 Human GU
C 104	13	4.1	20	8	ABT43241	Abt43241 Neurobl
C 105	13	4.1	20	8	ABT32412	Abt32412 Neuroblas
C 106	13	4.1	20	9	ACD23026	ACD23026 Human NEM
C 107	13	4.1	20	10	ADF66274	Adf66274 Rat GAPDH
C 108	13	4.1	20	12	ADN72398	Adn72398 Human E2-
C 109	13	4.1	20	12	ADN48621	Adn48621 Human Not
C 110	13	4.1	20	12	ADN48691	Adn48691 Human Not
C 111	13	4.1	20	12	ADP56791	Adp56791 Antisense
C 112	13	4.1	20	12	ADP56863	Adp56863 Human AMA
C 113	13	4.1	21	2	AAT89733	Aat89733 PCR prime
C 114	13	4.1	21	2	AAT89721	Aat89721 PCR prime
C 115	13	4.1	21	2	AAZ47454	Aaz47454 Antisense
C 116	13	4.1	21	3	AAZ35710	Aaz35710 Human uro
C 117	13	4.1	21	3	AAZ35710	Aaz35710 Human uro
C 118	13	4.1	21	6	ABN86474	Abn86474 Human Rec
C 119	13	4.1	21	6	ABN86474	Abn86474 Human Rec
C 120	13	4.1	21	10	ADD14547	Add14547 Human src
C 121	13	4.1	21	10	ADF37724	Adf37724 Human VRG
C 122	13	4.1	21	10	ADG39869	Adg39869 FLT1-targ
C 123	13	4.1	22	12	ADJ37418	Adj37418 Human Flt
C 124	13	4.1	22	8	ACA28540	Aca28540 PCR prime
C 125	13	4.1	22	8	ACA64608	Aca64608 C. elegans
C 126	13	4.1	23	2	AAQ37589	Aaq37589 HCV conse
C 127	13	4.1	23	6	AAT64903	Aat64903 Hepatitis
C 128	13	4.1	23	9	ABK66685	Abk66685 Human gen
C 129	13	4.1	23	9	AAI56651	Aai56651 Human gen
C 130	13	4.1	23	10	ADG37720	Adg37720 Human VEG
C 131	13	4.1	23	10	ADG37816	Adg37816 Human VEG
C 132	13	4.1	23	10	ADG29494	Adg29494 FLT1 siNA
C 133	13	4.1	23	10	ADG29865	Adg29865 FLT1-targ
C 134	13	4.1	23	12	ADO22145	Ado22145 Real-time
C 135	13	4.1	24	2	AAQ37582	Aaq37582 HCV conse
C 136	13	4.1	24	2	AAI64896	Aai64896 Hepatitis
C 137	13	4.1	24	6	ABI82437	Abi82437 Capture o
C 138	13	4.1	24	6	ABI82436	Abi82436 Capture o
C 139	13	4.1	24	6	ABI92632	Abi92632 Capture o
C 140	13	4.1	24	6	ABI92822	Abi92822 Capture o
C 141	13	4.1	24	6	ABI92823	Abi92823 Capture o
C 142	13	4.1	24	6	ABI92823	Abi92823 Capture o
C 143	13	4.1	24	6	ABI91703	Abi91703 Capture o
C 144	13	4.1	24	8	AAI51407	Aai51407 Complemen
C 145	13	4.1	25	3	AAI51407	Aai51407 Complemen
C 146	13	4.1	25	3	AAI51407	Aai51407 Complemen
C 147	13	4.1	25	4	AAI51407	Aai51407 Complemen
C 148	13	4.1	25	5	AAI51407	Aai51407 Complemen
C 149	13	4.1	25	6	AAI51407	Aai51407 Complemen
C 150	13	4.1	25	6	AAI51407	Aai51407 Complemen

ALIGNMENTS

RESULT 1
AAAF30355
ID AAF30355 standard; DNA; 28 BP.
XX
AC AAF30355;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human checkpoint gene chr5' PCR primer.
XX
KM Checkpoint with forkhead associated domain and ring finger; Chr5; human;
XX
KM mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;

KW	ubiquitin-protein ligase; PCR primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	MO200109150-A2.
XX	
PD	08-FEB-2001.
XX	
PF	14-JUN-2000; 2000MO-US016391.
XX	
PR	29-JUL-1999; 99US-0146194P.
XX	
PA	(WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX	
PI	Halazonetis T, Scolnick D;
XX	
DR	WPI; 2001-182927/18.
XX	
PT	Novel nucleic acid sequence of mitotic checkpoint gene encoding a
PT	checkpoint with forkhead-associated domain and ring finger protein, for
PT	diagnosing tumorigenic cells and in screening for anticancer drugs.
XX	
PS	Example 3; Page 38; 85pp; English.
XX	
CC	The present sequence is that of a 5' PCR primer, used with the 3' primer
CC	given in AAF30356, to amplify a cDNA fragment corresponding to
CC	nucleotides 352-1055 of the human chr5 sequence given in AAF30352. The
CC	chr5 gene encodes the human mitotic checkpoint protein Chtr (see
CC	AAAB20219), which is required for regulation of the transition of cells
CC	from prophase to metaphase during mitosis. Loss of expression of Chtr is
CC	associated with a predisposition to tumorigenesis upon exposure to
CC	mitotic stress. A set of primers (see AAF30353-76) was used to amplify
CC	regions spanning the entire chr5 coding region in order to determine
CC	whether the chr5 gene is mutated in any of the human cancer cell lines
CC	SW480, DLD1, HCT116, SAOS2, U2OS, IMR5 and NCP. A mutation leading
CC	to a Val-580 to Met amino acid substitution was identified in the chr5
CC	gene of U2OS cells. Chtr polypeptide was identified in the chr5
CC	methods of diagnosing tumorigenic cells and of screening for drugs which
CC	can inhibit the activity of Chtr in a cancer cell, rendering it more
CC	sensitive to additional antitumour therapies
CC	
SQ	Sequence 28 BP; 12 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
XX	
QY	Query Match 6.3%; Score 20; DB 5; Length 28;
QY	Best Local Similarity 100.0%; Pred. No. 6;
QY	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	230 CTGGAAGATACGACCCAG 249
DB	9 CTGGAAGATACGACCCAG 28
XX	
RESULT 2	
AAV09174/C	
ID AAV09174 standard; DNA; 20 BP.	
XX	
AC AAV09174;	
XX	
DT 09-JUN-1998 (first entry)	
XX	
DE Phosphorothiate oligonucleotide sequence 8051 targeting ILIR mRNA.	
XX	
KW Type I interleukin-1 receptor; ILIR; human; IL1 protein; hybridisation;	
KW inflammation; ss; 5' Cap region; phosphorothiate linkage.	
XX	
OS Synthetic.	
OS Homo sapiens.	
XX	
XX	
FT Key Location/Qualifiers	
FT modified_base 1..20	
FT /tag= a	
FT /note= "Phosphorothiate internucleotide linkage"	

PN WO9744656-A1.
 XX
 PD 27-NOV-1997.
 XX
 PF 12-MAY-1997; 97WO-US007147.
 XX
 PR 21-MAY-1996; 96US-00651692.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Miraglia L, Bennett CF, Dean N, Geiger T;
 XX
 DR WPI; 1998-018646/02.
 XX
 PT 2'-substituted oligonucleotide(s) specific for interleukin-1 receptor
 PT type I - used to modulate expression and detect overexpression of the
 PT receptor.
 XX
 PS Example 5; Page 19; 63pp; English.
 XX
 CC This is a novel oligomer comprising 20 covalently linked nucleotides
 CC which bind to the 5' Cap region of the interleukin-1 receptor (IL1R)
 CC mRNA. Expression of IL1R, in cells and tissues can be modulated by
 CC compositions comprising oligomers which are able to specifically
 CC hybridise with target areas of its encoding sequence. The composition can
 CC be used for treatment of disease in humans caused by excessive receptor
 CC expression, e.g. inflammation. When labelled they can be used
 CC diagnostically to determine overexpression of IL1R, also to determine
 CC localisation and distribution of this expression for research, diagnostic
 CC or therapeutic purposes
 CC
 SQ Sequence 20 BP; 1 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 5.0%; Score 16; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCGCGCGCGCGCGCG 58
 DB 19 GCGCGCGCGCGCGCG 4

RESULT 3
 AAX63292
 ID AAX63292 standard; RNA; 18 BP.

AC AAX63292;

DT 16-JUL-1999 (first entry)

DE Delta-9 desaturase hairpin ribozyme substrate SEQ ID NO:1167.

XX Maize; corn; Zea mays; delta-9 desaturase; GBS8; target; substrate;
 KM granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
 KM modulation; gene expression; transgenic plant; cleavage; canola plant;
 KM caffeine synthesis; coffee plant; nicotine production; tobacco;
 KM fruit ripening; flower pigmentation; lignin production; ss.

XX Zea mays.

OS WO9710328-A2.

PN 20-MAR-1997.

PD 12-JUL-1996; 96WO-US011689.

PR 13-JUL-1995; 95US-0001135P.

PA (RIBO-) RIBOZYME PHARM INC.

PA (DOMC) DOWELANCO.

PI Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA,
 PI Young SA, Folkerts O, Merlo DJ;

XX WPI; 1997-202224/18.

XX Ribozyme which modulates plant gene expression - preferably modulates
 PT expression of DELTA-9 desaturase or granule bound starch synthase in
 PT maize or canola.
 XX

PS Claim 40; Page 93; 155pp; English.

XX The present invention describes an enzymatic nucleic acid molecule (1)
 CC with RNA cleaving activity, which modulates the expression of a plant
 CC gene. Also described is a gene comprising a cDNA sequence encoding maize
 CC Delta-9 desaturase. (1) can be used to modulate expression of a gene.
 CC Preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
 CC gene, in a plant (preferably a maize or canola plant). (1) can be used to
 CC modulate caffeine synthesis in a coffee plant, nicotine production in a
 CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
 CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
 CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
 CC plant

SQ Sequence 18 BP; 1 A; 11 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 4.7%; Score 15; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCGCGAGC 53
 DB 4 CGCGCGCGCGCGAGC 18

RESULT 4
 AAX63294
 ID AAX63294 standard; RNA; 18 BP.

AC AAX63294;

DT 16-JUL-1999 (first entry)

DE Delta-9 desaturase hairpin ribozyme substrate SEQ ID NO:1169.

XX Maize; corn; Zea mays; delta-9 desaturase; GBS8; target; substrate;
 KM granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
 KM modulation; gene expression; transgenic plant; cleavage; canola plant;
 KM caffeine synthesis; coffee plant; nicotine production; tobacco;
 KM fruit ripening; flower pigmentation; lignin production; ss.

XX Zea mays.

OS WO9710328-A2.

PN 20-MAR-1997.

PD 12-JUL-1996; 96WO-US011689.

PR 13-JUL-1995; 95US-0001135P.

PA (RIBO-) RIBOZYME PHARM INC.

PA (DOMC) DOWELANCO.

PI Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA,
 PI Young SA, Folkerts O, Merlo DJ;

DR WPI; 1997-202224/18.

PT Ribozyme which modulates plant gene expression - preferably modulates
 PT expression of DELTA-9 desaturase or granule bound starch synthase in
 PT maize or canola.

PS Claim 40; Page 93; 155pp; English.

CC The present invention describes an enzymatic nucleic acid molecule (1)

CC with RNA cleaving activity, which modulates the expression of a plant
CC gene. Also described is a gene comprising a cDNA sequence encoding maize
CC Delta-9 desaturase. (1) can be used to modulate expression of a gene,
CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
CC gene, in a plant (preferably a maize or canola plant). (1) can be used to
CC modulate caffeine synthesis in a coffee plant, nicotine production in a
CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
CC plant
XX
SQ Sequence 18 BP; 2 A; 10 C; 6 G; 0 T; 0 U; 0 Other;
XX
Query Match 4.7%; Score 15; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 39 CGCCGCGCGCGCAGC 53
Db 1 CGCCGCGCGCGCAGC 15
XX
RESULT 5
AC137850/c
ID AC137850 standard; DNA; 25 BP.
XX
AC AC137850;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 37841.
XX
KM EST; ss; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; diallelic marker; polymorphism; human;
KM cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFV-) AFFMERTIX INC.
XX
PI Miltmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 37841; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compound. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-

CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termin of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 8 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
XX
Query Match 4.7%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 176 GTCTCTGGAGATCAC 190
Db 17 GTCTCTGGAGATCAC 3
XX
RESULT 6
AAL42088
ID AAL42088 standard; DNA; 27 BP.
XX
AC AAL42088;
XX
DT 27-MAY-2002 (first entry)
XX
DE Human glutathione S-transferase GSTT1 allele-specific PCR primer (T1R).
XX
KM Human; ss; allele-specific; PCR; primer; glutathione S-transferase; GST;
KM GSTM1; GSTM3; GSTP1; GSTT1; cancer; cancer treatment; chemotherapy;
KM genetic characterization; T1R.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO200208465-A1.
XX
PD 31-JAN-2002.
XX
PF 20-JUL-2001; 2001WO-US022923.
XX
PR 20-JUL-2000; 2000US-0219531P.
XX
PA (UTAH) UNIV UTAH RES FOUNO.
XX
PI Keller C, Ballard L, Lemons R, Ali-Osman F;
XX
DR WPI; 2002-241577/29.
XX
PT Detecting glutathione S-transferase alleles, by amplifying portions of
PT genomic DNA samples with primers specific for GSTM1 and CDK2, for GSTT1
PT and GSTM3, and for GSTP1, and detecting alleles and gene dosages.
XX
PS Claim 29; Page 5; 37pp; English.
XX
CC The invention comprises a method for detecting the presence of alleles of
CC the glutathione S-transferase (GST) genes GSTM1, GSTM3, GSTP1 and GSTT1.
CC The method of the invention involves the use of specifically claimed GST
CC allele-specific PCR primers. Cancer research has shown that the presence
CC of various GST polymorphisms correlates with altered risk for certain
CC cancers and altered response and toxicity from currently used cancer
CC treatments (e.g. chemotherapy). The method of the invention is useful for
CC identifying the alleles of GST present in a sample of genetic material
CC and characterizing the genetic makeup of a subject. The present DNA
CC sequence represents the GSTT1 allele-specific PCR primer (T1R)
XX
SQ Sequence 27 BP; 5 A; 3 C; 10 G; 9 T; 0 U; 0 Other;
XX
Query Match 4.7%; Score 15; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 TACAGACTGGGAGT 314
|||||
Db 6 TACAGACTGGGAGT 20

RESULT 7

ADCS5392
ID ADCS5392 standard; DNA; 28 BP.

AC ADCS5392;

DT 18-DEC-2003 (first entry)

DE Human purine receptor TG20022 PCR primer Seq ID9.

KW purine receptor; TG20022; novel G-protein coupled receptor;
KW signal transduction; human; P2Y receptor; PCR; primer; ss.

OS Homo sapiens.

PN JP2003038184-A.

PD 12-FEB-2003.

PF 06-JUL-2001; 2001JP-00206914.

PR 06-JUL-2001; 2001JP-00206914.

PA (TANA) TANABE SEIVAKU CO.

DR WPI; 2003-700043/67.

PT Novel purine receptor polypeptide, termed TG20022, useful for screening
PT or identifying ligand, agonist or antagonist of purine receptor
PT polypeptide.

PS Example 1; SEQ ID NO 9; 23pp; Japanese.

CC This invention relates to a human purine receptor polypeptide (a P2Y
CC receptor), termed TG20022 selected from a 331 amino acid sequence, given
CC in the specification. The receptor of the invention is a novel G-protein
CC coupled receptor. Involved in signal transduction in many different
CC pathways. The polypeptide is useful for screening or identifying a
CC ligand, agonist or antagonist of the receptor of the invention, or for
CC detecting the function or activity of the polypeptide. The polypeptide is
CC useful as a therapeutic agent. The present sequence is that of a PCR
CC primer which was used for amplification of a region of the human TG20022
CC gene during the exemplification of the invention.

XX Sequence 28 BP; 9 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 4.7%; Score 15; DB 10; Length 28;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 AGGTGACACTGGAG 236
|||||
Db 14 AGGTGACACTGGAG 28

RESULT 8

ACDS6641
ID ACD65641 standard; RNA; 17 BP.

AC ACD65641;

DT 30-SEP-2003 (first entry)

DE HCV minus strand DNAzyme substrate sequence #2160.

KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;

KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.

OS Hepatitis C virus.

PN WO200281494-A1.

PD 17-OCT-2002.

PF 26-MAR-2002; 2002WO-US009187.

PR 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00817478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEEP/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX Blact L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P,

PI Draper K, Roberts E;

XX WPI; 2003-229207/22.

DR Novel compound useful for treating cirrhosis, liver failure,

XX hepatocellular carcinoma, or condition associated with hepatitis C virus

PT infection.

PT Claim 1; Page 313; 387pp; English.

PS The present invention relates to nucleic acid molecules which modulate

XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed

CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

CC transcriptase and/or HBV reverse transcriptase primer sequences, as well

CC as oligonucleotides that specifically bind the Enhancer I region of HBV

CC DNA. The nucleic acids may be used to modulate the expression of HBV

CC genes and HBV viral replication. Also disclosed is a method for screening

CC compounds and/or potential therapies directed against HBV. The compounds and

CC methods of the invention are useful for the treatment of degenerative and

CC disease states related to HBV and HCV infection, replication and gene

CC expression such as cirrhosis, liver failure, and hepatocellular

CC carcinoma. The present sequence represents a substrate for one of the HCV

CC DNAzyme or minus strand DNAzyme sequences disclosed in the present

CC invention

XX Sequence 17 BP; 3 A; 6 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 4.4%; Score 14; DB 8; Length 17;

Best Local Similarity 85.7%; Pred. No. 7.5e+03;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 139 ACGAGTGGGACC 152
|||||
Db 4 ACGAGGUTGGGACC 17

RESULT 9

ACD57028/c
 ID ACD57028 standard; RNA; 17 BP.
 AC ACD57028;
 XX
 XX
 XX 23-SEP-2003 (first entry)
 DE HCV DNAzyme substrate sequence #118.
 XX
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KM RNA stability; RNA expression; RNA synthesis; antisense;
 KM enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
 KM amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KM HBV reverse transcriptase; Enhancer I region; viral replication;
 KM degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KM liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KM virucide; antiinflammatory; substrate; ss.
 XX
 XX Hepatitis C virus.
 OS
 XX
 XX WO200281494-A1.
 PN
 XX 17-OCT-2002.
 PD
 XX
 XX 26-MAR-2002; 2002WO-US009187.
 PF
 XX 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 XX WPI; 2003-229207/22.
 DR
 XX
 XX
 XX Claim 1; Page 236; 387dp; English.
 PS
 XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNAzyme or minus strand DNAzyme sequences disclosed in the present
 CC invention
 CC
 XX Sequence 17 BP; 2 A; 6 G; 0 T; 3 U; 0 Other;

Query Match 4.4%; Score 14; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 139 ACGAGGTGCGACC 152
 DB 15 ACGAGGTGCGACC 2
 RESULT 10
 ID ACD65642
 AC ACD65642;
 XX
 XX 30-SEP-2003 (first entry)
 DT
 XX
 XX HCV minus strand DNAzyme substrate sequence #2161.
 DE
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KM RNA stability; RNA expression; RNA synthesis; antisense;
 KM enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
 KM amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KM HBV reverse transcriptase; Enhancer I region; viral replication;
 KM degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KM liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KM virucide; antiinflammatory; substrate; ss.
 XX
 XX Hepatitis C virus.
 OS
 XX
 XX WO200281494-A1.
 PN
 XX 17-OCT-2002.
 PD
 XX
 XX 26-MAR-2002; 2002WO-US009187.
 PF
 XX 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 XX WPI; 2003-229207/22.
 DR
 XX
 XX
 XX Claim 1; Page 313; 387dp; English.
 PS
 XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV

CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC invention
XX
SQ Sequence 17 BP; 3 A; 5 C; 6 G; 0 T; 3 U; 0 Other;
Query Match 4.4%; Score 14; DB 8; Length 17;
Best Local Similarity 85.7%; Pred. No. 7.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 139 ACGAGGTTGCGACC 152
Db 1 ACGAGGTTGCGACC 14
RESULT 11
AD152305/C
ID AD152305 standard; DNA; 17 BP.
XX
AC AD152305;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SegID4608.
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytoskeletal; virulence; neuroprotective; neurotropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumours and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 4808; 30pp; French.
XX
XX This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 6 A; 6 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 4.4%; Score 14; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 175 GGTCCTGAGATC 188
Db 14 GGTCCTGAGATC 1
RESULT 12
AD187191
ID AD187191 standard; RNA; 17 BP.
XX
AC AD187191;
XX
DT 03-JUN-2004 (first entry)
XX
DE HCV DNAzyme substrate sequence #4437.
XX
KW sb; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KW HCV infection; type I interferon; DNAzyme.
XX
OS Hepatitis C virus.
XX
PN US2003125270-A1.
XX
PD 03-JUL-2003.
XX
PF 18-DEC-2000; 2000US-00740332.
XX
PR 18-DEC-2000; 2000US-00740332.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blact L, Mcswigen J, Roberts E, Pavco PA, Macejack D;
XX
DR WPI; 2004-031273/03.
XX
PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX
PS Claim 1; SEQ ID NO 4437; 19pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNAzyme substrate
CC sequence.
XX
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 0 T; 3 U; 0 Other;
Query Match 4.4%; Score 14; DB 12; Length 17;
Best Local Similarity 85.7%; Pred. No. 7.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 139 ACGAGGTTGCGACC 152
Db 4 ACGAGGTTGCGACC 17
RESULT 13.

```

AD182872/c
ID AD182872 standard; RNA; 17 BP.
XX
AC AD182872;
XX
DT 03-JUN-2004 (first entry)
XX
DE HCV DNAzyme substrate sequence #118.
XX
KW ss: enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KW HCV infection; type I interferon; DNAzyme.
XX
OS Hepatitis C virus.
XX
PN US2003125270-A1.
XX
PD 03-JUN-2003.
XX
PF 18-DEC-2000; 2000US-00740332.
XX
PR 18-DEC-2000; 2000US-00740332.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J.
PA (ROBE/) ROBERTS E.
PA (PAC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mewissen J, Roberts E, Pavco PA, Macejack D;
XX
DR WPI; 2004-031273/03.
XX
PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX
PS Claim 1; SEQ ID NO 118; 198bp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNAzyme substrate
CC sequence.
XX
SQ Sequence 17 BP; 2 A; 6 C; 6 G; 0 T; 3 U; 0 Other;
XX
Query Match 4.4%; Score 14; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 139 ACGAGTTGCGACC 152
DB 15 ACGAGTTGCGACC 2
XX
RESULT 14.
ID ADM94802/c
ID ADM94802 standard; DNA; 18 BP.
XX
AC ADM94802;
XX
DT 17-JUN-2004 (first entry)
XX
DE Hepatitis C virus DNA sequence-specific probe #16.
XX
KW DNA sequence detection; Hepatitis C virus; probe; ss.
XX
OS Hepatitis C virus.
XX
PN JP2004073064-A.

```

```

XX
PD 11-MAR-2004.
XX
PF 15-AUG-2002; 2002JP-00237045.
XX
PR 15-AUG-2002; 2002JP-00237045.
XX
PA (TOKE ) TOSHIBA KK.
XX
DR WPI; 2004-220125/21.
XX
PT Novel nucleic acid fragment comprising sequence complementary to first
PT and second target sequence and arbitrary sequences, useful as probe for
PT detecting hepatitis-C virus or for hybridizing target nucleic acid.
XX
PS Example 1; SEQ ID NO 16; 21bp; Japanese.
XX
CC The invention comprises a method for detecting a specific DNA sequence,
CC such as a specific DNA sequence from Hepatitis C virus. The method of the
CC invention is useful for detecting Hepatitis C virus and for amplifying a
CC DNA sequence from Hepatitis C virus. The present DNA sequence represents
CC a Hepatitis C virus-specific probe that is used in the method of the
CC invention.
XX
SQ Sequence 18 BP; 3 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match 4.4%; Score 14; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 139 ACGAGTTGCGACC 152
DB 18 ACGAGTTGCGACC 5
XX
RESULT 15.
ID ADM95053/c
ID ADM95053 standard; DNA; 18 BP.
XX
AC ADM95053;
XX
DT 17-JUN-2004 (first entry)
XX
DE Hepatitis C virus (HCV) oligonucleotide probe SeqID26.
XX
KW target nucleic acid hybridisation; spacer; nucleic acid probe;
KW human Hepatitis-C virus; HCV; probe; ss.
XX
OS Hepatitis C virus.
XX
PN JP2004073065-A.
XX
PD 11-MAR-2004.
XX
PF 15-AUG-2002; 2002JP-00237046.
XX
PR 15-AUG-2002; 2002JP-00237046.
XX
PA (TOKE ) TOSHIBA KK.
XX
DR WPI; 2004-342964/32.
XX
PT Novel nucleic acid fragment comprising sequence complementary to first
PT target sequence, second target sequence and spacer, useful as nucleic
PT acid probe for detecting target nucleic acid and as primer for extending
PT target nucleic acid.
XX
PS Example 1; SEQ ID NO 26; 24bp; Japanese.
XX
CC This invention relates to a novel nucleic acid fragment for hybridising a
CC target nucleic acid which contains a first target sequence and a second
CC target sequence, which comprises a sequence complementary to the first
CC target sequence and the second target sequence, and a spacer. The

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CC invention is useful as a reagent such as a nucleic acid probe for
CC detecting target nucleic acid or as a primer for extending target nucleic
CC acid. In particular, the invention is useful for detecting human
CC hepatitis-C virus. The invention enables a highly sensitive and specific
CC detection of a target nucleic acid, as a probe, and efficient extension
CC of target nucleic acid, as a primer. The present sequence is that of an
CC oligonucleotide probe which was used for detection of a region of the
CC hepatitis C virus genome during the exemplification of the invention.
XX
SQ Sequence 18 BP; 3 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 4.4%; Score 14; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 139 ACGAGGTTGGCACC 152
Db 18 ACGAGGTTGGCACC 5

RESULT 16

ADD00364/C

ID ADD00364 standard; RNA; 19 BP.

AC ADD00364;

DT 01-JAN-2004 (first entry)

DE HCV coding region-derived 50% conserved RNA sequence 310.

XX HCV infection; replication; pathogenesis; virulence; vaccine;
KW gene therapy; ds.

OS Hepatitis C virus.

XX WO2003016572-A1.

XX 27-FEB-2003.

PF 16-AUG-2002; 2002WO-US021843.

XX 17-AUG-2001; 2001US-0313076P.

PR 20-DEC-2001; 2001US-0344116P.

PR 01-FEB-2002; 2002US-0353750P.

PA (EILY) LILLY & CO ELI.

XX Zhao G, Lu J, Glass JI, Martinez A, Yang Y;

XX WPI; 2003-268345/26.

PT New double stranded RNA oligonucleotide, useful for preparing a

PT composition for treating or preventing hepatitis C virus.

XX Disclosure; Page 70; 173pp; English.

CC The invention relates to a novel isolated double stranded RNA
CC oligonucleotide about 19 to about 25 ribonucleotides in length or its
CC equivalent. One strand of the oligonucleotide comprises the same
CC nucleotide sequence as a region of a hepatitis C virus (HCV) target RNA
CC polynucleotide sequence required for hepatitis C virus infection,
CC replication or pathogenesis in vitro or in vivo in a host cell. The
CC oligonucleotide of the invention demonstrates virucide activity and may
CC be useful for preparing a composition or vaccine for treating or
CC preventing hepatitis C virus, as well as during gene therapy procedures.
CC The current sequence is that of the HCV coding region-derived conserved
CC RNA sequence of the invention.

SQ Sequence 19 BP; 4 A; 6 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 139 ACGAGGTTGGCACC 152
Db 15 ACGAGGTTGGCACC 2

RESULT 17

ADD00365/C

ID ADD00365 standard; RNA; 19 BP.

AC ADD00365;

DT 01-JAN-2004 (first entry)

DE HCV coding region-derived 50% conserved RNA sequence 311.

XX HCV infection; replication; pathogenesis; virulence; vaccine;
KW gene therapy; ds.

OS Hepatitis C virus.

XX WO2003016572-A1.

XX 27-FEB-2003.

PF 16-AUG-2002; 2002WO-US021843.

XX 17-AUG-2001; 2001US-0313076P.

PR 20-DEC-2001; 2001US-0344116P.

PR 01-FEB-2002; 2002US-0353750P.

PA (EILY) LILLY & CO ELI.

XX Zhao G, Lu J, Glass JI, Martinez A, Yang Y;

XX WPI; 2003-268345/26.

PT New double stranded RNA oligonucleotide, useful for preparing a

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CC The invention relates to a novel isolated double stranded RNA
CC oligonucleotide about 19 to about 25 ribonucleotides in length or its
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CC nucleotide sequence as a region of a hepatitis C virus (HCV) target RNA
CC polynucleotide sequence required for hepatitis C virus infection,
CC replication or pathogenesis in vitro or in vivo in a host cell. The
CC oligonucleotide of the invention demonstrates virucide activity and may
CC be useful for preparing a composition or vaccine for treating or
CC preventing hepatitis C virus, as well as during gene therapy procedures.
CC The current sequence is that of the HCV coding region-derived conserved
CC RNA sequence of the invention.

SQ Sequence 19 BP; 4 A; 5 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 139 ACGAGGTTGGCACC 152
Db 14 ACGAGGTTGGCACC 1

RESULT 18

ADD00363/C

ID ADD00363 standard; RNA; 19 BP.

AC ADD00363;

DT 01-JAN-2004 (first entry)

XX 01-JAN-2004 (first entry)

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DE HCV coding region-derived 50% conserved RNA sequence 309.
XX
XX HCV infection; replication; pathogenesis; virucide; vaccine;
XX gene therapy; ds.
XX
XX Hepatitis C virus.
XX
XX WO2003016572-A1.
XX
XX 27-FEB-2003.
XX
XX 16-AUG-2002; 2002WO-US021843.
XX
XX 17-AUG-2001; 2001US-0313076P.
XX 20-DEC-2001; 2001US-0344116P.
XX 01-FEB-2002; 2002US-0353750P.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Zhao G, Lu J, Glass JI, Martinez A, Yang Y;
XX WPI; 2003-268345/26.
XX
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XX composition for treating or preventing hepatitis C virus.
XX
XX Disclosure; Page 70; 173pp; English.
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XX polynucleotide sequence required for hepatitis C virus infection.
XX replication or pathogenesis in vitro or in vivo in a host cell. The
XX oligonucleotide of the invention demonstrates virucide activity and may
XX be useful for preparing a composition or vaccine for treating or
XX preventing hepatitis C virus, as well as during gene therapy procedures.
XX The current sequence is that of the HCV coding region-derived conserved
XX RNA sequence of the invention.
XX
XX Sequence 19 BP; 3 A; 6 C; 7 G; 0 T; 3 U; 0 Other;
SQ
Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 139 ACGAGTTGCGACC 152
DB 16 ACGAGTTGCGACC 3
RESULT 19
ADD00360/C
ID ADD00360 standard; RNA; 19 BP.
XX
XX ADD00360;
XX
XX 01-JAN-2004 (first entry)
XX
XX HCV coding region-derived 50% conserved RNA sequence 306.
XX
XX HCV infection; replication; pathogenesis; virucide; vaccine;
XX gene therapy; ds.
XX
XX Hepatitis C virus.
XX
XX WO2003016572-A1.
XX
XX 27-FEB-2003.
XX
XX 16-AUG-2002; 2002WO-US021843.
XX
XX 17-AUG-2001; 2001US-0313076P.

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PR 20-DEC-2001; 2001US-0344116P.
PR 01-FEB-2002; 2002US-0353750P.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Zhao G, Lu J, Glass JI, Martinez A, Yang Y;
XX WPI; 2003-268345/26.
XX
XX New double stranded RNA oligonucleotide, useful for preparing a
XX composition for treating or preventing hepatitis C virus.
XX
XX Disclosure; Page 69; 173pp; English.
XX
XX The invention relates to a novel isolated double stranded RNA
XX oligonucleotide about 19 to about 25 ribonucleotides in length or its
XX equivalent. One strand of the oligonucleotide comprises the same
XX nucleotide sequence as a region of a hepatitis C virus (HCV) target RNA
XX polynucleotide sequence required for hepatitis C virus infection.
XX replication or pathogenesis in vitro or in vivo in a host cell. The
XX oligonucleotide of the invention demonstrates virucide activity and may
XX be useful for preparing a composition or vaccine for treating or
XX preventing hepatitis C virus, as well as during gene therapy procedures.
XX The current sequence is that of the HCV coding region-derived conserved
XX RNA sequence of the invention.
XX
XX Sequence 19 BP; 3 A; 7 C; 6 G; 0 T; 3 U; 0 Other;
SQ
Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 139 ACGAGTTGCGACC 152
DB 19 ACGAGTTGCGACC 6
RESULT 20
ADD00361/C
ID ADD00361 standard; RNA; 19 BP.
XX
XX ADD00361;
XX
XX 01-JAN-2004 (first entry)
XX
XX HCV coding region-derived 50% conserved RNA sequence 307.
XX
XX HCV infection; replication; pathogenesis; virucide; vaccine;
XX gene therapy; ds.
XX
XX Hepatitis C virus.
XX
XX WO2003016572-A1.
XX
XX 27-FEB-2003.
XX
XX 16-AUG-2002; 2002WO-US021843.
XX
XX 17-AUG-2001; 2001US-0313076P.
XX 20-DEC-2001; 2001US-0344116P.
XX 01-FEB-2002; 2002US-0353750P.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Zhao G, Lu J, Glass JI, Martinez A, Yang Y;
XX WPI; 2003-268345/26.
XX
XX New double stranded RNA oligonucleotide, useful for preparing a
XX composition for treating or preventing hepatitis C virus.
XX
XX Disclosure; Page 69; 173pp; English.
XX

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CC The invention relates to a novel isolated double stranded RNA
CC oligonucleotide about 19 to about 25 ribonucleotides in length or its
CC equivalent. One strand of the oligonucleotide comprises the same
CC nucleotide sequence as a region of a hepatitis C virus (HCV) target RNA
CC polynucleotide sequence required for hepatitis C virus infection,
CC replication or pathogenesis in vitro or in vivo in a host cell. The
CC oligonucleotide of the invention demonstrates virucide activity and may
CC be useful for preparing a composition or vaccine for treating or
CC preventing hepatitis C virus, as well as during gene therapy procedures.
CC The current sequence is that of the HCV coding region-derived conserved
CC RNA sequence of the invention.
SQ Sequence 19 BP; 3 A; 6 C; 7 G; 0 T; 3 U; 0 Other;
QY Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 139 ACGAGTTGGCACC 152
18 ACGAGTTGGCACC 5
RESULT 21
ADD00362/c
ID ADD00362 standard; RNA; 19 BP.
AC ADD00362;
XX
DT 01-JAN-2004 (first entry)
XX
DE HCV coding region-derived 50% conserved RNA sequence 308.
XX
KM HCV infection; replication; pathogenesis; virucide; vaccine;
KM gene therapy; de.
XX
OS Hepatitis C virus.
OS
PN WO2003016572-A1.
XX
PD 27-FEB-2003.
XX
PF 16-AUG-2002; 2002WO-US021843.
XX
PR 17-AUG-2001; 2001US-0313076P.
PR 20-DEC-2001; 2001US-0344116P.
PR 01-FEB-2002; 2002US-0353750P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Zhao G, Lu J, Glass JI, Martinez A, Yang Y;
PI WPI; 2003-268345/26.
XX
DR
XX
PT New double stranded RNA oligonucleotide, useful for preparing a
PT composition for treating or preventing hepatitis C virus.
XX
PS Disclosure; Page 70; 173pp; English.
XX
CC The invention relates to a novel isolated double stranded RNA
CC oligonucleotide about 19 to about 25 ribonucleotides in length or its
CC equivalent. One strand of the oligonucleotide comprises the same
CC nucleotide sequence as a region of a hepatitis C virus (HCV) target RNA
CC polynucleotide sequence required for hepatitis C virus infection,
CC replication or pathogenesis in vitro or in vivo in a host cell. The
CC oligonucleotide of the invention demonstrates virucide activity and may
CC be useful for preparing a composition or vaccine for treating or
CC preventing hepatitis C virus, as well as during gene therapy procedures.
CC The current sequence is that of the HCV coding region-derived conserved
CC RNA sequence of the invention.
SQ Sequence 19 BP; 3 A; 6 C; 7 G; 0 T; 3 U; 0 Other;

QY Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 139 ACGAGTTGGCACC 152
17 ACGAGTTGGCACC 4
RESULT 22
ADFS2686
ID ADFS2686 standard; RNA; 19 BP.
AC ADFS2686;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus siRNA antisense strand SeqID1276.
XX
KM short interfering nucleic acid; siNA; virus replication inhibition;
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KM hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KM hepatocellular cancer; cirrhosis; ss.
XX
OS Hepatitis C virus.
OS
XX
FN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mewissen J, Beigelman I, Macejak D, Morrissey D;
PI WPI; 2003-689778/65.
XX
DR
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 1276; 183pp; English.
XX
CC This invention relates to novel double-stranded short interfering nucleic
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (AS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC AS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA/s of the invention may be used to inhibit
CC replication of HCV in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.
XX

Sequence 19 BP, 3 A, 6 C, 6 G, 0 T, 4 U, 0 Other;
Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 85.7%; Pred. No. 7.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 139 ACGAGGTTGCGACC 152
|||||:|||||
5 ACGAGGUGCGACC 18
Db
RESULT 23
ADFS2703
ID ADFS2703 standard; RNA, 19 BP.
XX ADFS2703;
AC ADFS2703;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus siNA antisense strand SeqID1293.
XX
KM short interfering nucleic acid; siNA; virus replication inhibition;
KM hepatitis C virus; HCV; sugar modification; vironcide; antiinflammatory;
KM hepatocellular cancer; cytosolic; RNA interference; HCV infection; liver failure;
KM hepatocellular cancer; cirrhosis; ss.
XX
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
DR WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 1293; 183bp; English.
XX
PS This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC vironcide, antiinflammatory, hepatotropic or cytosolic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different

CC strains.
XX
SQ Sequence 19 BP, 3 A, 7 C, 6 G, 0 T, 3 U, 0 Other;
XX
Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 85.7%; Pred. No. 7.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 139 ACGAGGTTGCGACC 152
|||||:|||||
4 ACGAGGUGCGACC 17
Db
RESULT 24
ADFS2726
ID ADFS2726 standard; RNA, 19 BP.
XX ADFS2726;
AC ADFS2726;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus siNA antisense strand SeqID1316.
XX
KM short interfering nucleic acid; siNA; virus replication inhibition;
KM hepatitis C virus; HCV; sugar modification; vironcide; antiinflammatory;
KM hepatocellular cancer; cytosolic; RNA interference; HCV infection; liver failure;
KM hepatocellular cancer; cirrhosis; ss.
XX
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
DR WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 1316; 183bp; English.
XX
PS This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC vironcide, antiinflammatory, hepatotropic or cytosolic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,

CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.
XX
SQ Sequence 19 BP; 3 A; 6 C; 7 G; 0 T; 3 U; 0 Other;
Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 85.7%; Pred. No. 7.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 139 ACGAGTTGCGACC 152
|||||
1 ACGAGTUGCGACC 14
Db
RESULT 25
ADFS2030/C
ID ADFS2030 standard; RNA; 19 BP.
XX
AC ADFS2030;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID620.
XX
KM short interfering nucleic acid; siNA; virus replication inhibition;
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KM hepatocellular cancer; cirrhosis; ss.
XX
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
DR WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 620; 183pp; English.
XX
PS This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC modulation, antiinflammatory, hepatotropic or cytostatic activities by
CC interference. The siNA's of the invention or activity of HCV RNA, by RNA
CC modification. The invention may allow development of compounds with
CC modulation, antiinflammatory, hepatotropic or cytostatic activities by
CC interference. The siNA's of the invention or activity of HCV RNA, by RNA
CC modification of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure, hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,

CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.
XX
SQ Sequence 19 BP; 3 A; 7 C; 6 G; 0 T; 3 U; 0 Other;
Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 139 ACGAGTTGCGACC 152
|||||
19 ACGAGTTGCGACC 6
Db
RESULT 26
ADFS1994/C
ID ADFS1994 standard; RNA; 19 BP.
XX
AC ADFS1994;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID584.
XX
KM short interfering nucleic acid; siNA; virus replication inhibition;
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KM hepatocellular cancer; cirrhosis; ss.
XX
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
DR WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 584; 183pp; English.
XX
PS This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC modulation, antiinflammatory, hepatotropic or cytostatic activities by
CC interference. The siNA's of the invention or activity of HCV RNA, by RNA
CC modification of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure, hepatocellular cancer

CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siRNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.
SQ Sequence 19 BP; 3 A; 6 C; 7 G; 0 T; 3 U; 0 Other;
Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 139 ACGAGGTTGCGACC 152
DB 17 ACGAGGTTGCGACC 4
RESULT 27
ADFS2685
ID ADFS2685 standard; RNA; 19 BP.
AC ADFS2685;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus siRNA antisense strand SegID1275.
XX
KM short interfering nucleic acid; siRNA; virus replication inhibition;
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KM hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KM hepatocellular cancer; cirrhosis; ss.
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI McSwiggen J, Beigelman L, Macejak D, Morrissey D;
XX
PT WPI; 2003-689778/65.
XX
DR New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 1275; 183bp; English.
XX
CC This invention relates to novel double-stranded short interfering nucleic
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siRNA's of the invention may be used to inhibit

CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siRNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.
SQ Sequence 19 BP; 3 A; 7 C; 5 G; 0 T; 4 U; 0 Other;
Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 85.7%; Pred. No. 7.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 139 ACGAGGTTGCGACC 152
DB 6 ACGAGGUUCGACC 19
RESULT 28
ADFS2698
ID ADFS2698 standard; RNA; 19 BP.
AC ADFS2698;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus siRNA antisense strand SegID1288.
XX
KM short interfering nucleic acid; siRNA; virus replication inhibition;
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KM hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KM hepatocellular cancer; cirrhosis; ss.
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI McSwiggen J, Beigelman L, Macejak D, Morrissey D;
XX
PT WPI; 2003-689778/65.
XX
DR New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 1288; 183bp; English.
XX
CC This invention relates to novel double-stranded short interfering nucleic
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by

CC	modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC	interference. The siRNA of the invention may be used to inhibit
CC	replication of HCV, in cells, tissue explants or organisms, for treating
CC	HCV infection and its consequences (liver failure; hepatocellular cancer
CC	and cirrhosis), and also for drug screening, diagnosis, target
CC	identification and validation, genetic engineering, pharmacogenomics,
CC	studying gene function and gene mapping (for example of single-nucleotide
CC	polymorphisms). The chemical modification improves stability, activity,
CC	cellular uptake and/or binding affinity. The siRNA can be directed to
CC	conserved regions of HCV genes, so are active against many different
CC	strains.
XX	
XX	Sequence 19 BP; 3 A; 7 C; 6 G; 0 T; 3 U; 0 Other;
SO	
Query Match	4.4%; Score 14; DB 10; Length 19;
Best Local Similarity	85.7%; Pred. No. 7.5e+03;
Matches 12; Conservative	2; Mismatches 0; Indels 0; Gaps 0;
OY	139 ACGAGTTGCGACC 152
	:
Db	2 ACGAGGUGCGACC 15
RESULT 29	
ADFS2007/c	
ID	ADFS2007 standard; RNA; 19 BP.
XX	
AC	ADFS2007;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Hepatitis C virus short interfering nucleic acid sense strand SeqID597.
XX	
KW	short interfering nucleic acid; siNA; virus replication inhibition;
KW	hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW	hepatotropic; cytosolic; RNA interference; HCV infection; liver failure;
KW	hepatocellular cancer; cirrhosis; ss.
XX	
OS	Hepatitis C virus.
XX	
PN	WO2003070750-A2.
XX	
PD	28-AUG-2003.
XX	
PF	20-FEB-2003; 2003WO-US005043.
XX	
PR	20-FEB-2002; 2002US-0358580P.
PR	11-MAR-2002; 2002US-0363124P.
PR	26-MAR-2002; 2002WO-US009187.
PR	06-JUN-2002; 2002US-0386782P.
PR	05-AUG-2002; 2002US-0401104P.
PR	29-AUG-2002; 2002US-0406784P.
PR	05-SEP-2002; 2002US-0408378P.
PR	09-SEP-2002; 2002US-0409293P.
PR	15-JAN-2003; 2003US-0440129P.
XX	
PA	(SIRN-) siRNA THERAPEUTICS INC.
XX	
PI	McWiggen J, Beigelman L, Macejak D, Morrissey D;
XX	
DR	WPI; 2003-689778/65.
XX	
PT	New double-stranded short interfering nucleic acid comprises sugar-
PT	modified pyrimidine bases useful for treating infection with hepatitis C
XX	
XX	virus.
PS	
XX	Example 3; SEQ ID NO 597; 183bp; English.
CC	
CC	This invention relates to novel double-stranded short interfering nucleic
CC	acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC	one strand is an antisense strand (AS) that is complementary to (part
CC	of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC	AS), and where most of the pyrimidine nucleotides comprise a sugar

CC	modification. The invention may allow development of compounds with
CC	vintucide), antiinflammatory, hepatotropic or cytostatic activities by
CC	molecular (inhibition) of expression or activity of HCV RNA, by RNA
CC	interference. The siNA's of the invention may be used to inhibit
CC	replication of HCV, in cells, tissue explants or organisms, for treating
CC	HCV infection and its consequences (liver failure; hepatocellular cancer
CC	and cirrhosis), and also for drug screening, diagnosis, target
CC	identification and validation, genetic engineering, pharmacogenomics,
CC	studying gene function and gene mapping (for example of single-nucleotide
CC	polymorphisms). The chemical modification improves stability, activity,
CC	cellular uptake and/or binding affinity. The siNA can be directed to
CC	conserved regions of HCV genes, so are active against many different
CC	strains.
SQ	Sequence 19 BP; 3 A; 6 C; 7 G; 0 T; 3 U; 0 Other;
Query Match	4.4%; Score 14; DB 10; Length 19;
Best Local Similarity	100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	139 ACAGGTTGCAGAC 152 16 ACAGGTTGCAGACC 3
Dn	
RESULT 30	
ADFS1990/C	
ID	ADFS1990 standard; RNA, 19 BP.
XX	ADFS1990;
XX	
DT	12-FEB-2004 (first entry)
DE	
XX	Hepatitis C virus short interfering nucleic acid sense strand SeqID580.
KW	short interfering nucleic acid; siNA; virus replication inhibition;
RN	hepatitis C virus; HCV; sugar modification; vintucide; antiinflammatory;
KM	hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KV	hepatocellular cancer; cirrhosis; ss.
XX	
OS	Hepatitis C virus.
XX	
PN	WO2003070750-A2.
PD	28-AUG-2003.
XX	
PF	20-FEB-2003; 2003WO-US005043.
XX	
PR	20-FEB-2002; 2002US-0358580P.
PR	11-MAR-2002; 2002US-0363124P.
PR	26-MAR-2002; 2002WO-US009187.
PR	06-JUN-2002; 2002US-0386782P.
PR	05-AUG-2002; 2002US-0401104P.
PR	29-AUG-2002; 2002US-0406784P.
PR	05-SEP-2002; 2002US-0408378P.
PR	09-SEP-2002; 2002US-0409293P.
PR	15-JAN-2003; 2003US-0440129P.
XX	
PA	(SIRN-) SIRNA THERAPEUTICS INC.
PI	
PJ	Mcewigen J, Beigelman L, Macejak D, Morrissey D;
XX	
DR	WPI; 2003-689776/65.
XX	
PT	New double-stranded short interfering nucleic acid comprises sugar-
PT	modified pyrimidine bases useful for treating infection with hepatitis C
XX	virus.
PS	Example 3; SEQ ID NO 580; 183bp; English.
XX	
XX	This invention relates to novel double-stranded short interfering nucleic
XX	acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX	one strand is an antisense strand (ASS) that is complementary to (part
CC	of)

CC (of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siRNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siRNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.

SO Sequence 19 BP, 4 A, 6 C, 6 G, 0 T, 3 U, 0 Other;

Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 ACGAGGTTGCGACC 152
Db 15 ACGAGGTTGCGACC 2

RESULT 31
ADFS2690
ID ADFS2690 standard; RNA; 19 BP.
XX
AC ADFS2690;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus siRNA antisense strand SeqID1280.
XX
KW short interfering nucleic acid; siRNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-036782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
DR WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
PS Example 3; SEQ ID NO 1280; 183bp; English.
CC This invention relates to novel double-stranded short interfering nucleic

CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siRNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siRNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.

SO Sequence 19 BP, 3 A, 7 C, 6 G, 0 T, 3 U, 0 Other;

Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 85.7%; Pred. No. 7.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 139 ACGAGGTTGCGACC 152
Db 3 ACGAGGTTGCGACC 16

RESULT 32
ADFS2002/c
ID ADFS2002 standard; RNA; 19 BP.
XX
AC ADFS2002;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID592.
XX
KW short interfering nucleic acid; siRNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-036782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
DR WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
PS Example 3; SEQ ID NO 592; 183bp; English.

XX This invention relates to novel double-stranded short interfering nucleic acids (siNA) that inhibits replication of hepatitis C virus (HCV), where one strand is an antisense strand (AS) that is complementary to (part of) an HCV RNA (portion) and a sense strand (SS) that is complementary to AS, and where most of the pyrimidine nucleotides comprise a sugar modification. The invention may allow development of compounds with vitucide, antiinflammatory, hepatotropic or cytostatic activities by modulation (inhibition) of expression or activity of HCV RNA, by RNA interference. The siNA's of the invention may be used to inhibit replication of HCV, in cells, tissue explants or organisms, for treating HCV infection and its consequences (liver failure; hepatocellular cancer and cirrhosis), and also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (for example of single-nucleotide polymorphisms). The chemical modification improves stability, activity, cellular uptake and/or binding affinity. The siNA can be directed to conserved regions of HCV genes, so are active against many different strains.

XX
XX
SQ Sequence 19 BP; 3 A; 6 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 139 ACGAGTTGCGACC 152
Db 18 ACGAGTTGCGACC 5

RESULT 33
ADP51989/C
ID ADF51989 standard; RNA; 19 BP.

XX ADF51989;
XX
XX 12-FEB-2004 (first entry)

XX Hepatitis C virus short interfering nucleic acid sense strand SeqID579.

XX short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; vitucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.

XX Hepatitis C virus.
XX
XX WO2003070750-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409292P.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX McEwiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.

XX Example 3; SEQ ID NO 579; 183bp; English.

PS
XX This invention relates to novel double-stranded short interfering nucleic acids (siNA) that inhibits replication of hepatitis C virus (HCV), where one strand is an antisense strand (AS) that is complementary to (part of) an HCV RNA (portion) and a sense strand (SS) that is complementary to AS, and where most of the pyrimidine nucleotides comprise a sugar modification. The invention may allow development of compounds with vitucide, antiinflammatory, hepatotropic or cytostatic activities by modulation (inhibition) of expression or activity of HCV RNA, by RNA interference. The siNA's of the invention may be used to inhibit replication of HCV, in cells, tissue explants or organisms, for treating HCV infection and its consequences (liver failure; hepatocellular cancer and cirrhosis), and also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (for example of single-nucleotide polymorphisms). The chemical modification improves stability, activity, cellular uptake and/or binding affinity. The siNA can be directed to conserved regions of HCV genes, so are active against many different strains.

XX
XX
SQ Sequence 19 BP; 4 A; 5 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 139 ACGAGTTGCGACC 152
Db 14 ACGAGTTGCGACC 1

RESULT 34
ADP05478/C
ID ADB05478 standard; DNA; 19 BP.

XX ADB05478;
XX
XX 29-JUL-2004 (first entry)

XX Hepatitis C virus probe #6.

XX ss; probe; hepatitis C virus; infection; hepatitis B virus.

XX Hepatitis C virus.
XX
XX JP2004113195-A.
XX
XX 15-APR-2004.
XX
XX 27-SEP-2002; 2002JP-00284453.
XX
XX 27-SEP-2002; 2002JP-00284453.
XX
XX (TOKE) TOSHIBA KK.
XX
XX WPI; 2004-360138/34.
XX
XX
XX Determining genotype or mutant of target nucleic acid by selecting
XX genotype or mutant sequence, amplifying nucleic acid having specific
XX sequence, hybridizing probe to nucleic acid, detecting nucleic acid,
XX analyzing hybridization pattern.
XX
XX Example; SEQ ID NO 6; 41pp; Japanese.

XX The invention relates to a method of determining genotype or mutant of
XX target nucleic acid comprising selecting the sequence characteristic of
XX the genotype or mutant, amplifying the nucleic acid containing the
XX characteristic sequence, allowing a probe specific to the genotype or
XX mutant to hybridise the amplified nucleic acid, detecting the nucleic
XX acid hybridised to the probe and analysing the hybridisation pattern. The
XX method is useful for determining the genotype or mutant of target nucleic

CC acid, preferably hepatitis C virus. The method is useful for immobilising
 CC an nucleic acid fragment to a solid support. The method is useful for
 CC purifying and amplifying desired viral genome, preferably hepatitis B
 CC virus. The method is useful for amplifying desired nucleic acid and for
 CC discriminating the genotype and mutant of hepatitis B virus. The method
 CC is useful in detecting the genotype of patient infected with viral
 CC hepatitis, estimating the illness condition of patient, and predicting
 CC the treatment for the infection. The method efficiently and simply
 CC determines the genotype or mutant of target nucleic acid. The method is
 CC simple and rapid for discriminating genotype and mutant of hepatitis B
 CC virus at higher rate. The present sequence represents a hepatitis C virus
 CC probe.

SQ Sequence 19 BP; 3 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 4.4%; Score 14; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 ACCGAGTTGGGACC 152
 |||||
 Db 18 ACGAGTTGGGACC 5

RESULT 35
 AAV09175/c
 ID AAV09175 standard; DNA; 20 BP.

AC AAV09175;
 DT 09-JUN-1998 (first entry)

DE Phosphorothioate oligonucleotide sequence 8054 targeting IL1R mRNA.

KM Type I interleukin-1 receptor; IL1R; human; IL1 protein; hybridisation;
 KW inflammation; ss; 5' Cap region; phosphorothioate linkage.

OS Synthetic.
 OS Homo sapiens.

PH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 /note= "Phosphorothioate internucleotide linkage"

PN WO9744656-A1.

XX 27-NOV-1997.

PF 12-MAY-1997; 97WO-US007147.

PR 21-MAY-1996; 96US-00651692.

PA (ISIS-) ISIS PHARM INC.

PI Miraglia L, Bennett CF, Dean N, Geisler T;

DR WPI; 1998-018646/02.

PT 2'-substituted oligonucleotide(s) specific for interleukin-1 receptor
 PT type I - used to modulate expression and detect overexpression of the
 PT receptor.

XX Example 5; Page 19; 63pp; English.

CC This is a novel oligomer comprising 20 covalently linked nucleotides
 CC which bind to the 5' Cap region of the interleukin-1 receptor (IL1R)
 CC mRNA. Expression of IL1R in cells and tissues can be modulated by
 CC compositions comprising oligomers which are able to specifically
 CC hybridise with target areas of its encoding sequence. The composition can
 CC be used for treatment of disease in humans caused by excessive receptor
 CC expression, e.g. inflammation. When labelled they can be used
 CC diagnostically to determine overexpression of IL1R, also to determine

CC localisation and distribution of this expression for research, diagnostic
 CC or therapeutic purposes

SQ Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 4.4%; Score 14; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCCGCCGACCCCT 56
 |||||
 Db 14 GCCGCCGACCCCT 1

RESULT 36
 AAX93253/c
 ID AAX93253 standard; DNA; 20 BP.

AC AAX93253;

DT 13-SEP-1999 (first entry)

DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.

KM Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope; PCR primer; ss.

OS Synthetic.
 OS Chlamydia pneumoniae.

PN WO9272105-A2.

PD 03-JUN-1999.

PF 20-NOV-1998; 96WO-1B001890.

PR 21-NOV-1997; 97FR-00014673.

PR 04-NOV-1998; 98US-0107078P.

PA (GENEST) GENSET.

PI Griffiths R;

DR WPI; 1999-357842/30.

DE Genome sequence of Chlamydia pneumoniae.

PS Page 1575; Disclosure; 1912pp; English.

CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAX94584 - AAX95879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleic acid sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae

SQ Sequence 20 BP; 4 A; 9 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 4.4%; Score 14; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 GCGAGCGAGTTGC 148
 |||||
 Db 17 GCGAGCGAGTTGC 4

RESULT 37
AAC67142/c
ID AAC67142 standard; DNA; 20 BP.
XX
XX AAC67142;
XX
XX 03-APR-2001 (first entry)
XX
XX Human E2F transcription factor 3 mRNA antisense sequence SEQ ID NO: 15.
DE
XX Human; E2F transcription factor 3; antisense; E2F-3; cancer;
KM phosphorothioate backbone; infection; inflammation; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX US6165791-A.
PN
XX 26-DEC-2000.
PD
XX 24-FEB-2000; 2000US-00513729.
PF
XX 24-FEB-2000; 2000US-00513729.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Popoff I, Wyatt J;
PI
XX WPI; 2001-101698/11.
DR
XX
XX Novel antisense compounds targeted to E2F transcription factor 3 for
PT diagnosis, prophylaxis and treatment of diseases associated with E2F
PT transcription factor 3 such as infection, inflammation or tumor
PT formation.
XX
XX Example 15; Col 41:42; 41pp; English.
PS
XX The present invention provides antisense oligonucleotides with
CC phosphorothioate backbones directed at the human E2F transcription factor
CC 3 (E2F-3) coding sequences. These can be used in the therapy of diseases
CC which can be treated by modulating E2F-3 expression and to prevent
CC infection, inflammation and tumour formation
CC
XX Sequence 20 BP; 2 A; 7 C; 10 G; 1 T; 0 U; 0 Other;
SQ

Query Match 4.4%; Score 14; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 GTGCGCGCGCGCGC 50
Db 19 GTGCGCGCGCGCGC 6

RESULT 38
ABT08551
ID ABT08551 standard; DNA; 20 BP.
XX
XX ABT08551;
AC
XX 28-NOV-2002 (first entry)
XX
XX Human novel protein coding sequence NOVX PCR primer SEQ ID NO: 159.
DE
XX Human; NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic;
KM antiarteriosclerotic; antidiabetic; antiasmatic; antiinflammatory;
KM haemostatic; hypotensive; neuroprotective; anorectic; nootropic;
KM antidepressant; immunosuppressive; antibacterial; antiparasitic;
KM virostatic; tranquilizer; anticonvulsant; osteopathic; analgesic;
KM antiparkinsonian; dermatological; antifertility; cerebroprotective;
KM antidiabetic; PCR; primer; probe; ss.
XX
XX Homo sapiens.
OS
XX

PN WO200259315-A2.
XX
XX 01-AUG-2002.
PD
XX
XX 19-DEC-2001; 2001WO-US050076.
PF
XX
XX 19-DEC-2000; 2000US-0256619P.
PR
XX 19-JAN-2001; 2001US-0262959P.
PR
XX 28-FEB-2001; 2001US-0272408P.
PR
XX 20-APR-2001; 2001US-0285189P.
PR
XX 26-JUL-2001; 2001US-0308039P.
PR
XX 09-AUG-2001; 2001US-0311266P.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shinkels RA, Paturajan M, Vernet CAM, Casman SJ, Malyanar U;
PI Shenoy S, Spytek RA, Gangoli E, Miller C, Boldog F, Li L;
PI Taupier RJ, Kekuda R, Smithson G, Zernusen BD, Liu X, Colman SD;
PI Tchernev V, St J, Edinger S, Stone D, Sciore P, Millet I;
PI Rothenberg M;
XX
XX WPI; 2002-666903/71.
DR
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders e.g.
PT diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease
PT or Alzheimer's disease.
XX
XX Example 1; Page 286; 363pp; English.
PS
XX
XX The present invention provides the protein and coding sequences of
CC several novel human proteins, designated NOVX. These can be used in the
CC treatment of diseases such as cancers, Hodgkin's disease, Von Hippel-
CC Lindau syndrome, Alzheimer's disease, stroke, tuberculous sclerosis,
CC hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral
CC palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia
CC telangiectasia, leukodystrophies, addiction, anxiety, depression, pain,
CC obesity, Crohn's disease, osteoporosis, inflammatory bowel disease,
CC infertility, atherosclerosis, hypertension, scleroderma, haemophilia,
CC diabetes, pancreatitis, autoimmune disease, asthma, arthritis,
CC immunodeficiencies, HIV, viral, bacterial or parasitic infections, or
CC graft-versus-host disease. The present sequence is an oligonucleotide
CC used to isolate a coding sequence of the invention
XX
XX Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
SQ

Query Match 4.4%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 241 CAGCACCAGTGAA 254
Db 7 CAGCACCAGTGAA 20

RESULT 39
ADJ34405
ID ADJ34405 standard; DNA; 20 BP.
XX
XX ADJ34405;
AC
XX 06-MAY-2004 (first entry)
XX
XX Human secreted protein NOV5 RTQ PCR primer #2.
DE
XX Human; ss; PCR; NOVX; secreted protein; cancer; diabetes; obesity;
KM endocrine disorder; CNS disorder; inflammatory disorder; gene therapy;
KM primer; RTQ PCR; real time quantitative PCR.
XX
XX Homo sapiens.
OS
XX
XX WO2004000997-A2.
PN
XX

PD 31-DEC-2003.
 XX
 PF 04-JUN-2003; 2003WO-US017512.
 XX
 PR 19-MAR-2002; 2002US-0365491P.
 PR 04-JUN-2002; 2002US-0385504P.
 PR 05-JUN-2002; 2002US-0386041P.
 PR 06-JUN-2002; 2002US-0386453P.
 PR 06-JUN-2002; 2002US-0386974P.
 PR 07-JUN-2002; 2002US-0386816P.
 PR 07-JUN-2002; 2002US-0387002P.
 PR 10-JUN-2002; 2002US-0387540P.
 PR 11-JUN-2002; 2002US-0387659P.
 PR 12-JUN-2002; 2002US-0387934P.
 PR 13-JUN-2002; 2002US-0389123P.
 PR 17-JUN-2002; 2002US-0389729P.
 PR 17-JUN-2002; 2002US-0389742P.
 PR 19-JUN-2002; 2002US-039006P.
 PR 17-JUL-2002; 2002US-0396706P.
 PR 12-AUG-2002; 2002US-0402832P.
 PR 13-AUG-2002; 2002US-0403486P.
 PR 14-AUG-2002; 2002US-0403522P.
 PR 15-AUG-2002; 2002US-0403748P.
 PR 06-NOV-2002; 2002US-0387037P.
 PR 03-JUN-2003; 2003US-00454246.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Anderson DW, Boldog FL, Burgess CE, Caeman SJ, Edinger SR,
 PI Eisen A, Ellerman K, Gerlach VL, Gorman L, Guo X, Gusev VY, Ji W,
 PI Li L, McDougall JR, Malyanhar UM, Millet I, Ort T, Padigan M,
 PI Prayaga SK, Paturajan M, Pena CEA, Peyman JA, Rieger DK,
 PI Rothenberg ME, Sciore P, Shenoy SG, Smithson G, Spletter KA, Stone DJ,
 PI Taupier RJ, Tchernev VT, Vernet CAM, Voss EZ, Zernhusen BD, Zhong M,
 XX
 XX WPI; 2004-082483/08.

PT New isolated NOVX polypeptides useful for treating, preventing and
 PT diagnosing pathological conditions with NOVX-associated disorders, such
 PT as cancer, obesity, diabetes and inflammatory or CNS diseases.
 XX

PS Example D; SEQ ID NO 294; 418bp; English.

XX The invention relates to a new isolated polypeptide (designated NOVX)
 CC comprising one of 141 fully defined sequences, their mature forms, a
 CC protein comprising one or more conservative substitutions or having at
 CC least 95% identity to one of the 141 proteins. Also included are a
 CC composition comprising NOVX or a NOVX nucleic acid molecule (NA), a kit
 CC comprising the composition of NOVX in one or more containers, an isolated
 CC nucleic acid molecule encoding a NOVX protein, producing NOVX (comprising
 CC culturing a cell under conditions that lead to expression of the
 CC polypeptide, where the cell comprises a vector comprising NOVX NA),
 CC identifying an agent that binds to NOVX, identifying a potential
 CC therapeutic agent for use in the treatment of a pathology that is related
 CC to aberrant expression or physiological interactions of NOVX, screening
 CC for a modulator of activity of or latency or predisposition to a
 CC pathology associated with NOVX, modulating the activity of NOVX, treating
 CC or preventing a pathology associated with NOVX, treating a pathological
 CC state in a mammal, a vector comprising the NOVX nucleic acid molecule, a
 CC cell comprising the vector, an antibody that immunospecifically binds to
 CC NOVX, determining the presence or amount of NOVX or the nucleic acid
 CC molecule in a sample, and determining the presence of or predisposition
 CC to a disease associated with altered levels of expression of NOVX or the
 CC nucleic acid molecule in a first mammalian subject. The methods and
 CC compositions of the present invention are useful for the diagnosis and
 CC treatment of disorders associated with aberrant expression or activity of
 CC the NOVX polypeptide, such as cancer, diabetes, obesity, and endocrine,
 CC CNS and inflammatory disorders. They can also be used in various
 CC detection and screening assays, chromosome mapping, tissue typing, gene
 CC therapy and predictive medicine. The present sequence is an RTG (real
 CC time quantitative) PCR primer for an mRNA encoding a NOVX protein.
 XX

Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 4.4%; Score 14; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 7.5e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 CAGCACCACTGGCA 254
 Db 7 CAGCACCACTGGCA 20

RESULT 40
 ADO09916
 ID ADO09916 standard; DNA; 20 BP.

AC ADO09916;

DT 01-JUL-2004 (first entry)

DE Human NOVX reverse primer #15.

XX human; NOVX; immunogen; vaccine; cancer; diabetes; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; asthma; allergy; emphysema;
 KW bronchitis; autoimmune disease; graft-versus-host disease; arthritis;
 KW scleroderma; systemic lupus erythematosus; bacterial infection;
 KW cystic fibrosis; coronary artery disease; stroke; hypertension;
 KW myocardial infarction; haemophilia; idiopathic thrombocytopenic purpura;
 KW hyperlipidemia; obesity; cirrhosis; inflammatory bowel disease;
 KW Crohn's disease; ulcers; muscular dystrophy; myasthenia gravis;
 KW endometriosis; psoriasis; alopecia; uveitis;
 KW amyotrophic lateral sclerosis; osteoporosis;
 KW liver disease; epilepsy; multiple sclerosis; anxiety; pain; fertility;
 KW glomerulonephritis; polycystic kidney disease; ss; PCR; primer.

OS Homo sapiens.

XX US2004018970-A1.

PD 29-JAN-2004.

PF 27-MAR-2002; 2002US-00107782.

XX 19-DEC-2000; 2000US-0256619P.
 PR 19-JAN-2001; 2001US-0262959P.
 PR 28-FEB-2001; 2001US-0272408P.
 PR 28-MAR-2001; 2001US-0279344P.
 PR 20-APR-2001; 2001US-0285189P.
 PR 26-JUL-2001; 2001US-0308039P.
 PR 09-AUG-2001; 2001US-0311266P.
 PR 19-DEC-2001; 2001US-00028248.

XX (SHIM/) SHIMKETS R. A.
 PA (PAT/) PATURAJAN M.
 PA (VERN/) VERNET C. A. M.
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 PA (MALY/) MALYANKAR U. M.
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 PA (SPYK/) SPYTEK K. A.
 PA (GANG/) GANGOLI E. A.
 PA (MILL/) MILLER C. E.
 PA (BOLD/) BOLDOG F. L.
 PA (LIL/) LI L.
 PA (TAUP/) TAUPIER R. J.
 PA (KEKU/) KEKUDA R.
 PA (SMIT/) SMITHSON G.
 PA (ZERN/) ZERNHUSEN B. D.
 PA (LITX/) LITX X.
 PA (COLM/) COLMAN S. D.
 PA (TCHE/) TCHERNEV V. T.
 PA (SITJ/) SI J.
 PA (EDIN/) EDINGER S. R.
 PA (STON/) STONE D. J.
 PA (SCIO/) SCIORE P.
 PA (MILL/) MILLER I.

PA (ROTH/) ROTHENBERG M E.
 XX
 PI Shinkets RA, Paturajan M, Vernet CAM, Casman SJ, Malyanar UM,
 PI Shenoy SG, Spytek KA, Gangoli EA, Miller CE, Boldog FL, Li L,
 PI Taupier RJ, Kekuda R, Smithson G, Zernusen BD, Liu X, Colman SD,
 PI Tchernev VT, St J, Edinger SR, Stone DJ, Sclere P, Millet I,
 PI Rothenberg ME,
 XX
 DR WPI: 2004-122080/12.
 XX
 PT New NOXV polypeptides and nucleic acid molecules, useful for diagnosing,
 PT preventing or treating NOXV-associated disorders e.g. cancer, diabetes,
 PT Alzheimer's disease, stroke, arthritis, hypertension or myocardial
 PT interaction.
 XX
 PS Example 1; SEQ ID NO 159; 240pp; English.
 XX
 CC The invention relates to an isolated NOXV polypeptide. A therapeutic,
 CC i.e. the NOXV polypeptide, nucleic acid and antibody, is useful for
 CC manufacturing a medicament for treating a syndrome associated with a
 CC human disease, e.g. a NOXV-associated disorder. The NOXV polypeptides can
 CC be used as immunogens or as vaccines. The NOXV polypeptide, nucleic acid
 CC or antibody is useful for diagnosing, treating or preventing a NOXV-
 CC associated disorder, e.g. cancer, diabetes, Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease, asthma, allergies, emphysema,
 CC bronchitis, autoimmune disease, graft-versus-host disease, arthritis,
 CC eczema, systemic lupus erythematosus, bacterial infections, cystic
 CC fibrosis, coronary artery disease, stroke, hypertension, myocardial
 CC infarction, haemophilia, idiopathic thrombocytopenic purpura,
 CC hyperlipidaemia, obesity, cirrhosis, inflammatory bowel disease, Crohn's
 CC disease, ulcers, muscular dystrophy, myasthenia gravis, endometriosis,
 CC prostatic, alopecia, uveitis, amyotrophic lateral sclerosis,
 CC osteoporosis, osteoarthritis, liver disease, epilepsy, multiple
 CC sclerosis, anxiety, pain, fertility, glomerulonephritis, or polycystic
 CC kidney disease. The NOXV polypeptides and nucleic acid molecules are
 CC useful for determining the presence of or predisposition to a disease
 CC associated with altered levels of the NOXV polypeptide or the nucleic
 CC acid molecule, or for screening for molecules that inhibit or enhance
 CC NOXV activity or function. The nucleic acids may be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine, or
 CC pharmacogenomics. The present sequence represents a human NOXV protein
 CC PCR primer.
 XX
 SQ Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 4.4%; Score 14; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 241 CAGCAGCAGTGGA 254
 DB 7 CAGCAGCAGTGGA 20
 XX
 RESULT 41
 AAL41635/c
 ID AAL41635 standard; DNA; 22 BP.
 XX
 AC AAL41635;
 XX
 DT 19-APR-2002 (first entry)
 XX
 DE Human colon cancer related cDNA PCR primer SEQ ID NO: 53.
 XX
 XX Human colon cancer; cytostatic; drug design; adenomatous polyp;
 KM colorectal carcinoma; high metastatic potential colon tumour;
 KM metastatic colon cancer; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX W0200196523-A2.
 PN
 XX 20-DEC-2001.
 PD

XX
 PF 15-JUN-2001; 2001WO-US019313.
 XX
 PR 15-JUN-2000; 2000US-0211835P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Kennedy GC, Kang S, Reinhard C, Jefferson AB;
 XX
 DR WPI: 2002-164362/21.
 XX
 PT Detecting a cancerous colon cell, useful for diagnosing colon cancer and
 PT for rational drug and therapy design, comprises detecting at least one
 PT differentially expressed gene product.
 XX
 PS Example 4; Page 57; 135pp; English.
 XX
 CC The present invention relates to methods for detecting a cancerous colon
 CC cell involving detecting at least one differentially expressed gene such
 CC as those given in AAL41595-AAL41611. This is useful for diagnosing colon
 CC cancer, in rational drug and therapy design, and for identifying
 CC additional genes linked to the development or inhibition of development
 CC of colon cancer. Examples of colon cancer which can be detected include
 CC adenomatous polyp, colorectal carcinoma, high metastatic potential colon
 CC tumours and metastatic colon cancer. The present sequence is a PCR primer
 CC used to isolate colon cancer associated protein coding sequences
 XX
 SQ Sequence 22 BP; 2 A; 11 C; 1 G; 8 T; 0 U; 0 Other;
 XX
 Query Match 4.4%; Score 14; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 7.6e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 112 GAGCGGAGTGGA 125
 DB 22 GAGCGGAGTGGA 9
 XX
 RESULT 42
 ADH93941
 ID ADH93941 standard; DNA; 22 BP.
 XX
 AC ADH93941;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human gene PCR primer #786.
 XX
 XX human; gene sequence; single nucleotide polymorphism; SNP;
 KM disease diagnosis; ss; PCR; primer.
 XX
 OS Homo sapiens.
 XX
 PN JP2003174883-A.
 XX
 PD 24-JUN-2003.
 XX
 PF 11-DEC-2001; 2001JP-00377637.
 XX
 PR 11-DEC-2001; 2001JP-00377637.
 XX
 PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
 XX
 DR WPI: 2003-819215/77.
 XX
 XX Polynucleotide for detecting single nucleotide polymorphisms existing in
 PT human gene, contains isolated human gene having specified sequence.
 XX
 XX Claim 2; SEQ ID NO 1778; 529pp; Japanese.
 PS
 XX
 CC The invention comprises isolated human gene sequences and PCR primer
 CC sequences which can be used to detect single nucleotide polymorphisms
 CC (SNPs). The DNA sequences of the invention are useful for detecting SNPs

CC existing in human genes and for the diagnosis of human disease. The
 CC present DNA sequence represents a human gene PCR primer of the invention.
 XX
 SO Sequence 22 BP; 6 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 4.4%; Score 14; DB 10; Length 22;
 Best Local Similarity 100.0%; Pred. No. 7.6e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 ACATGCCCTTACA 303
 DB 3 ACATGCCCTTACA 16

RESULT 43
 ADK98335
 ID ADK98335 standard; DNA; 24 BP.

AC ADK98335;

DT 06-MAY-2004 (first entry)

DE Primer of the invention #4055.

XX human; single nucleotide polymorphism; SNP; ss; primer.

OS Synthetic.

PN JP2003259875-A.

PD 16-SEP-2003.

PF 08-MAR-2002; 2002JP-00064373.

PR 08-MAR-2002; 2002JP-00064373.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

DR WPI; 2004-093977/10.

PT Novel polynucleotide useful for PCR amplification along with two DNA
 PT fragment from another set of sequences, or for detecting single
 PT nucleotide polymorphism in human gene.

PS Claim 2; SEQ ID NO 7364; 2627bp; Japanese.

CC The present invention relates to a polynucleotide isolated from a human
 CC gene and is useful for detecting a single nucleotide polymorphism in a
 CC human gene or for diagnosing of disease. The invention enables the
 CC detection of a single nucleotide polymorphism in a human gene. The
 CC present sequence represents a primer of the invention.

SO Sequence 24 BP; 8 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 4.4%; Score 14; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.6e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 TTGTTAAGAGCAG 289
 DB 4 TTGTTAAGAGCAG 17

RESULT 44
 AAQ34273/C
 ID AAQ34273 standard; DNA; 25 BP.

AC AAQ34273;

DT 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

DE Upstream PCR primer TGLA137UP1.

XX PCR; selection; microsatellite; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.

OS Bos taurus.

PN WO923102-A1.

PD 06-AUG-1992.

PF 15-JAN-1992; 92WO-US000340.

PR 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

PI Georges M, Massey JW;

DR WPI; 1992-284684/34.

PT Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.

PS Table 8; Page 439; 517pp; English.

CC The sequence shows an upstream PCR primer for in vitro amplification of
 CC bovine microsatellite sequences obtd. by screening library of bovine MbOI
 CC DNA fragments of between 250 and 500 bp with an (AC)₁₅ and a (TC)₁₅
 CC oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming
 CC independent distribution of microsatellites and MbOI sites, the frequency
 CC of (T)₆n > 9 microsatellites in the bovine genome is estimated at
 CC >100,000. The sequence information for ca. 230 such bovine
 CC microsatellites is summarised in the specification and indexed herein
 CC (see below). For each such microsatellite sequence sufficient information
 CC was obtd. to generate the required PCR primers for in vitro amplification
 CC of the corresp. microsatellite (using the program OPTIPRIM). The
 CC microsatellites may be used to identify individuals, for parentage
 CC testing, and in the genetic mapping of economic trait loci, or genes
 CC involved in the determination of economically important traits esp. in cattle,
 CC to allow selective breeding. See also AAQ33501-34440. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

SO Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 4.4%; Score 14; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 7.6e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 CAGTGATTACAG 268
 DB 19 CAGTGATTACAG 6

RESULT 45
 ACK00756/C
 ID ACK00756 standard; DNA; 25 BP.

AC ACK00756;

DT 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 100737.

KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; diallelic marker; polymorphism; human;
 KW cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFYF-) AFFYMETRIX INC.
XX
PI Mltmann MP;
XX WPI; 2003-567953/53.
DR
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 100737; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 9 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 4.4%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 ACTGCTCTCTGAG 185
DB 20 ACTGCTCTCTGAG 7
RESULT 46
ACI86610/C
ID ACI86610 standard; DNA; 25 BP.
XX
AC ACT86610;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 86601.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX

PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFYF-) AFFYMETRIX INC.
XX
PI Mltmann MP;
XX WPI; 2003-567953/53.
DR
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 86601; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 4.4%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 ACTGCTCTCTGAG 185
DB 16 ACTGCTCTCTGAG 3
RESULT 47
ACK00130/C
ID ACK00130 standard; DNA; 25 BP.
XX
AC ACK00130;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 100111.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX

PA (AFVY-) AFFYMETRIX INC.

XX Miltmann MP;

XX WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 100111; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at uspto.uspto.gov/sequence.html

XX Sequence 25 BP; 8 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

SO Query Match 4.4%; Score 14; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.6e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 ACTGGTCTCTGGAG 185

Db 18 ACTGGTCTCTGGAG 5

RESULT 48

ID ADP15727 standard; DNA; 25 BP.

AC ADP15727;

DT 26-AUG-2004 (first entry)

XX Renal cell carcinoma differentially expressed gene probe #2132.

KW ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.

OS Homo sapiens.

PN W02004048933-A2.

PD 10-JUN-2004.

PF 21-NOV-2003; 2003WO-US037481.

PR 21-NOV-2002; 2002US-0427982P.

PR 03-APR-2003; 2003US-0459782P.

PA (AMHP) WYETH.

PA (TWIN/) TWINE N C.

PA (BURC/) BURCZYNSKI M E.

PA (TREP/) TREPICCHIO W L.

PA (DORN/) DORNER A.

PA (STOV/) STOVER J A.

PA (SLOW/) SLOWIN D K.

PI Twine NC, Burczynski ME, Trepicchio WL, Dornier A, Stover JA,

PI Slow DK;

DR WPI; 2004-460799/43.

XX Diagnosing non-blood disease such as solid tumor, involves comparing

PT differential expression profile of specific genes in peripheral blood

PT sample of subject with reference expression profile of specific genes.

XX Disclosure; SEQ ID NO 2463; 350pp; English.

CC The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.

XX Sequence 25 BP; 2 A; 6 C; 10 G; 7 T; 0 U; 0 Other;

SO Query Match 4.4%; Score 14; DB 12; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.6e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 GGGACGGCTCTGTC 71

Db 4 GGGACGGCTCTGTC 17

RESULT 49

ID ABQ80298/c standard; DNA; 26 BP.

AC ABQ80298;

DT 27-JUN-2003 (first entry)

XX Primer Telo-1F.

KW Primer; PCR; amplify; regulation; cell growth; myocardial infarction;
KW osteoblast differentiation; CD49c; CD90; telomerase; p21; p53; CBFA1;
KW BSP; core binding factor 1; bone sialoprotein; degeneration; trauma;
KW acute injury; cardiac neurological; spinal cord injury;
KW amyotrophic lateral sclerosis; Parkinson's disease; stroke;
KW traumatic brain injury; Fabry disease condition; brain tumour;
KW metachromatic dyscystrophy; adrenal leukodystrophy; Canavan disease;
KW Pelizaeus Merzbacher; Nieman-pick; congestive heart failure; ss.

OS Homo sapiens.

PN W02003025149-A2.

PD 27-MAR-2003.

PF 20-SEP-2002; 2002WO-US029971.

PR 20-SEP-2002; 2002WO-US029971.

PA (AMHP) WYETH.

```

PR 21-SEP-2001; 2001US-00960244.
XX
XX (NEUR-) NEURONYX INC.
XX
XX Ho TW, Kopen GC, Righter WF, Rutkowski JL, Herring WJ, Ragalia V,
XX Wagner J,
XX
XX WPI; 2003-354604/33.
XX
XX New substantially homogenous cell population that co-express CD49c, CD90
XX and telomerase, useful for treating degenerative, traumatic, acute
XX injury, cardiac or neurological conditions in humans.
XX
XX Example 5; Page 42; 95pp; English.
XX
XX The sequences given in AB080288-99 are primers which were used to
XX determine the expression of transcripts encoding regulators of cell
XX growth and osteoblast differentiation. These primers were used to test
XX the cell populations of the invention which co-express CD49c, CD90 and
XX telomerase. The expression of transcripts for telomerase, p21, p53, CBF1
XX and B2P were determined using quantitative PCR. Cell populations which co
XX -express CD49c and CD90 express telomerase at the level of approximately
XX 13 transcripts/10 power 6 transcripts of 18S rRNA, and these populations
XX continue to proliferate at a constant rate. Compositions containing the
XX cell populations of the invention are useful in treating humans suffering
XX from a degenerative, traumatic, acute injury, cardiac or neurological
XX condition, e.g., such as spinal cord injury, amyotrophic lateral
XX sclerosis, Parkinson's disease, stroke, traumatic brain injury, Fabry
XX disease condition, metachromatic dystrophy, adrenoleukodystrophy,
XX Canavan disease, Pelizaeus Merzbacher, Niemann-Pick or brain tumour,
XX myocardial infarction or congestive heart failure. This primer is
XX deposited under Genbank ID AF015950 and its bp location is 1500-1525 bp
XX
XX Sequence 26 BP; 8 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 4.4%; Score 14; DB 10; Length 26;
XX Best Local Similarity 100.0%; Pred.No. 7.6e+03;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 105 TCCTGAGGAGCGG 118
XX |||||
XX 24 TCCTGAGGAGCGG 11
XX
XX Db
XX
XX RESULT 50
XX ADK0061/C
XX ID ADK0061 standard; DNA; 26 BP.
XX
XX ADK0061;
XX
XX 17-JUN-2004 (first entry)
XX
XX Human telomerase quantitative PCR primer seq id 11.
XX
XX cardiant; homogenous cell population; CD49c; CD90;
XX cardiac-related transcription factor; myocardial infarction;
XX congestive heart; quantitative PCR; primer; ss; human; 18S RNA;
XX cell growth regulator; osteoblast differentiation regulator; telomerase.
XX
XX Homo sapiens.
XX
XX US2004058412-A1.
XX
XX 25-MAR-2004.
XX
XX 20-SEP-2002; 2002US-00251685.
XX
XX 20-SEP-2002; 2002US-00251685.
XX
XX (NEUR-) NEURONYX INC.
XX
XX Ho TW, Kopen GC, Righter WF, Rutkowski JL, Wagner J, Herring WJ,
XX Ragalia V,

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XX
XX WPI; 2004-258792/25.
XX
XX Homogenous cell population comprising cardiac-related transcription
XX factor, useful for preparing a pharmaceutical composition for treating
XX myocardial infarction in humans.
XX
XX Example 5; SEQ ID NO 11; 25pp; English.
XX
XX The invention describes a homogenous cell population comprising CD49c,
XX CD90 and cardiac-related transcription factor. The cell population is
XX useful in a pharmaceutical composition for treating a myocardial
XX infarction, e.g. congestive heart in a human. This sequence represents a
XX quantitative PCR primer for human telomerase used to determine the
XX expression of transcripts encoding regulators of cell growth and
XX osteoblast differentiation by cell populations expressing CD49c and CD90.
XX
XX Sequence 26 BP; 8 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 4.4%; Score 14; DB 12; Length 26;
XX Best Local Similarity 100.0%; Pred.No. 7.6e+03;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 105 TCCTGAGGAGCGG 118
XX |||||
XX 24 TCCTGAGGAGCGG 11
XX
XX Db
XX
XX RESULT 51
XX ABX67739
XX ID ABX67739 standard; DNA; 30 BP.
XX
XX ABX67739;
XX
XX 07-MAY-2003 (first entry)
XX
XX Novel Helicobacter pylori gene PCR primer #710.
XX
XX Protein-protein interaction; ulcer; selected interacting domain; SID;
XX PCR; primer; ss.
XX
XX Helicobacter pylori.
XX
XX W020026501-A2.
XX
XX 29-AUG-2002.
XX
XX 28-DEC-2001; 2001WO-EP015428.
XX
XX 02-JAN-2001; 2001US-0259302P.
XX
XX (HYBR-) HYBRIGENICS.
XX PA (INSP ) INST PASTEUR.
XX
XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;
XX
XX WPI; 2002-674910/72.
XX
XX New complexes of protein-protein interactions in Helicobacter pylori,
XX useful for identifying modulating compounds for treating or preventing
XX ulcers in mammals.
XX
XX Example 9; Page 510; 642pp; English.
XX
XX The invention describes a complex of protein-protein interactions in
XX Helicobacter pylori selected from 421 complexes given in the
XX specification. The complex of protein-protein interactions are useful for
XX screening for agents which modulate the interaction of proteins.
XX Modulating compounds which binds to a targeted bacterial protein may be
XX used for treating or preventing ulcers in a human or animal. This
XX sequence represents a primer used to isolate polynucleotides encoding
XX Helicobacter pylori proteins for studies on protein-protein interactions
XX

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```

SQ Sequence 30 BP; 12 A; 5 C; 7 G; 3 T; 3 U; 0 Other;
Query Match 4.4%; Score 14; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 201 TAGTGATGAAAA 214
DB 14 TAGTGATGAAAA 27

RESULT 52
ADP89508/c
ID ADP89508 standard; DNA; 30 BP.
AC ADP89508;
XX
XX 26-FEB-2004 (first entry)
DE HIV-1 Rev NLS (-) oligo related to Rev nucleolus transfer signal.
XX
XX expression vector; NEGP reporter; long terminal repeat; LTR;
KM Rev protein nucleolus transfer signal; anti-HIV; vaccine; HIV-1; ss;
XX Rev NLS (-).
XX
XX Human immunodeficiency virus 1.
XX
XX JF2003230387-A.
XX
XX 19-AUG-2003.
XX
XX 07-FEB-2002; 2002JP-00031473.
XX
XX 07-FEB-2002; 2002JP-00031473.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (KOKU-) KOKURITSU YOB0 EISEI KENKYUSHO.
XX
XX WPI; 2003-820212/77.
XX
XX Novel expression vector comprising NEGP reporter gene linked downstream
PT of HIV-long terminal repeat, and a Rev protein nucleolus transfer signal
XX is linked downstream of reporter gene.
XX
XX Example 1; SEQ ID NO 5; 15pp; Japanese.
XX
XX The invention relates to a novel expression vector comprising an NEGP
CC reporter gene linked downstream of a HIV long terminal repeat (LTR) where
CC a Rev protein nucleolus transfer signal is linked downstream of the
CC reporter gene. The vector of the invention may be useful for infecting a
CC cell with HIV-1 and measuring the infectivity of HIV-1 in a cell, as well
CC as for producing HIV-1 clones, which in turn may be useful for anti-HIV
CC strategies such as vaccine development. The current sequence is that of
CC the HIV-1 Rev NLS (-) oligonucleotide of the invention which is related
CC to HIV-1 Rev protein nucleolus transfer signal peptide.
XX
XX
SQ Sequence 30 BP; 2 A; 10 C; 15 G; 3 T; 0 U; 0 Other;
Query Match 4.4%; Score 14; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 37 GTGCGCGCGCGCGC 50
DB 21 GTGCGCGCGCGCGC 8

RESULT 53
ABC96919/c
ID ABC96919 standard; DNA; 13 BP.
AC ABC96919;
XX
XX

DT 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 96936 for detecting SNP TSC0024052.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX MO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-1B000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIDENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 96936; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 4.1%; Score 13; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 198 TTGTAGTGATGA 210
DB 13 TTGTAGTGATGA 1

RESULT 54
ABF95242
ID ABF95242 standard; DNA; 13 BP.
AC ABF95242;
XX
XX 22-FEB-2002 (first entry)
DE
XX Oligonucleotide SEQ ID NO 195239 for detecting SNP TSC0048037.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
```

```
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 195239; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
OY Query Match 4.1%; Score 13; DB 5; Length 13;
OY Best Local Similarity 100.0%; Pred. No. 2.5e+04;
OY Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 193 TAGAATTGTAGTG 205
Db 1 TAGAATTGTAGTG 13
RESULT 55
ABF95243/c
ID ABF95243 standard; DNA; 13 BP.
XX AC ABF95243;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 195240 for detecting SNP TSC0048037.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
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PT methylation status.
XX PS Claim 1; SEQ ID NO 195240; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
OY Query Match 4.1%; Score 13; DB 5; Length 13;
OY Best Local Similarity 100.0%; Pred. No. 2.5e+04;
OY Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY Db 193 TAGAATTGTAGTG 205
OY 13 TAGAATTGTAGTG 1
RESULT 56
ABC96918
ID ABC96918 standard; DNA; 13 BP.
XX AC ABC96918;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 96935 for detecting SNP TSC0024052.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 96935; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
```

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 4.1%; Score 13; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 TTGTAGTGGATGA 210
|||||
DB 1 TTGTAGTGGATGA 13

RESULT 57

AAA26133
ID AAA26133 standard; DNA; 14 BP.

AC AAA26133;

DT 19-JUL-2000 (first entry)

DE Oestrogen receptor hairpin ribozyme target sequence SEQ ID NO:2631.

XX Oestrogen receptor; C-raf; K-raf; bcl-2; ribozyme; cleavage;

KM hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;

KM gene expression modification; cancer; phosphorothioate; endonuclease;

XX anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.

XX Homo sapiens.

PN WO954459-A2.

PD 28-OCT-1999.

PF 19-APR-1999; 99WO-US008547.

XX 20-APR-1998; 98US-0082404P.

PR 23-JUN-1998; 98US-00103636.

XX (RIBO-) RIBOZYME PHARM INC.

PI Thompson JD, Beigelman L, Mcswiggen JA, Karpelisky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Wolff T, Haeblerl P;

PI Metulic-Adamic J;

XX WPI; 2000-013248/01.

DR New nucleic acids that interact, and optionally cleave, target sequences,

PT used to treat cancer.

XX Claim 79; Page 99; 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably

CC with a target sequence and contain at least one phosphorodithiolate

CC link, having endonuclease activity. (A), and more generally any catalytic

CC nucleic acid (A') that modulates expression of the oestrogen receptor

CC gene, are used to treat cancer (particularly of breast or endometrium),

CC in vivo or by transforming cells ex vivo and implanting treated cells, or

CC for other conditions associated with levels of oestrogen receptor.

CC Because of the high selectivity for targeted RNA, (A) can also be used to

CC correlate inhibition of gene expression with alterations in phenotype,

CC particularly for identification of therapeutic targets, and as research

CC reagents (for RNA, in the same way that restriction endonucleases are

CC used with DNA). The combination of modifications in (A) improves

CC resistance to nucleases, binding affinity and/or activity. AAA23503 to

CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and

CC AAA25993 to AAA26105 represent their corresponding target sequences.

CC sequences, and AAA26107 to AAA26218 represent their corresponding target

CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and

CC antisense oligonucleotides used in the exemplification of the present

CC invention

XX Sequence 14 BP; 1 A; 8 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 4.1%; Score 13; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CCGCGCGCGCAGC 53
|||||
DB 1 CCGCGCGCGCAGC 13

RESULT 58

ABN83308/C
ID ABN83308 standard; DNA; 14 BP.

AC ABN83308;

DT 08-AUG-2002 (first entry)

DE HLA-DQB1 gene probe 37b.

XX Human; HLA-DQB1; probe; autoimmune disease; ankylosing spondylitis;

KM insulin-dependent diabetes; rheumatoid arthritis; lupus; scleroderma;

KM human leukocyte antigen; ss.

OS Homo sapiens.

PN WO200240711-A1.

PD 23-MAY-2002.

PF 16-NOV-2001; 2001WO-FR003599.

PR 17-NOV-2000; 2000FR-00014896.

XX (INMR) BIOMERIEUX SA.

PI Mouglin B;

XX WPI; 2002-454864/48.

DR Assessing genetic predisposition to autoimmune diseases, specifically

XX type I diabetes, by detecting polymorphisms associated with

PT susceptibility, resistance or neutrality.

XX Claim 10; Page 43; 57pp; French.

XX The present invention relates to a method for analysing genetic

CC predisposition to an autoimmune disease. The method comprises producing

CC at least one amplification product from a polymorphic region associated

CC with the disease, and testing it for hybridisation to probes specific for

CC susceptibility, resistance and neutrality. The method is used to

CC determine susceptibility to insulin-dependent diabetes, but can also be

CC applied to rheumatoid arthritis, ankylosing spondylitis, lupus and

CC scleroderma. The present sequence is a probe for HLA (human leukocyte

CC antigen) DQB1 gene detection. The HLA-DQB1 gene is known to be associated

CC with insulin-dependent diabetes

XX Sequence 14 BP; 3 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

XX Query Match 4.1%; Score 13; DB 6; Length 14;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+04;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 96 CCGACGTCCTCTCT 108
|||||
XX DB 13 CCGACGTCCTCTCT 1

RESULT 59
AA262579/c

ID AA262579 standard; RNA; 15 BP.
XX
AC AA262579;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for HH ribozyme HCV-3349 which cleaves HCV RNA at nt. 3349.
XX
KM Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KM cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KM autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX
FN W09955847-A2.
XX
PD 04-NOV-1999.
XX
PF 26-APR-1999; 99MO-US009027.
XX
PR 27-APR-1998; 98US-0083217P.
PR 18-SEP-1998; 98US-0100842P.
PR 25-FEB-1999; 99US-00257608.
PR 23-MAR-1999; 99US-00274553.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PI Blatt L, McSwigen JA, Roberts E, Pavco PA, Macejak D;
XX WPI; 2000-062023/05.
DR
PT Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
PS Claim 1; Page 56; 123pp; English.
XX
CC The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesized to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX
SQ Sequence 15 BP; 1 A; 9 C; 3 G; 0 T; 2 U; 0 Other;
Query Match 4.1%; Score 13; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 129 TCGGGCGGAGACG 141
DB 15 TCGGGCGGAGACG 3
RESULT 60
ABX00430/C
ID ABX00430 standard; RNA; 15 BP.
XX
AC ABX00430;
XX
DT 23-DEC-2002 (first entry)
XX
DE Hepatitis C virus substrate #212 for HCV hammerhead ribozyme #212.
XX

KM Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KM HCV ribozyme; HCV expression; HCV replication; cirrhosis; viruside;
KM liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KM type I interferon; interferon alpha; interferon beta; cytosolic;
KM interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KM substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS Hepatitis C virus.
XX
FN US202082225-A1.
XX
PD 27-JUN-2002.
XX
PF 23-MAR-1999; 99US-00274553.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, McSwigen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
DR
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS Claim 1; Page 27; 80pp; English.
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/pispid/Identry.html
XX
SQ Sequence 15 BP; 1 A; 9 C; 3 G; 0 T; 2 U; 0 Other;
Query Match 4.1%; Score 13; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 129 TCGGGCGGAGACG 141
DB 15 TCGGGCGGAGACG 3
RESULT 61
AAQ26476
ID AAQ26476 standard; DNA; 16 BP.
XX
AC AAQ26476;
XX
DT 25-MAR-2003 (revised)
DT 08-JAN-1993 (first entry)
XX
DE Probe DB69.
XX
KM PCR; polymerase chain reaction; amplify; class II HLA DQB1; probe;

KM insulin-dependent diabetes mellitus; IDDM; non-coding strand; forensics;
XX ss.
OS Synthetic.
XX WO9211389-A1.
XX 09-JUL-1992.
XX 20-DEC-1991; 91WO-US009796.
XX 21-DEC-1990; 90US-00632180.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Erlich HA, Bugawan T;
XX WPI; 1992-250108/30.
XX Novel method for typing HLA DQB1 alleles - for tissue typing, determining
PT identity, and for studying disease susceptibility.
XX Disclosure; Page 30; 37pp; English.
XX The sequences given in AAQ26461-81 are probes which were used within the
CC scope of the invention to type class II HLA DQB1 alleles. These probes
CC were used to screen sequences amplified from the DQB1 gene second exon
CC sequence. This method could be used to identify new DQB1 alleles. This
CC method provides a simple, rapid and precise system for serological
CC including those alleles which cannot be distinguished by serological
CC methods. The presence or absence of a particular HLA DQB1 allele serves
CC as an indicator of susceptibility to insulin-dependent diabetes mellitus
CC (IDDM). Accurate DQ typing is particularly important in the field of
CC organ transplantation and in the study of the molecular basis of disease
CC susceptibility. Moreover, samples from unusual sources, eg. ancient DNA
CC or forensic samples, can be typed, even when the DNA sample is degraded
CC or only present in a small amount. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 16 BP; 3 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 4.1%; Score 13; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 96 CGCAGCTCTCTCT 108
DB 4 CGCAGCTCTCTCT 16
RESULT 62
ID AAQ26453 standard; DNA; 16 BP.
XX
XX AAQ26453;
XX 25-MAR-2003 (revised)
DT 08-JAN-1993 (first entry)
XX
DE Probe DB69.
XX
XX PCR; polymerase chain reaction; amplify; class II HLA DQB1; probe;
KM insulin-dependent diabetes mellitus; IDDM; forensics; ss.
XX Synthetic.
XX WO9211389-A1.
XX 09-JUL-1992.
XX 20-DEC-1991; 91WO-US009796.
XX 21-DEC-1990; 90US-00632180.
XX

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Erlich HA, Bugawan T;
XX WPI; 1992-250108/30.
XX Novel method for typing HLA DQB1 alleles - for tissue typing, determining
PT identity, and for studying disease susceptibility.
XX Disclosure; Page 12; 37pp; English.
XX The sequences given in AAQ26442-57 are probes which were used within the
CC scope of the invention to type class II HLA DQB1 alleles. These probes
CC were used to screen sequences amplified from the DQB1 gene second exon
CC sequence. This method could be used to identify new DQB1 alleles. This
CC method provides a simple, rapid and precise system for serological
CC including those alleles which cannot be distinguished by serological
CC methods. The presence or absence of a particular HLA DQB1 allele serves
CC as an indicator of susceptibility to insulin-dependent diabetes mellitus
CC (IDDM). Accurate DQ typing is particularly important in the field of
CC organ transplantation and in the study of the molecular basis of disease
CC susceptibility. Moreover, samples from unusual sources, eg. ancient DNA
CC or forensic samples, can be typed, even when the DNA sample is degraded
CC or only present in a small amount. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 16 BP; 3 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 4.1%; Score 13; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 96 CGCAGCTCTCTCT 108
DB 4 CGCAGCTCTCTCT 16
RESULT 63
ID ABL31182/C
XX ABL31182 standard; DNA; 16 BP.
XX
XX ABL31182;
XX 21-MAR-2002 (first entry)
DT
XX
DE Human HLA genotyping oligonucleotide SEQ ID NO 671.
XX
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;
KM immunogenetic; transplantation; genetic disease; ss.
XX Homo sapiens.
XX WO200192572-A1.
XX 06-DEC-2001.
PF 01-JUN-2001; 2001WO-JP004662.
XX
XX 01-JUN-2000; 2000JP-00164798.
XX
XX (NISH) NISSHINO IND INC.
PA (SYST-) SYSTEM RES INC.
XX
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
XX WPI; 2002-122074/16.
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
PT individuals e.g. by determining immunogenetic differences when
PT transplanting between them.
XX
PS Claim 10; Page 220; 345pp; Japanese.

XX The invention relates to a typing kit for judging human leukocyte antigen
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC oligonucleotides (ABV30512-ABV31809) originating in the sequences of
CC genes e.g. belonging to HLA class I antigens on human genome and
CC containing gene polymorphisms as alloantigens have been immobilised as
CC primers for amplification of cleaved nucleic acids relating to gene
CC polymorphisms. The method is useful for judging HLA genotypes of
CC individuals by determining immunogenetic differences before transplanting
CC between them, providing genetic information to decide compatibility of
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC pancreas, Langerhans islet in pancreas and cornea, susceptibility
CC diagnosis of genetic diseases and identifying individuals

XX
SQ Sequence 16 BP; 4 A; 3 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 4.1%; Score 13; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 CGCAGCTCTCTCT 108
Db 15 CGCAGCTCTCTCT 3

RESULT 64
ABV78964 standard; DNA; 17 BP.

XX
AC ABV78964;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 210.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP129046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
PS Example 2; Page 91; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop

CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention

XX
SQ Sequence 17 BP; 6 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 4.1%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 GGAAGGCAAGCAG 37
Db 5 GGAAGGCAAGCAG 17

RESULT 65
ABV78965 standard; DNA; 17 BP.

XX
AC ABV78965;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 211.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP129046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
PS Example 2; Page 91; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL

CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTP-L-5 (S for short) compared to HTP-L (L for long). HTP-L
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTP-L plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTP-L is
 CC important in regulating male germ cell development, and the HTP-L gene was
 CC mapped to human chromosome 10p12.1. HTP-L and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTP-L, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTP-L. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTP-L proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 5 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 4.1%; Score 13; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GGAAGGCAAGCAG 37
 |||||
 DB 4 GGAAGGCAAGCAG 16

RESULT 66
 ABV78968
 ID ABV78968 standard; DNA; 17 BP.
 AC ABV78968;
 XX
 DT 03-JAN-2003 (first entry)

DE Human HTP-L scanning oligonucleotide SEQ ID 214.
 XX
 DE Human; gene therapy; tumour suppressor; HTP-L; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX
 OS Homo sapiens.
 OS
 PN EP1229046-A2.
 PN
 PD 07-AUG-2002.
 PD
 XX
 PF 28-JAN-2002; 2002EP-00001167.
 PF
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 PR
 PR 30-JAN-2001; 2001WO-US000664.
 PR
 PR 30-JAN-2001; 2001WO-US000665.
 PR
 PR 30-JAN-2001; 2001WO-US000667.
 PR
 PR 30-JAN-2001; 2001WO-US000668.
 PR
 PR 30-JAN-2001; 2001WO-US000669.
 PR
 PR 23-MAY-2001; 2001US-00864761.
 PR
 PR 09-OCT-2001; 2001US-0327898P.
 PR
 XX
 PA (AEOM-) AEOMICA INC.
 PA
 PI Zhan J;
 PI
 DR WPI; 2002-676582/73.
 DR
 XX
 XX Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTP-L.
 XX
 PS Example 2; Page 91; 718pp; English.
 XX

CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABV8519 to ABV8520). HTP-L
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTP-L-5 (S for short) compared to HTP-L (L for long). HTP-L
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTP-L plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTP-L is
 CC important in regulating male germ cell development, and the HTP-L gene was
 CC mapped to human chromosome 10p12.1. HTP-L and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTP-L, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTP-L. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTP-L proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 4.1%; Score 13; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GGAAGGCAAGCAG 37
 |||||
 DB 1 GGAAGGCAAGCAG 13

RESULT 67
 ABV78967
 ID ABV78967 standard; DNA; 17 BP.
 AC ABV78967;
 XX
 DT 03-JAN-2003 (first entry)

DE Human HTP-L scanning oligonucleotide SEQ ID 213.
 XX
 DE Human; gene therapy; tumour suppressor; HTP-L; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX
 OS Homo sapiens.
 OS
 PN EP1229046-A2.
 PN
 PD 07-AUG-2002.
 PD
 XX
 PF 28-JAN-2002; 2002EP-00001167.
 PF
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 PR
 PR 30-JAN-2001; 2001WO-US000664.
 PR
 PR 30-JAN-2001; 2001WO-US000665.
 PR
 PR 30-JAN-2001; 2001WO-US000667.
 PR
 PR 30-JAN-2001; 2001WO-US000668.
 PR
 PR 30-JAN-2001; 2001WO-US000669.
 PR
 PR 23-MAY-2001; 2001US-00864761.
 PR
 PR 09-OCT-2001; 2001US-0327898P.
 PR
 XX
 PA (AEOM-) AEOMICA INC.
 PA
 PI Zhan J;
 PI
 DR WPI; 2002-676582/73.
 DR
 XX
 XX Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTP-L.
 XX

PS Example 2; Page 91; 718bp; English.
 XX
 CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 4.1%; Score 13; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 GGAAAGGCAGCAG 37
 Db 2 GGAAAGGCAGCAG 14
 RESULT 68
 ABV78966
 ID ABV78966 standard; DNA; 17 BP.
 XX
 AC ABV78966;
 DT 03-JAN-2003 (first entry)
 DE Human HTPL scanning oligonucleotide SEQ ID 212.
 XX
 KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1229046-A2.
 XX
 PD 07-AUG-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001167.
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 09-OCT-2001; 2001US-0327898P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Zhan J;
 XX
 DR WPI; 2002-676582/73.
 XX
 PT Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and

PT for treating subjects having defects in HTPL.
 XX
 PS Example 2; Page 91; 718bp; English.
 XX
 CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 5 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 4.1%; Score 13; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 GGAAAGGCAGCAG 37
 Db 3 GGAAAGGCAGCAG 15
 RESULT 69
 ABK19313/C
 ID ABK19313 standard; RNA; 17 BP.
 XX
 AC ABK19313;
 DT 09-APR-2002 (first entry)
 DE Human ERG amberzyme target sequence Seq ID No 1960.
 XX
 KW Human; hammerhead ribozyme; cytosolic; antitumour; antidiabetic;
 KW opthalmological; antiarthritic; antiproliferative; virocidic; osteopathic;
 KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiodioma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Ostler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
 KW amberzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO200188124-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 16-MAY-2001; 2001WO-US015866.
 XX
 PR 16-MAY-2000; 2000US-00572021.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI (GLAX) GLAXO GROUP LTD.
 XX
 DR Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 XX
 PT WPI; 2002-082995/11.
 PT Novel polynucleotide which down regulates expression of Ets-related gene,

PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
PS Claim 4; Page 125; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic degeneration, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting the cell with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 4 A; 1 C; 10 G; 0 T; 2 U; 0 Other;
Query Match 4.1%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 154 TTCTTCCCGCAGC 166
DB 17 TTCTTCCCGCAGC 5
RESULT 70
ABK19314/c
ID ABK19314 standard; RNA; 17 BP.
AC ABK19314;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG Amberzyme target sequence Seq ID No 1961.
XX
KW Human; hammerhead ribozyme; cytosolic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; vitruclide; osteopathic;
KW vulnerrary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic degeneration; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenunay-Weber syndrome; leukemia; ss;
KW Osler-Weber-rendu syndrome; leukemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.

PA (GLAXO) GLAXO GROUP LTD.
XX
XX Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
PI WPI; 2002-082995/11.
DR
XX
PT Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
PS Claim 4; Page 125; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting the cell with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 4 A; 1 C; 11 G; 0 T; 1 U; 0 Other;
Query Match 4.1%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 154 TTCTTCCCGCAGC 166
DB 16 TTCTTCCCGCAGC 4
RESULT 71
ABK19315/c
ID ABK19315 standard; RNA; 17 BP.
AC ABK19315;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG Amberzyme target sequence Seq ID No 1962.
XX
KW Human; hammerhead ribozyme; cytosolic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; vitruclide; osteopathic;
KW vulnerrary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic degeneration; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenunay-Weber syndrome; leukemia; ss;
KW Osler-Weber-rendu syndrome; leukemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.

PD 22-NOV-2001.
XX
XX 16-MAY-2001; 2001WO-US015866.
XX
XX 16-MAY-2000; 2000US-00572021.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (GLAXO) GLAXO GROUP LTD.
XX
XX Jarvie T, Von Carlowitz I, Mcswigen JA, McLaughlin F, Randi AM;
PI WPI; 2002-082995/11.
XX
XX Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
XX Claim 4; Page 125; 149pp; English.
XX
XX The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Redu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
XX Sequence 17 BP; 4 A; 2 C; 10 G; 0 T; 1 U; 0 Other;
SQ
Query Match 4.1%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 154 TTCCTTCCCGCAGC 166
Db 15 TTCCTTCCCGCAGC 3
RESULT 72
ABV89388
ID ABV89388 standard; DNA; 17 BP.
XX
XX ABV89388;
AC
XX 23-DEC-2002 (first entry)
DT
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 101.
DE
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KM gene therapy; transgenic; ss.
XX
XX Homo sapiens.
OS
XX EPI239051-A2.
PN

XX
PD 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
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XX 30-JAN-2001; 2001WO-US000670.
XX 23-MAY-2001; 2001US-00864761.
XX 10-OCT-2001; 2001US-0328205P.
XX
XX (ABOM-) ABOMICA INC.
XX
XX Shannon M;
PI
XX WPI; 2002-684061/74.
DR
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 101; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (II), comprising a sequence of 730 amino
CC acids (SI, ABB81999), a sequence having 65% sequence identity to (SI),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (II) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (II) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
XX Sequence 17 BP; 2 A; 3 C; 10 G; 2 T; 0 U; 0 Other;
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Best Local Similarity 100.0%; Pred. No. 2.5e+04;
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Db 5 GCGCGGAGGAGCG 17
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ID ABV89391 standard; DNA; 17 BP.
XX
XX ABV89391;
AC
XX 23-DEC-2002 (first entry)
DT
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 104.
DE
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KM gene therapy; transgenic; ss.
XX
XX


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OS Homo sapiens.
XX
XX EP1239051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
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XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 23-MAY-2001; 2001US-00864761.
XX 10-OCT-2001; 2001US-0328205P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M;
XX
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 104; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino acids (S1, ABB83999), a sequence having 65% sequence identity to (S1), (S1) having 95% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSHL1 is a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPases as well as downstream components of the signal transduction pathway. (I) is useful for identifying a specific binding partner. (I) and nucleic acids (II) encoding (I) are useful for diagnosing, monitoring disease and treating caused by altered expression of human POSHL1 including diagnosing and treating cancer, they useful in the development of vaccines and (II) is useful in gene therapy. (II) is useful for constructing microarrays which are useful for measuring and for surveying gene expression and creating transgenic non-human animals capable of producing the proteins. The present sequence is that of a scanning oligonucleotide useful in examples of the invention. Note: The present sequence did not form part of the printed specification, but is based on sequence information supplied to Derwent by the European Patent Office
XX
XX SEQ Sequence 17 BP; 2 A; 3 C; 11 G; 1 T; 0 U; 0 Other;
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XX Query Match 4.1%; Score 13; DB 6; Length 17;
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XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Db
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XX AC ABV89392;
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XX DT 23-DEC-2002 (first entry)
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XX XX Human; POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX
XX KM
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KM Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
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XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 23-MAY-2001; 2001US-00864761.
XX 10-OCT-2001; 2001US-0328205P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M;
XX
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 105; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino acids (S1, ABB83999), a sequence having 65% sequence identity to (S1), (S1) having 95% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSHL1 is a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPases as well as downstream components of the signal transduction pathway. (I) is useful for identifying a specific binding partner. (I) and nucleic acids (II) encoding (I) are useful for diagnosing, monitoring disease and treating caused by altered expression of human POSHL1 including diagnosing and treating cancer, they useful in the development of vaccines and (II) is useful in gene therapy. (II) is useful for constructing microarrays which are useful for measuring and for surveying gene expression and creating transgenic non-human animals capable of producing the proteins. The present sequence is that of a scanning oligonucleotide useful in examples of the invention. Note: The present sequence did not form part of the printed specification, but is based on sequence information supplied to Derwent by the European Patent Office
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XX Best Local Similarity 100.0%; Pred. No. 2.5e+04;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX AC ABV89390;
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XX DT 23-DEC-2002 (first entry)
XX
XX DE Human; POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;
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XX XX
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DE Human POSHL1 scanning oligonucleotide SEQ ID NO 103.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.

XX Homo sapiens.

OS EPI239051-A2.

PN 11-SEP-2002.

PD 28-JAN-2002; 2002EP-00001165.

PF 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

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PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 23-MAY-2001; 2001US-00864761.

PR 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

XX Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL

FT -1, useful for treating disorders associated with decreased expression or

PT activity of human POSHL1.

XX Example 2; SEQ ID NO 103; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling

CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino

CC acids (S1, ABB8399), a sequence having 65% sequence identity to (S1),

CC (S1) having 95% deviations, especially conservative substitutions or a

CC fragment of the sequences comprising at least 8 contiguous amino acids.

CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an

CC adaptor protein that interacts with Rho family small GTPases as well as

CC downstream components of the signal transduction pathway. (I) is useful

CC for identifying a specific binding partner. (I) and nucleic acids (II)

CC encoding (I) are useful for diagnosing, monitoring disease and treating

CC caused by altered expression of human POSHL1 including diagnosing and

CC treating cancer, they useful in the development of vaccines and (II) is

CC useful in gene therapy. (II) is useful for constructing microarrays which

CC are useful for measuring and for surveying gene expression and creating

CC transgenic non-human animals capable of producing the proteins. The

CC present sequence is that of a scanning oligonucleotide useful in examples

CC of the invention. Note: The present sequence did not form part of the

CC printed specification, but is based on sequence information supplied to

CC Derwent by the European Patent Office

XX Sequence 17 BP; 2 A; 3 C; 11 G; 1 T; 0 U; 0 Other;

XX Query Match 4.1%; Score 13; DB 6; Length 17;

XX Best Local Similarity 100.0%; Pred.No. 2.5e+04;

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XX 78 GCGCGAGAGAGAG 90

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XX 3 GCGCGAGAGAGAG 15

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136 13 4.1 25 15 US-10-098-263B-14545 Sequence 14545, A
C 137 13 4.1 25 15 US-10-098-263B-30220 Sequence 30220, A
C 138 13 4.1 25 15 US-10-098-263B-47078 Sequence 47078, A
C 139 13 4.1 25 15 US-10-098-263B-57624 Sequence 57624, A
C 140 13 4.1 25 15 US-10-098-263B-79683 Sequence 79683, A
C 141 13 4.1 25 15 US-10-098-263B-80406 Sequence 80406, A
142 13 4.1 25 15 US-10-098-263B-81420 Sequence 81420, A
143 13 4.1 25 15 US-10-098-263B-85086 Sequence 85086, A
C 144 13 4.1 25 15 US-10-098-263B-94187 Sequence 94187, A
145 13 4.1 25 15 US-10-098-263B-103434 Sequence 103434, A
146 13 4.1 25 15 US-10-098-263B-107646 Sequence 107646, A
C 147 13 4.1 25 15 US-10-098-263B-108888 Sequence 108888, A
148 13 4.1 25 15 US-10-061-201-2163 Sequence 2163, App
149 13 4.1 25 15 US-10-061-201-2164 Sequence 2164, App
150 13 4.1 25 15 US-10-061-201-2165 Sequence 2165, App
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ALIGNMENTS

RESULT 1
US-10-751-736-15592/c
; Sequence 15592, Application US/10751736

```
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15592
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
; US-10-751-736-15593

Query Match          5.0%; Score 16; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 TGGGACCTTCTCTCC 161
      |||||
      21 TGGGACCTTCTCTCC 6

RESULT 2
US-10-751-736-15593/c
; Sequence 15593, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US/10/751,736
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15593
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
; US-10-751-736-15593

Query Match          5.0%; Score 16; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 TGGGACCTTCTCTCC 161
      |||||
      21 TGGGACCTTCTCTCC 6

RESULT 3
US-10-751-736-15685/c
; Sequence 15685, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
```

TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 15685
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-751-736-15685

Query Match 5.0%; Score 16; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 TGCACCTTCTTC 161
DB 18 TGCACCTTCTTC 3

RESULT 4
US-10-751-736-15686/c
Sequence 15686, Application US/10751736
Publication No. US20040265230A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
FILE OF INVENTION: CANCERS
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 15686
LENGTH: 21
TYPE: RNA
ORGANISM: RNAI
US-10-751-736-15686

Query Match 5.0%; Score 16; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 TGCACCTTCTTC 161
DB 16 TGCACCTTCTTC 1

RESULT 5
US-09-961-077-1167
Sequence 1167, Application US/09961077
Publication No. US20030014775A1
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
Edington, Brent E.
McSwiggen, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.
Folkerts, Otto
Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
IN PLANTS

NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/961,077
FILING DATE: 21-Sep-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,645
FILING DATE: July 12, 1996
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994

ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1167:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1167:
US-09-961-077-1167

Query Match 4.7%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 GCGCGCGCGCAGC 53
DB 4 GCGCGCGCGCAGC 18

RESULT 6
US-09-961-077-1169
Sequence 1169, Application US/09961077
Publication No. US20030014775A1
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
Edington, Brent E.
McSwiggen, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.
Folkerts, Otto
Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street

Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/961,077
FILING DATE: 21-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,645
FILING DATE: July 12, 1996
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1169:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1169:
US-09-961-077-1169
Query Match 4.7%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 39 CGCGCGCGCGCGCAGC 53
DB 1 CGCGCGCGCGCGCAGC 15
RESULT 7
US-10-764-238-78
Sequence 78, Application US/10764238
Publication No. US20040219616A1
GENERAL INFORMATION:
APPLICANT: Elix Therapeutics Ltd.
APPLICANT: Seery, Liam
APPLICANT: Hayes, Ian
APPLICANT: Murphy, Finbarr
TITLE OF INVENTION: Apoptosis-Related Kinase/GPCRs
FILE REFERENCE: 8912/2012
CURRENT APPLICATION NUMBER: US/10/764,238
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/457,533
PRIOR FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: UK 0301566.5
PRIOR FILING DATE: 2003-01-23
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.2
SEQ ID NO 78
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: qPCR Forward Primer (GPR86)

US-10-764-238-78
Query Match 4.7%; Score 15; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 222 AGGTGACACTGGAG 236
DB 1 AGGTGACACTGGAG 15
RESULT 8
US-10-751-736-15688/C
Sequence 15688, Application US/10751736
Publication No. US20040265230A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 15688
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-751-736-15688
Query Match 4.7%; Score 15; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 146 TCGACCTTCTCCTTC 160
DB 15 TCGACCTTCTCCTTC 1
RESULT 9
US-10-098-263B-37841/C
Sequence 37841, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 37841
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-263B-37841
Query Match 4.7%; Score 15; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 GTCTCTGGAGATCAG 190
DB 17 GTCTCTGGAGATCAG 3

```
RESULT 10
US-10-296-012-13
; Sequence 13, Application US/10296012
; Publication No. US20040023238A1
; GENERAL INFORMATION:
; APPLICANT: Keller, Charles
; APPLICANT: Ballard, Linda
; APPLICANT: Lemons, Richard
; APPLICANT: All-Oman, Francis
; TITLE OF INVENTION: High-Throughput Glutathione S-Transferase Polymorphic Allele Assay
; FILE REFERENCE: 1321.2.48
; CURRENT APPLICATION NUMBER: US/10/296,012
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: 60/219,531
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide.
US-10-296-012-13

Query Match      4.7%; Score 15; DB 16; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      300 TACAGACTGGGAGT 314
Db      6 TACAGACTGGGAGT 20

RESULT 11
US-10-189-576-9
; Sequence 9, Application US/10189576
; Publication No. US20030059878A1
; GENERAL INFORMATION:
; APPLICANT: ONUKI, Tetsuo
; APPLICANT: KOGUCHI, Yutaka
; APPLICANT: TSUDA, Naoki
; TITLE OF INVENTION: A NOVEL PURINOCEPTOR AND THE GENE THEREOF
; FILE REFERENCE: ONUKI-1A
; CURRENT APPLICATION NUMBER: US/10/189,576
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificially synthesized primer sequence
US-10-189-576-9

Query Match      4.7%; Score 15; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      222 AGGTGACACTGGAG 236
Db      14 AGGTGACACTGGAG 28

RESULT 12
US-09-740-332-118/c
; Sequence 118, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
```

```
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 118
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-118

Query Match      4.4%; Score 14; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      139 ACGAGTTGGGACC 152
Db      15 ACGAGTTGGGACC 2

RESULT 13
US-09-740-332-4437
; Sequence 4437, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4437
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4437

Query Match      4.4%; Score 14; DB 10; Length 17;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      139 ACGAGTTGGGACC 152
Db      4 ACGAGTTGGGACC 17

RESULT 14
US-09-740-332-4438
; Sequence 4438, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4438
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
```

```
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4438
```

```
Query Match          4.4%; Score 14; DB 10; Length 17;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      139 ACGAGTTGCGACC 152
         |||||:|||||
Db       1 ACGAGGUGCGACC 14
```

```
RESULT 15
US-09-817-879-118/c
Sequence 118, Application US/09817879
Publication No. US2003017311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
FILE REFERENCE: MEBH00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 118
LENGTH: 17
TYPE: RNA
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-118
```

```
Query Match          4.4%; Score 14; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      139 ACGAGTTGCGACC 152
         |||||:|||||
Db       15 ACGAGTTGCGACC 2
```

```
RESULT 16
US-09-817-879-4437
Sequence 4437, Application US/09817879
Publication No. US2003017311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
FILE REFERENCE: MEBH00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4437
LENGTH: 17
TYPE: RNA
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4437
```

```
Query Match          4.4%; Score 14; DB 10; Length 17;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      139 ACGAGTTGCGACC 152
         |||||:|||||
Db       4 ACGAGGUGCGACC 17
```

```
RESULT 17
US-09-817-879-4438
Sequence 4438, Application US/09817879
Publication No. US2003017311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
FILE REFERENCE: MEBH00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4438
LENGTH: 17
TYPE: RNA
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4438
```

```
Query Match          4.4%; Score 14; DB 10; Length 17;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      139 ACGAGTTGCGACC 152
         |||||:|||||
Db       1 ACGAGGUGCGACC 14
```

```
RESULT 18
US-10-712-672-98/c
Sequence 98, Application US/10712672
Publication No. US20040102413A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Chowitra, Bharat
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
FILE REFERENCE: MEBH00-882-C (400/019)
CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US/09/653,225
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/197,769
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/150,713
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 98
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-712-672-98
```

```
Query Match          4.4%; Score 14; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      105 TCTTGAGGAGCGG 118
         |||||:|||||
Db       17 TCTTGAGGAGCGG 4
```


RESULT 19

US-10-712-672-99/C
; Sequence 99, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Chowitra, Bharat
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 99
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-99

Query Match 4.4%; Score 14; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 TCCTGAGGAGCGG 118

Db 16 TCCTGAGGAGCGG 3

RESULT 20

US-10-712-672-811/C
; Sequence 811, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Chowitra, Bharat
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 811
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-811

Query Match 4.4%; Score 14; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 TCCTGAGGAGCGG 118

Db 15 TCCTGAGGAGCGG 2

RESULT 21

US-10-712-672-812/C
; Sequence 812, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Chowitra, Bharat
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 812
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-812

Query Match 4.4%; Score 14; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 TCCTGAGGAGCGG 118

Db 14 TCCTGAGGAGCGG 1

RESULT 22

US-10-669-841-2711/C
; Sequence 2711, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwigen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07

```
/ PRIOR APPLICATION NUMBER: US 09/504,321
/ PRIOR FILING DATE: 2000-02-15
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 16207
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2711
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: oligonucleotide substrate
/ US-10-669-841-2711

Query Match      4.4%; Score 14; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      139 ACGAGGTGGGACC 152
Db      15 ACGAGGTGGGACC 2

RESULT 23
/ US-10-669-841-7030
/ Sequence 7030, Application US/10669841
/ Publication No. US20040127446A1
/ GENERAL INFORMATION:
/ APPLICANT: Sirna Therapeutics, Inc.
/ APPLICANT: Lawrence, Blact
/ APPLICANT: Dennis, Macejak
/ APPLICANT: James, McSwiggan
/ APPLICANT: David, Morrissey
/ APPLICANT: Pamela, Pavco
/ APPLICANT: Patricia, Lee
/ APPLICANT: Kenneth, Draper
/ APPLICANT: Elisabeth, Roberts
/ TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPB
/ FILE REFERENCE: 400/042US (MHB02-249-E)
/ CURRENT FILING DATE: 2003-09-23
/ PRIOR APPLICATION NUMBER: US/10/669,841
/ PRIOR FILING DATE: 2002-03-26
/ PRIOR APPLICATION NUMBER: PCT/US02/09187
/ PRIOR FILING DATE: 2001-06-08
/ PRIOR APPLICATION NUMBER: US 60/296,876
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: US 60/335,059
/ PRIOR FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: US 60/358,580
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/363,124
/ PRIOR FILING DATE: 2002-03-11
/ PRIOR APPLICATION NUMBER: US 09/817,879
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: US 09/740,332
/ PRIOR FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: US 09/611,931
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: US 09/504,321
/ PRIOR FILING DATE: 2000-02-15
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 16207
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 7030
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
```

```
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: oligonucleotide substrate
/ US-10-669-841-7030

Query Match      4.4%; Score 14; DB 17; Length 17;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      139 ACGAGGTGGGACC 152
Db      4 ACGAGGTGGGACC 17

RESULT 24
/ US-10-669-841-7031
/ Sequence 7031, Application US/10669841
/ Publication No. US20040127446A1
/ GENERAL INFORMATION:
/ APPLICANT: Sirna Therapeutics, Inc.
/ APPLICANT: Lawrence, Blact
/ APPLICANT: Dennis, Macejak
/ APPLICANT: James, McSwiggan
/ APPLICANT: David, Morrissey
/ APPLICANT: Pamela, Pavco
/ APPLICANT: Patricia, Lee
/ APPLICANT: Kenneth, Draper
/ APPLICANT: Elisabeth, Roberts
/ TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPB
/ FILE REFERENCE: 400/042US (MHB02-249-E)
/ CURRENT FILING DATE: 2003-09-23
/ PRIOR APPLICATION NUMBER: PCT/US02/09187
/ PRIOR FILING DATE: 2002-03-26
/ PRIOR APPLICATION NUMBER: US 60/296,876
/ PRIOR FILING DATE: 2001-06-08
/ PRIOR APPLICATION NUMBER: US 60/335,059
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: US 60/337,055
/ PRIOR FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: US 60/358,580
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/363,124
/ PRIOR FILING DATE: 2002-03-11
/ PRIOR APPLICATION NUMBER: US 09/817,879
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: US 09/740,332
/ PRIOR FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: US 09/611,931
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: US 09/504,321
/ PRIOR FILING DATE: 2000-02-15
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 16207
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 7031
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: oligonucleotide substrate
/ US-10-669-841-7031

Query Match      4.4%; Score 14; DB 17; Length 17;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

OY 139 ACGAGTTGGCACC 152
|||:|||||
DB 1 ACGAGGUGCGACC 14

RESULT 25

US-09-955-2598-24
; Sequence 24, Application US/09955259B
; Publication No. US20030104607A1
; GENERAL INFORMATION:
; APPLICANT: Annibali, Nestor
; TITLE OF INVENTION: Expression of a Human Insulin Precursor In P. Pastoris
; FILE REFERENCE: 52071.4
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-955-2598-24

Query Match 4.4%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 CAGCACCAGTGAA 254
|||:|||||
DB 3 CAGCACCAGTGAA 16

RESULT 26

US-10-667-271-579/C
; Sequence 579, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 579
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-667-271-579

Query Match 4.4%; Score 14; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 139 ACGAGTTGGCACC 152
|||:|||||
DB 14 ACGAGTTGGCACC 1

RESULT 27

US-10-667-271-580/C
; Sequence 580, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 580
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-667-271-580

Query Match 4.4%; Score 14; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 139 ACGAGTTGGCACC 152
|||:|||||
DB 15 ACGAGTTGGCACC 2

RESULT 28

```
US-10-667-271-584/c
; Sequence 584, Application US/10667271
; Publication No.: US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: MCSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 584
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-584

Query Match          4.4%; Score 14; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      139 ACGAGGTTGCGACC 152
Db      17 ACGAGGTTGCGACC 4

RESULT 29
US-10-667-271-592/c
; Sequence 592, Application US/10667271
; Publication No.: US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: MCSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
```

```
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 592
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-667-271-592

Query Match          4.4%; Score 14; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      139 ACGAGGTTGCGACC 152
Db      18 ACGAGGTTGCGACC 5

RESULT 30
US-10-667-271-597/c
; Sequence 597, Application US/10667271
; Publication No.: US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: MCSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
```

```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 597
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-597
```

Query Match

```

4.4%; Score 14; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 139 ACGAGTTGCGACC 152

Db 16 ACGAGTTGCGACC 3

```

RESULT 31
US-10-667-271-620/c
; Sequence 620, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-05-23
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 620
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-620
```

```

Query Match
4.4%; Score 14; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 139 ACGAGTTGCGACC 152

Db 19 ACGAGTTGCGACC 6

```

RESULT 32
US-10-667-271-1275
; Sequence 1275, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1275
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1275
```

```

Query Match
4.4%; Score 14; DB 18; Length 19;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

OY 139 ACGAGTTGCGACC 152

Db 6 ACGAGTUGCGACC 19

```

RESULT 33
US-10-667-271-1276
; Sequence 1276, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
```

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; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1276
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1276
```

```

Query Match      4.4%; Score 14; DB 18; Length 19;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      139 ACGAGTTGGGACC 152
Db      5 ACGAGGUGGCGACC 18
```

RESULT 34

```

US-10-667-271-1280
; Sequence 1280, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```

; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1280
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1280
```

```

Query Match      4.4%; Score 14; DB 18; Length 19;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      139 ACGAGTTGGGACC 152
Db      3 ACGAGGUGGCGACC 16
```

RESULT 35

```

US-10-667-271-1288
; Sequence 1288, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1288
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1288
```

```

Query Match      4.4%; Score 14; DB 18; Length 19;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      139 ACGAGTTGGGACC 152
Db      2 ACGAGGUGGCGACC 15
```

```
RESULT 36
US-10-667-271-1293
; Sequence 1293, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US/10/667,271
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1293
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1293

Query Match      4.4%  Score 14; DB 18; Length 19;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      139 ACGAGTTGCGACC 152
Db      4 ACGAGTUGCGACC 17

RESULT 37
US-10-667-271-1316
; Sequence 1316, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US/10/667,271
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
```

```
;; PRIOR APPLICATION NUMBER: PCT / US03/05043
;; PRIOR FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: PCT / US02/09187
;; PRIOR FILING DATE: 2002-03-26
;; PRIOR APPLICATION NUMBER: USSN 60/401,104
;; PRIOR FILING DATE: 2002-08-05
;; PRIOR APPLICATION NUMBER: USSN 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: USSN 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: USSN 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: USSN 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: USSN 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: USSN 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1705
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 1316
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1316

Query Match      4.4%  Score 14; DB 18; Length 19;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      139 ACGAGTTGCGACC 152
Db      1 ACGAGTUGCGACC 14

RESULT 38
US-10-028-248A-159
; Sequence 159, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Pachturajan, Meera
; APPLICANT: Verneet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Malpankar, Uriel
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gangolli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Boldog, Perenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glenda
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchernov, Veltzar
; APPLICANT: Si, Jingsheng
; APPLICANT: Bdingert, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Sclote, Paul
; APPLICANT: Miller, Isabelle
; APPLICANT: Rotherberg, Mark
; TITLE OF INVENTION: NO. US20030235882A1 Nucleic Acids and Polypeptides and Methods
; FILE REFERENCE: 21402-222
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US/10/028,248A
; PRIOR APPLICATION NUMBER: 60/256619
```

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; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
; US-10-028-248A-159
```

```
Query Match
Best Local Similarity 100.0%; Score 14; DB 15; Length 20;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 241 CAGCACGAGTGGAA 254
Db 7 CAGCACGAGTGGAA 20
```

```
RESULT 39
US-10-289-762-2554/C
; Sequence 2554, Application US/10289762
; Publication No. US2004006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2554
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; US-10-289-762-2554
```

```
Query Match
Best Local Similarity 100.0%; Score 14; DB 15; Length 20;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 135 GGAGACGAGGTGC 148
Db 17 GGAGACGAGGTGC 4
```

```
RESULT 40
US-10-107-782-159
; Sequence 159, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie
; APPLICANT: Colman, Steve,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gangoli, Neha,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malyanekar, Uriel,
```

```
; APPLICANT: Miller, Charles,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Patnursajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shinkete, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glenda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Taupier, Raymond, Jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zethusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10/107,782
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272,408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285,189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308,039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311,266
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/279,344
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 159
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
; US-10-107-782-159
```

```
Query Match
Best Local Similarity 100.0%; Score 14; DB 16; Length 20;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 241 CAGCACGAGTGGAA 254
Db 7 CAGCACGAGTGGAA 20
```

```
RESULT 41
US-10-751-736-15496/C
; Sequence 15496, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15496
```


LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-751-736-15496

Query Match 4.4%; Score 14; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 146 TGCAGCTTCTCCTT 159
Db 14 TGCAGCTTCTCCTT 1

RESULT 42
US-09-883-152-53/c
Sequence 53, Application US/09883152
Publication No. US2003008284A1
GENERAL INFORMATION:
APPLICANT: Kennedy, Giulia
APPLICANT: Kang, Sammo
APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne Bennett
TITLE OF INVENTION: POLYNUCLEOTIDES RELATED TO COLON CANCER
FILE REFERENCE: 2300-1663
CURRENT APPLICATION NUMBER: US/09/883,152
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/211,835
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 53
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-883-152-53

Query Match 4.4%; Score 14; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 112 GAACGGGAGTGGA 125
Db 22 GAACGGGAGTGGA 9

RESULT 43
US-10-098-263B-86601/c
Sequence 86601, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 86601
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-86601

Query Match 4.4%; Score 14; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 172 ACTGCTCTCTGAG 185

Db 16 ACTGCTCTCTGAG 3

RESULT 44
US-10-098-263B-100111/c
Sequence 100111, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 100111
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-100111

Query Match 4.4%; Score 14; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 172 ACTGCTCTCTGAG 185
Db 18 ACTGCTCTCTGAG 5

RESULT 45
US-10-098-263B-100737/c
Sequence 100737, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 100737
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-100737

Query Match 4.4%; Score 14; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 172 ACTGCTCTCTGAG 185
Db 20 ACTGCTCTCTGAG 7

RESULT 46
US-10-717-597-2463
Sequence 2463, Application US/10717597
Publication No. US20040110221A1
GENERAL INFORMATION:
APPLICANT: Wylech
APPLICANT: Burczynski, Michael E.
APPLICANT: Twine, Natalie C.
APPLICANT: Dorneer, Andrew J.
APPLICANT: Trepichio, William L.
APPLICANT: Stonim, Donna K.

Query Match 4.4%; Score 14; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2463
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-2463

Query Match
Best Local Similarity 100.0%; Score 14; DB 17; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GGGACGGCTCTCTGC 71
DB 4 GGGACGGCTCTCTGC 17

RESULT 47
US-09-960-244A-11/c
; Sequence 11, Application US/09960244A
; Publication No. US20030059414A1
; GENERAL INFORMATION:
; APPLICANT: Ho, Tony W.
; APPLICANT: Kopen, Gene C.
; APPLICANT: Righter, William F.
; APPLICANT: Rutkowski, J. Lynn
; TITLE OF INVENTION: CELL POPULATIONS WHICH CO-EXPRESS CD49c
; TITLE OF INVENTION: AND CD90
; FILE REFERENCE: 2831.2003-000
; CURRENT APPLICATION NUMBER: US/09/960,244A
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primers
US-09-960-244A-11

Query Match
Best Local Similarity 100.0%; Score 14; DB 10; Length 26;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 TCCTGAGGAAGCGG 118
DB 24 TCCTGAGGAAGCGG 11

RESULT 48
US-10-251-685-11/c
; Sequence 11, Application US/10251685
; Publication No. US20040058412A1
; GENERAL INFORMATION:
; APPLICANT: Ho, Tony W.
; APPLICANT: Kopen, Gene C.
; APPLICANT: Righter, William F.
; APPLICANT: Rutkowski, J. Lynn
; APPLICANT: Wagner, Joseph
; APPLICANT: Herring, W. Joseph
; APPLICANT: Ragaglia, Vanessa
; TITLE OF INVENTION: CELL POPULATIONS WHICH CO-EXPRESS CD49c
```

```

; TITLE OF INVENTION: AND CD90
; FILE REFERENCE: 2831.2003-001
; CURRENT APPLICATION NUMBER: US/10/251,685
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primers
US-10-251-685-11

Query Match
Best Local Similarity 100.0%; Score 14; DB 16; Length 26;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 TCCTGAGGAAGCGG 118
DB 24 TCCTGAGGAAGCGG 11

RESULT 49
US-10-257-017B-96935
; Sequence 96935, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 96935
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024052
US-10-257-017B-96935

Query Match
Best Local Similarity 100.0%; Score 13; DB 18; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 TTGTAGTGATGA 210
DB 1 TTGTAGTGATGA 13

RESULT 50
US-10-257-017B-96936/c
; Sequence 96936, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 96936
```

```

; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024052
US-10-257-017B-96936

Query Match          4.1%; Score 13; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      198 TTGTAGTGTGATGA 210
      |||||
Db      13 TTGTAGTGTGATGA 1

RESULT 51
US-10-257-017B-195239
; Sequence 195239, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 195239
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0048037
US-10-257-017B-195239

Query Match          4.1%; Score 13; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      193 TAGAATTGTAGTG 205
      |||||
Db      1 TAGAATTGTAGTG 13

RESULT 52
US-10-257-017B-195240/C
; Sequence 195240, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 195240
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0048037
US-10-257-017B-195240
```

```

Query Match          4.1%; Score 13; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      193 TAGAATTGTAGTG 205
      |||||
Db      13 TAGAATTGTAGTG 1

RESULT 53
US-10-416-928-11/C
; Sequence 11, Application US/10416928
; Publication No. US20040033516A1
; GENERAL INFORMATION:
; APPLICANT: Biometreux S.A.
; TITLE OF INVENTION: METHOD FOR ANALYZING A PATIENT'S PREDISPOSITION TO INSULIN-DEPEND
; FILE REFERENCE: BONN-104
; CURRENT APPLICATION NUMBER: US/10/416,928
; CURRENT FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-416-928-11

Query Match          4.1%; Score 13; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      96 CGCAGCTCTCTCT 108
      |||||
Db      13 CGCAGCTCTCTCT 1

RESULT 54
US-09-504-231A-212/C
; Sequence 212, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 212
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-212

Query Match          4.1%; Score 13; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 129 TCGGGCGGAGACG 141
|||||
Db 15 TCGGGCGGAGACG 3

RESULT 55
US-09-274-553D-212/c
; Sequence 212, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blact, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: EPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 212
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-212

Query Match 4.1%; Score 13; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 TCGGGCGGAGACG 141
|||||
Db 15 TCGGGCGGAGACG 3

RESULT 56
US-10-297-068-671/c
; Sequence 671, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 1314OP174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 671
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: capture
US-10-297-068-671

Query Match 4.1%; Score 13; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 96 CGCAGCTCCTCCT 108
|||||
Db 15 CGCAGCTCCTCCT 3

RESULT 57
US-09-864-785-2830/c
; Sequence 2830, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: 400/022 (MHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2830
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2830

Query Match 4.1%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 TTCCTTCCCGACG 166
|||||
Db 17 TTCCTTCCCGACG 5

RESULT 58
US-09-864-785-2831/c
; Sequence 2831, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: 400/022 (MHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2831
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2831

Query Match 4.1%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 TTCCTTCCCGACG 166
|||||
Db 16 TTCCTTCCCGACG 4

RESULT 59

US-09-864-785-2832/c
; Sequence 2832, Application US/09864785
; Patent No. US2002017558A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: 400/022 (MBH80-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2832
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2832

Query Match 4.1%; Score 13; DB 9; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 154 TTCTTCCCGCAGC 166

Db 15 TTCTTCCCGCAGC 3

RESULT 60

US-09-740-332-117/c
; Sequence 117, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 117
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-117

Query Match 4.1%; Score 13; DB 10; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 140 CGAGTTCGACG 152

Db 17 CGAGTTCGACG 5

RESULT 61

US-09-817-879-117/c
; Sequence 117, Application US/09817879
; Publication No. US2003017111A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; FILE REFERENCE: MBH80-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 117
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-117

Query Match 4.1%; Score 13; DB 10; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 140 CGAGTTCGACG 152

Db 17 CGAGTTCGACG 5

RESULT 62

US-10-060-756A-210
; Sequence 210, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 210
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-210

Query Match 4.1%; Score 13; DB 14; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 GGAAGCGACGAG 37

Db 5 GGAAGCGACGAG 17

RESULT 63

US-10-060-756A-211
; Sequence 211, Application US/10060756A
; Publication No. US20030046717A1

```
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 211
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-211
```

```
Query Match          4.1%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      25 GGAAGGCAAGCAG 37
         |||||
         4 GGAAGGCAAGCAG 16
DB
```

```
RESULT 64
US-10-060-756A-212
; Sequence 212, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 212
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-212
```

```
Query Match          4.1%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      25 GGAAGGCAAGCAG 37
         |||||
         3 GGAAGGCAAGCAG 15
DB
```

```
RESULT 65
US-10-060-756A-213
; Sequence 213, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 213
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-213
```

```
Query Match          4.1%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      25 GGAAGGCAAGCAG 37
         |||||
         2 GGAAGGCAAGCAG 14
DB
```

```
RESULT 66
US-10-060-756A-214
; Sequence 214, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
```

```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 214
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-214

Query Match          4.1%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      25 GGAGGCGAGGAGG 37
Db      1 GGAGGCGAGGAGG 13

RESULT 67
US-10-061-201-101
; Sequence 101, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 101
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-101

Query Match          4.1%; Score 13; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78 GCGCGGAGGAGG 90
Db      5 GCGCGGAGGAGG 17

RESULT 68
US-10-061-201-102
; Sequence 102, Application US/10061201
; Publication No. US20030166229A1
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; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10

US-10-061-201-102

Query Match          4.1%; Score 13; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78 GCGCGGAGGAGG 90
Db      4 GCGCGGAGGAGG 16

RESULT 69
US-10-061-201-103
; Sequence 103, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
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; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 103
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-103
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Query Match          4.1%; Score 13; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      78 GCGCGAGAGAGAGG 90
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Db       3 GCGCGAGAGAGAGG 15
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RESULT 70
US-10-061-201-104
; Sequence 104, Application US/10061201
; Publication No. US20030162229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00671
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 104
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-104
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Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db       2 GCGCGAGAGAGAGG 14
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RESULT 71
US-10-061-201-105
; Sequence 105, Application US/10061201
; Publication No. US20030162229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
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; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 105
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-105
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Query Match          4.1%; Score 13; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      78 GCGCGAGAGAGG 90
      |||||
Db       1 GCGCGAGAGAGG 13
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RESULT 72
US-10-138-674-7348
; Sequence 7348, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: Wcswigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R-
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7348
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7348
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Query Match          4.1%; Score 13; DB 16; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      118 GGAGTGACCATC 130
      |||||
Db       2 GGAGTGACCATC 14
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RESULT 73
US-10-287-949A-7348
; Sequence 7348, Application US/10287949A
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Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7348
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-287-949A-7348

Query Match
Best Local Similarity 4.1%; Score 13; DB 17; Length 17;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 118 GGAGTGACACATC 130
Db 2 GGAGUGACCAUC 14

RESULT 74
US-10-712-672-100/c
Sequence 100, Application US/10712672
Publication No. US20040102413A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Chowrita, Bharat
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
FILE REFERENCE: MHB00-882-C (400/019)
CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US/09/653,225
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/197,769
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/150,713
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 100
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-712-672-100

Query Match
Best Local Similarity 4.1%; Score 13; DB 17; Length 17;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 105 TCCTGAGGAGCG 117
Db 13 TCCTGAGGAGCG 1

RESULT 75
US-10-712-672-810/c
Sequence 810, Application US/10712672
Publication No. US20040102413A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Chowrita, Bharat
APPLICANT: McSwiggen, Jim
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APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
FILE REFERENCE: MHB00-882-C (400/019)
CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US/09/653,225
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/197,769
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/150,713
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 810
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-712-672-810

Query Match
Best Local Similarity 4.1%; Score 13; DB 17; Length 17;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 106 CCTGAGGAGCG 118
Db 17 CCTGAGGAGCG 5

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Job time : 177.942 secs
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:25:00 : Search time 30.5987 Seconds
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7410.178 Million cell updates/sec

Title: US-10-048-046-1_COPY_81_399

Perfect score: 319
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Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 0

Total number of hits satisfying chosen parameters: 682300

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	5.0	20	2	US-08-651-692-1
2	15	4.7	18	3	US-08-679-645-1167
3	15	4.7	18	3	US-08-679-645-1169
4	15	4.7	24	2	US-08-863-639A-27
5	14	4.4	20	2	US-08-651-692-2
6	14	4.4	20	3	US-09-513-729B-15
7	14	4.4	20	4	US-09-198-452A-2554
8	13	4.1	15	1	US-08-182-968A-190
9	13	4.1	15	2	US-08-774-306A-190
10	13	4.1	15	3	US-09-064-156A-190
11	13	4.1	20	2	US-09-018-595B-7
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13	13	4.1	20	4	US-09-844-521-40
14	13	4.1	22	4	US-09-438-906-10
15	13	4.1	23	1	US-08-240-547-21
16	13	4.1	23	2	US-08-859-998-773
17	13	4.1	23	3	US-09-225-928-773
18	13	4.1	23	4	US-09-225-201B-773
19	13	4.1	24	1	US-08-240-547-14
20	13	4.1	29	4	US-09-344-529-18
21	13	4.1	30	4	US-09-747-391-276
22	12	3.8	12	2	US-08-863-639A-95
23	12	3.8	14	1	US-08-609-657-10
24	12	3.8	14	3	US-08-985-162-1759
25	12	3.8	14	4	US-09-401-063-1759
26	12	3.8	15	2	US-08-863-639A-21
27	12	3.8	15	3	US-08-618-834C-1

28	12	3.8	15	3	US-08-618-834C-7	Sequence 7, Appli
29	12	3.8	15	4	US-08-730-635-13	Sequence 13, Appli
30	12	3.8	16	3	US-08-954-210-11	Sequence 21, Appli
31	12	3.8	16	3	US-08-618-834C-5	Sequence 5, Appli
32	12	3.8	16	4	US-09-431-419A-11	Sequence 11, Appli
33	12	3.8	16	4	US-09-371-772B-5650	Sequence 5650, Ap
34	12	3.8	17	2	US-08-704-473-8	Sequence 8, Appli
35	12	3.8	17	3	US-08-909-742-3	Sequence 9, Appli
36	12	3.8	17	3	US-08-909-742-4	Sequence 4, Appli
37	12	3.8	17	3	US-08-954-210-71	Sequence 71, Appli
38	12	3.8	17	3	US-08-998-099-133	Sequence 133, Ap
39	12	3.8	17	3	US-08-998-099-134	Sequence 134, Ap
40	12	3.8	17	3	US-09-412-289-3	Sequence 3, Appli
41	12	3.8	17	3	US-09-431-419A-71	Sequence 4, Appli
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43	12	3.8	17	4	US-09-343-698-2	Sequence 2, Appli
44	12	3.8	17	4	US-09-371-772B-4397	Sequence 4397, Ap
45	12	3.8	17	4	US-08-325-955-1	Sequence 1, Appli
46	12	3.8	17	4	US-08-325-955-2	Sequence 2, Appli
47	12	3.8	17	4	US-08-866-108A-8273	Sequence 8273, Ap
48	12	3.8	17	4	US-09-866-108A-8274	Sequence 8274, Ap
49	12	3.8	17	4	US-09-866-108A-8275	Sequence 8275, Ap
50	12	3.8	17	4	US-09-866-108A-8276	Sequence 8276, Ap
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55	12	3.8	18	1	US-09-205-204-10	Sequence 10, Appli
56	12	3.8	18	2	US-09-205-204-10	Sequence 10, Appli
57	12	3.8	18	2	US-08-857-946-14	Sequence 14, Appli
58	12	3.8	18	2	US-09-161-244-63	Sequence 63, Appli
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66	12	3.8	18	3	US-09-063-733A-21	Sequence 21, Appli
67	12	3.8	18	4	US-09-679-298A-25	Sequence 25, Appli
68	12	3.8	18	4	US-09-077-940A-8	Sequence 8, Appli
69	12	3.8	18	4	US-09-500-700-68	Sequence 68, Appli
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71	12	3.8	20	1	US-08-715-142-16	Sequence 16, Appli
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79	12	3.8	20	3	US-09-490-692-145	Sequence 145, App
80	12	3.8	20	3	US-09-517-884A-13	Sequence 13, Appli
81	12	3.8	20	3	US-09-101-886B-60	Sequence 60, Appli
82	12	3.8	20	3	US-09-030-701-65	Sequence 65, Appli
83	12	3.8	20	3	US-09-467-082-12	Sequence 12, Appli
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98	12	3.8	20	3	US-09-467-082-27	Sequence 27, Appli
99	12	3.8	20	3	US-09-467-082-28	Sequence 28, Appli
100	12	3.8	20	3	US-09-467-082-29	Sequence 29, Appli

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C 103	12	3.8	21	2	US-08-863-6399-68	Sequence 68, Appl 1
C 104	12	3.8	21	2	US-08-863-6399-71	Sequence 71, Appl 1
C 105	12	3.8	21	2	US-08-863-6399-71	Sequence 71, Appl 1
C 106	12	3.8	21	3	US-09-099-053-18	Sequence 18, Appl 1
C 107	12	3.8	21	4	US-08-649-950-52	Sequence 52, Appl 1
C 108	12	3.8	21	4	US-09-475-9479-51	Sequence 51, Appl 1
C 109	12	3.8	21	4	US-09-359-411-8	Sequence 8, Appl 1
C 110	12	3.8	21	4	US-09-422-978-4383	Sequence 4383, Appl 1
C 111	12	3.8	21	4	US-09-422-978-8165	Sequence 8165, Appl 1
C 112	12	3.8	21	4	US-09-422-978-9566	Sequence 9566, Appl 1
C 113	12	3.8	21	4	US-09-322-624-13	Sequence 13, Appl 1
C 114	12	3.8	22	3	US-09-082-762-6	Sequence 6, Appl 1
C 115	12	3.8	22	4	US-08-192-943-8	Sequence 8, Appl 1
C 116	12	3.8	22	4	US-09-818-780-15	Sequence 15, Appl 1
C 117	12	3.8	23	4	US-09-177-650-11	Sequence 11, Appl 1
C 118	12	3.8	23	4	US-09-177-650-65	Sequence 65, Appl 1
C 119	12	3.8	24	2	US-08-570-155-16	Sequence 16, Appl 1
C 120	12	3.8	24	3	US-08-570-155-17	Sequence 17, Appl 1
C 121	12	3.8	24	3	US-08-707-743-8	Sequence 8, Appl 1
C 122	12	3.8	24	3	US-08-283-3009-23	Sequence 23, Appl 1
C 123	12	3.8	24	3	US-09-443-303-16	Sequence 16, Appl 1
C 124	12	3.8	24	4	US-09-318-138-42	Sequence 42, Appl 1
C 125	12	3.8	24	4	US-09-318-138-42	Sequence 42, Appl 1
C 126	12	3.8	24	4	US-09-315-152-6	Sequence 6, Appl 1
C 127	12	3.8	24	5	PCT-US95-09345-23	Sequence 23, Appl 1
C 128	12	3.8	25	1	US-08-174-144-3	Sequence 3, Appl 1
C 129	12	3.8	25	1	US-08-775-164-3	Sequence 3, Appl 1
C 130	12	3.8	25	2	US-08-775-609-3	Sequence 3, Appl 1
C 131	12	3.8	25	2	US-08-775-609-3	Sequence 3, Appl 1
C 132	12	3.8	25	2	US-08-860-174-14	Sequence 14, Appl 1
C 133	12	3.8	25	3	US-08-622-2779-17	Sequence 17, Appl 1
C 134	12	3.8	25	3	US-09-171-025-19	Sequence 19, Appl 1
C 135	12	3.8	25	4	US-09-742-693-1	Sequence 1, Appl 1
C 136	12	3.8	25	4	US-09-866-1089-13165	Sequence 13165, Appl 1
C 137	12	3.8	25	4	US-09-866-1089-13166	Sequence 13166, Appl 1
C 138	12	3.8	25	4	US-09-866-1089-13167	Sequence 13167, Appl 1
C 139	12	3.8	25	4	US-09-866-1089-13168	Sequence 13168, Appl 1
C 140	12	3.8	25	4	US-09-866-1089-13169	Sequence 13169, Appl 1
C 141	12	3.8	25	4	US-09-866-1089-13170	Sequence 13170, Appl 1
C 142	12	3.8	25	4	US-09-866-1089-13171	Sequence 13171, Appl 1
C 143	12	3.8	25	4	US-09-866-1089-13172	Sequence 13172, Appl 1
C 144	12	3.8	25	4	US-09-866-1089-13173	Sequence 13173, Appl 1
C 145	12	3.8	25	4	US-09-866-1089-13174	Sequence 13174, Appl 1
C 146	12	3.8	25	4	US-09-866-1089-13175	Sequence 13175, Appl 1
C 147	12	3.8	25	4	US-09-866-1089-13176	Sequence 13176, Appl 1
C 148	12	3.8	25	4	US-09-866-1089-13177	Sequence 13177, Appl 1
C 149	12	3.8	25	4	US-09-866-1089-13178	Sequence 13178, Appl 1
C 150	12	3.8	25	5	PCT-US93-06828-3	Sequence 3, Appl 1

ALIGNMENTS

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1      RESULT 1
2      US-08-651-692-1/c
3      ; Sequence 1, Application US/08651692
4      ; Patent No. 5856099
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: Loren Miraglia, Thomas Geisler,
9      ; APPLICANT: Clarence Frank Bennett and Nicholas M. Dean
10     ; TITLE OF INVENTION: Compositions and Methods for
11     ; TITLE OF INVENTION: Modulating Type I Interleukin-1 Receptor Expression
12     ; NUMBER OF SEQUENCES: 42
13     ; CORRESPONDENCE ADDRESS:
14     ; ADDRESSEE: Law Offices of Jane Massey Licata
15     ; STREET: 210 Lake Drive East, Suite 201
16     ; CITY: Cherry Hill
17     ; STATE: NJ
18     ; COUNTRY: USA
19     ;
20     ; ZIP: 08002
21     ;
22     ; COMPUTER READABLE FORM:

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1 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
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3 MEDIUM TYPE: IBM PS/2
4 COMPUTER: IBM PS/2
5 OPERATING SYSTEM: PC-DOS
6 SOFTWARE: WORDPERFECT 5.1
7
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/651,692
10 FILING DATE: Herewith
11 CLASSIFICATION: 536
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER:
14 FILING DATE:
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Jane Massey Licata
17 REGISTRATION NUMBER: 32,257
18 REFERENCE/DOCKET NUMBER: ISPH-0144
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: (609) 779-2400
21 TELEFAX: (609) 779-8488
22 INFORMATION FOR SEQ ID NO: 1:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 20
25 TYPE: Nucleic Acid
26 STRANDEDNESS: Single
27 TOPOLOGY: Linear
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29 ANTI-SENSE: Yes
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31 US-08-651-692-1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1167:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-1167

Query Match 4.7%; Score 15; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCAGC 53
DB 4 CGCGCGCGCGCAGC 18

RESULT 3
US-08-679-645-1169
Sequence 1169, Application US/08679645
Patent No. 6350934
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
APPLICANT: Edington, Brent E.
APPLICANT: McSwiggen, James A.
APPLICANT: Merlo, Patricia Ann Owens
APPLICANT: Guo, Lining
APPLICANT: Skokut, Thomas A.
APPLICANT: Young, Scott A.
APPLICANT: Folkerts, Otto
APPLICANT: Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fitch Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: storage
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: July 12, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1169:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-1169

Query Match 4.7%; Score 15; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCAGC 53
DB 1 CGCGCGCGCGCAGC 15

RESULT 4
US-08-663-639A-27
Sequence 27, Application US/08663639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matsen, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel wordperfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Muech
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-663-639A-27

Query Match 4.7%; Score 15; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCAGC 53
DB 3 CGCGCGCGCGCAGC 17

RESULT 5
US-08-651-692-2/c
; Sequence 2, Application US/08651692
; Patent No. 5856099
; GENERAL INFORMATION:
; APPLICANT: Loren Miraglia, Thomas Gelger,
; APPLICANT: Clarence Frank Bennett and Nicholas M. Dean
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Modulating Type I Interleukin-1 Receptor Expression
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; MEDIUM TYPE: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION NUMBER: US/08/651,692
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-651-692-2

Query Match 4.4%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCGCGCGAGCCCT 56
DB 14 GCGCGCGAGCCCT 1

RESULT 6
US-09-513-729B-15/c
; Sequence 15, Application US/09513729B
; Patent No. 6165791
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF B2F TRANSCRIPTION FACTOR 3 EXPRESSION
; FILE REFERENCE: RTS-0112
; CURRENT APPLICATION NUMBER: US/09/513,729B
; CURRENT FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-513-729B-15

Query Match 4.4%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GTCGCGCGCGCGC 50
DB 19 GTCGCGCGCGCGC 6

RESULT 7
US-09-198-452A-2554/c
; Sequence 2554, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2554
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-2554

Query Match 4.4%; Score 14; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 GGAGACGAGGTTGC 148
DB 17 GGAGACGAGGTTGC 4

RESULT 8
US-08-182-968A-190/c
; Sequence 190, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/277
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-182-968A-190

Query Match 4.1%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 129 TCGGGCGGAGACG 141
Db 15 TCGGGCGGAGACG 3

RESULT 9
US-08-774-306A-190/C
Sequence 190, Application US/08774306A
Patent No. 5869253
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,306A
FILING DATE: December 26, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-774-306A-190
Query Match 4.1%; Score 13; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 129 TCGGGCGGAGACG 141
Db 15 TCGGGCGGAGACG 3

RESULT 10
US-09-064-156A-190/C
Sequence 190, Application US/09064156A
Patent No. 6132966
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 498
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,156A
FILING DATE: April 21, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/774,306
FILING DATE: December 26, 1996
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-064-156A-190
Query Match 4.1%; Score 13; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 129 TCGGGCGGAGACG 141
Db 15 TCGGGCGGAGACG 3
RESULT 11
US-09-018-595B-7
Sequence 7, Application US/09018595B
Patent No. 5962233
GENERAL INFORMATION:
APPLICANT: Perkin-Elmer Corporation,
Applied Biosystems Division

TITLE OF INVENTION: DETERMINATION OF GENOTYPE OF
TITLE OF INVENTION: AMPLIFICATION PRODUCTS AT MULTIPLE ALLELIC SITES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David J. Weitz,
ADDRESSEE: Wilson Sonsini Goodrich & Rosati
STREET: 650 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1050
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Wordperfect for windows 6.0,
SOFTWARE: ASCII (DOS) TEXT format
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,595B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: David J. Weitz
REGISTRATION NUMBER: 38,362
REFERENCE/DOCKET NUMBER: PELM-744
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 493-9300
TELEFAX: (650) 493-6811
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-018-595B-7

Query Match 4.1%; Score 13; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 CGCAGCTCTCTCT 108
DB 7 CGCAGCTCTCTCT 19

RESULT 12
US-09-324-709A-7
Sequence 7, Application US/09324709A
Patent No. 6154707
GENERAL INFORMATION:
APPLICANT: Perkin-Elmer Corporation,
APPLICANT: Applied Biosystems Division
TITLE OF INVENTION: FLUORESCENCE GENOTYPING AT MULTIPLE ALLELIC
TITLE OF INVENTION: SITES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David J. Weitz,
ADDRESSEE: Wilson Sonsini Goodrich & Rosati
STREET: 650 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1050
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Wordperfect for windows 6.0,
SOFTWARE: ASCII (DOS) TEXT format
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/324,709A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: David J. Weitz
REGISTRATION NUMBER: 38,362
REFERENCE/DOCKET NUMBER: 16842-758
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 493-9300
TELEFAX: (650) 493-6811
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-324-709A-7

Query Match 4.1%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 CGCAGCTCTCTCT 108
DB 7 CGCAGCTCTCTCT 19

RESULT 13
US-09-844-521-40/C
Sequence 40, Application US/09844521
Patent No. 6492172
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Harris Busch
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF GU PROTEIN EXPRESSION
FILE REFERENCE: RTS-0163
CURRENT APPLICATION NUMBER: US/09/844,521
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 40
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense oligonucleotide
US-09-844-521-40

Query Match 4.1%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 TGGGATGTCATC 319
DB 16 TGGGATGTCATC 4

RESULT 14
US-09-438-906-10
Sequence 10, Application US/09438906
Patent No. 6465185
GENERAL INFORMATION:
APPLICANT: Goldfine, Ira
APPLICANT: Triachitta, Vincenzo
APPLICANT: Pizzuti, Antonio
APPLICANT: Vigneri, Riccardo
APPLICANT: Filicchia, Lucia
TITLE OF INVENTION: Polymorphic Human PC-1 Sequences
FILE REFERENCE: 9076-089
CURRENT APPLICATION NUMBER: US/09/438,906

;; CURRENT FILING DATE: 1999-11-18
;; PRIOR APPLICATION NUMBER: 60/108,853
;; PRIOR FILING DATE: 1998-11-18
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 10
;; LENGTH: 22
;; TYPE: DNA
;; ORGANISM: H. sapiens
US-09-438-906-10

Query Match 4.1%; Score 13; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 TGAAGATACGAG 243
Db 6 TGAAGATACGAG 18

RESULT 15
US-08-240-547-21
; Sequence 21, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Siab Ph.D., Scacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-240-547-21

Query Match 4.1%; Score 13; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 140 CGAGGTTCCGACC 152
Db 1 CGAGGTTCCGACC 13

RESULT 16
US-08-859-998-773
; Sequence 773, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jikhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-May-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 773:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-773

Query Match 4.1%; Score 13; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CGGCTCTCGGCTC 74
Db 7 CGGCTCTCGGCTC 19

RESULT 17
US-09-225-928-773
; Sequence 773, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jikhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park

```
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 773:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 773:
US-09-225-928-773

Query Match
Best Local Similarity 4.1%; Score 13; DB 3; Length 23;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CGGCTCCTCGCTC 74
DB 7 CGGCTCCTCGCTC 19

RESULT 18
US-09-225-201B-773
Sequence 773. Application US/09225201B
Patent No. 5489455
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,201B
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 773:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 773:
US-09-225-201B-773

Query Match
Best Local Similarity 4.1%; Score 13; DB 4; Length 23;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CGGCTCCTCGCTC 74
DB 7 CGGCTCCTCGCTC 19

RESULT 19
US-08-240-547-14/C
Sequence 14. Application US/08240547
Patent No. 5527669
GENERAL INFORMATION:
APPLICANT: Resnick, Robert M.
Young, Karen K.Y.
TITLE OF INVENTION: Primers for Detection of
Hepatitis C and No. 5527669el Variants
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: U.S.A.
ZIP: 07110-1139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,547
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/918,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sias Ph.D., Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-240-547-14
```

Query Match

Best Local Similarity 4.1%; Score 13; DB 1; Length 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 140 CGAGTTTCGACC 152
Db 24 CGAGTTTCGACC 12

RESULT 20

US-09-344-529-18/c
Sequence 18, Application US/09344529
Patent No. 6429293

GENERAL INFORMATION:

APPLICANT: Hew, Choy L.
APPLICANT: HSC Research and Development Limited Partnership
TITLE OF INVENTION: Sculptin-Type Antifreeze Polypeptides and Nucleic Acids
FILE REFERENCE: 016252-002620US
CURRENT APPLICATION NUMBER: US/09/344,529
CURRENT FILING DATE: 1999-06-24
EARLIER APPLICATION NUMBER: US 60/090,794
EARLIER FILING DATE: 1998-06-26
EARLIER APPLICATION NUMBER: US 60/095,713
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: upper strand
US-09-344-529-18

Query Match

Best Local Similarity 4.1%; Score 13; DB 4; Length 29;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 TCGCGCGCGCGC 50
Db 27 TCGCGCGCGCGC 15

RESULT 21

US-09-747-391-276
Sequence 276, Application US/09747391
Patent No. 6670124

GENERAL INFORMATION:

APPLICANT: Chow, Robert
APPLICANT: Tonai, Richard
APPLICANT: StemCye, Inc.
TITLE OF INVENTION: High Throughput Methods of HLA Typing
FILE REFERENCE: 020035-000210US
CURRENT APPLICATION NUMBER: US/09/747,391
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/172,768
PRIOR FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 278
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 276
LENGTH: 30
TYPE: DNA
ORGANISM: Homo sapiens
US-09-747-391-276

Query Match

Best Local Similarity 4.1%; Score 13; DB 4; Length 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 CGCAGCTCTCTCT 108
Db 17 CGCAGCTCTCTCT 29

RESULT 22

US-08-863-639A-95/c
Sequence 95, Application US/08863639A
Patent No. 5981185

GENERAL INFORMATION:

APPLICANT: Watson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESS: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Joseph E. Muech
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 795-6321
TELEFAX: (626) 795-4000

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-95

Query Match

Best Local Similarity 3.8%; Score 12; DB 2; Length 12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 CGCGCGCGCGCG 50
Db 12 CGCGCGCGCGCG 1

RESULT 23

US-08-609-657-10
Sequence 10, Application US/08609657
Patent No. 5681706

GENERAL INFORMATION:

APPLICANT: Anderson, Garth R.
APPLICANT: Estes, Scott D.
APPLICANT: Stoler, Daniel L.
TITLE OF INVENTION: Mammalian Anoxia-Responsive Regulatory
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One Met Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391

Query Match

Best Local Similarity 3.8%; Score 12; DB 2; Length 12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 CGCGCGCGCGCG 50
Db 12 CGCGCGCGCGCG 1

MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,657
FILING DATE: 01 March 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 10 :
SEQUENCE CHARACTERISTICS:
LENGTH: 14 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: No
US-08-609-657-10

Query Match 3.8%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 GCACGCTCTCTCT 108
Db 3 GCACGCTCTCTCT 14

RESULT 24
US-08-985-162-1759
Sequence 1759, Application US/08985162
Patent No. 6057156
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1759:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-985-162-1759

Query Match 3.8%; Score 12; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCG 50
Db 2 CGCGCGCGCGCG 13

RESULT 25
US-09-401-063-1759
Sequence 1759, Application US/09401063
Patent No. 6623962
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1759:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-401-063-1759

Query Match 3.8%; Score 12; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCG 50
Db 2 CGCGCGCGCGCG 13

RESULT 26

US-08-863-639A-21/c
Sequence 21, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coaslin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel Wordperfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Muech
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-21

Query Match 3.8%; Score 12; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCG 50
Db 13 CGCGCGCGCGCG 2

RESULT 27

US-08-618-834C-1
Sequence 1, Application US/08618834C
Patent No. 6361937
GENERAL INFORMATION:
APPLICANT: Stryer, Lubert
TITLE OF INVENTION: Computer-Aided Nucleic Acid
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rittler, Van Pelt & Yi LLP
STREET: 4906 El Camino Real, Suite 205
CITY: Los Altos
STATE: CA

COUNTRY: USA
ZIP: 94022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,834C
FILING DATE: 19-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Rittler, Michael J.

REGISTRATION NUMBER: 36,653
REFERENCE/DOCKET NUMBER: AFFYP002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-903-3500
TELEFAX: 650-903-3501

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-618-834C-1

Query Match 3.8%; Score 12; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 TTGTAGTGATG 209
Db 3 TTGTAGTGATG 14

RESULT 28

US-08-618-834C-7
Sequence 7, Application US/08618834C
Patent No. 6361937
GENERAL INFORMATION:
APPLICANT: Stryer, Lubert
TITLE OF INVENTION: Computer-Aided Nucleic Acid
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rittler, Van Pelt & Yi LLP
STREET: 4906 El Camino Real, Suite 205
CITY: Los Altos
STATE: CA
COUNTRY: USA
ZIP: 94022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,834C
FILING DATE: 19-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Rittler, Michael J.
REGISTRATION NUMBER: 36,653
REFERENCE/DOCKET NUMBER: AFFYP002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-903-3500
TELEFAX: 650-903-3501

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-618-834C-7

Query Match 3.8%; Score 12; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 TTGTAGTGATG 209
DB 2 TTGTAGTGATG 13

RESULT 29
US-08-730-635-13/C
Sequence 13, Application US/08730635
Patent No. 6514693
GENERAL INFORMATION:
APPLICANT: Lamsdorp, Peter
TITLE OF INVENTION: Method for Detecting Multiple Copies of
TITLE OF INVENTION: a Repeat Sequence in a Nucleic Acid Molecule
Patent No. 6514693
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWSON & HOWSON
STREET: 321 No. 65146931sttown Road
CITY: Spring House
STATE: PA.
COUNTRY: U.S.A.
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/730,635
FILING DATE: 11-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: B&P/USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
TELEX: N/A
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-730-635-13

Query Match 3.8%; Score 12; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCG 50
DB 13 CGCGCGCGCGCG 2

RESULT 30
US-08-954-210-11/C
Sequence 11, Application US/08954210
Patent No. 6043077

GENERAL INFORMATION:
APPLICANT: Barber, Jack R.
APPLICANT: Welch, Peter J.
APPLICANT: Tiltz, Richard
APPLICANT: Yel, Soonpin
APPLICANT: Yu, Mang
TITLE OF INVENTION: HEPATITIS C VIRUS RIBOZYMES
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,210
FILING DATE: 20-OCT-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480124.403C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-954-210-11

Query Match 3.8%; Score 12; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 GAGGTTCGACG 152
DB 16 GAGGTTCGACG 5

RESULT 31
US-08-618-834C-5
Sequence 5, Application US/08618834C
Patent No. 6361937
GENERAL INFORMATION:
APPLICANT: Stryer, Lubert
TITLE OF INVENTION: Computer-Aided Nucleic Acid
TITLE OF INVENTION: Sequencing
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ritter, Van Pelt & Yi LLP
STREET: 4906 El Camino Real, Suite 205
CITY: Los Altos
STATE: CA
COUNTRY: USA
ZIP: 94022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,834C
FILING DATE: 19-MAR-1996
CLASSIFICATION: 435

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritzer, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: AFFY002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-618-834C-5

Query Match          3.8%; Score 12; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      198 TTGTAGTGATG 209
DB      3 TTGTAGTGATG 14

RESULT 32
US-09-431-419A-11/c
; Sequence 11, Application US/09431419A
; Patent No. 6458567
; GENERAL INFORMATION:
; APPLICANT: Barber, Jack R.
; APPLICANT: Welch, Peter J.
; APPLICANT: Tritz, Richard
; APPLICANT: Yei, Soompin
; APPLICANT: Yu, Mang
; TITLE OF INVENTION: HEPATITIS C VIRUS RIBOZYMES
; FILE REFERENCE: 480124.403C3
; CURRENT APPLICATION NUMBER: US/09/431.419A
; CURRENT FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Hepatitis C Virus
;
US-09-431-419A-11

Query Match          3.8%; Score 12; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      141 GAGGTTCGACC 152
DB      16 GAGGTTCGACC 5

RESULT 33
US-09-371-772B-5650/c
; Sequence 5650, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00,876-J (237/198)
; TITLE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
```

```

; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 1425
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5650
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-09-371-772B-5650

Query Match          3.8%; Score 12; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38 TCGCCGCCCGG 49
DB      12 TCGCCGCCCGG 1

RESULT 34
US-08-704-473-8
; Sequence 8, Application US/08704473
; Patent No. 5830850
; GENERAL INFORMATION:
; APPLICANT: Geld, Bruce
; APPLICANT: Chapman, Harold
; APPLICANT: Desnick, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: THE TREATMENT OF BONE RESORPTIVE DISORDERS,
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,473
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-704-473-8

Query Match          3.8%; Score 12; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 AATCCGATGGA 15
DB      6 AATCCGATGGA 17
```

RESULT 35
US-08-909-742-3
Sequence 3, Application US/08909742
Patent No. 6007991
GENERAL INFORMATION:
APPLICANT: Vimala S. Sivaraman
APPLICANT: Hsien-Yu Wang
APPLICANT: Craig C. Malbon
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-
TITLE OF INVENTION: ACTIVATED PROTEIN KINASES AS THERAPY FOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: USA
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,742
FILING DATE: August 12, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/831,994
FILING DATE: April 1, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/827,520
FILING DATE: March 28, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Adams, Lindsay S.
REGISTRATION NUMBER: 36,425
REFERENCE/DOCKET NUMBER: 178-225 CIP II
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
HYPOTHEICAL: NO
ANTI-SENSE: YES
US-08-909-742-3
Query Match 3.8%; Score 12; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 39 CGCGCGCGCGCG 50
DB 3 CGCGCGCGCGCG 14

RESULT 36
US-08-909-742-4
Sequence 4, Application US/08909742
Patent No. 6007991
GENERAL INFORMATION:
APPLICANT: Vimala S. Sivaraman
APPLICANT: Hsien-Yu Wang
APPLICANT: Craig C. Malbon
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-
TITLE OF INVENTION: ACTIVATED PROTEIN KINASES AS THERAPY FOR

TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: USA
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,742
FILING DATE: August 12, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/831,994
FILING DATE: April 1, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/827,520
FILING DATE: March 28, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Adams, Lindsay S.
REGISTRATION NUMBER: 36,425
REFERENCE/DOCKET NUMBER: 178-225 CIP II
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: YES
US-08-909-742-4
Query Match 3.8%; Score 12; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 39 CGCGCGCGCGCG 50
DB 3 CGCGCGCGCGCG 14

RESULT 37
US-08-954-210-71/c
Sequence 71, Application US/08954210
Patent No. 6043077
GENERAL INFORMATION:
APPLICANT: Barber, Jack R.
APPLICANT: Welch, Peter J.
APPLICANT: Tiltz, Richard
APPLICANT: Yel, Soomin
APPLICANT: Yu, Mang
TITLE OF INVENTION: HEPATITIS C VIRUS RIBOZYMES
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible


```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/954,210
APPLICATION NUMBER: US/08/954,210
FILING DATE: 20-OCT-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480124.403C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-954-210-71
```

```
Query Match          3.8% Score 12; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      141 GAGGTGGGACC 152
Db      16 GAGGTGGGACC 5
```

```
RESULT 38
US-08-998-099-133
Sequence 133, Application US/08998099A
Patent No. 6103890
GENERAL INFORMATION:
APPLICANT: JARVIS, THALE
APPLICANT: MCSWIGEN, JAMES A.
APPLICANT: STINGCOMB, DAN T.
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
FILE REFERENCE: 231/175
CURRENT APPLICATION NUMBER: US/08/998,099A
CURRENT FILING DATE: 1997-12-24
EARLIER APPLICATION NUMBER: 60/037,658
EARLIER FILING DATE: 1997-01-23
EARLIER APPLICATION NUMBER: 08/373,124
EARLIER FILING DATE: 1995-01-13
EARLIER APPLICATION NUMBER: 08/245,466
EARLIER FILING DATE: 1994-05-18
NUMBER OF SEQ ID NOS: 375
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 133
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-08-998-099-133
```

```
Query Match          3.8% Score 12; DB 3; Length 17;
Best Local Similarity 75.0%; Pred. No. 9.9e+03;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      155 TCCTTCCCGCAGC 166
Db      5 UCCUCCCCCAGC 16
```

```
RESULT 39
US-08-998-099-134
Sequence 134, Application US/08998099A
Patent No. 6103890
GENERAL INFORMATION:
APPLICANT: JARVIS, THALE
APPLICANT: MCSWIGEN, JAMES A.
```

```
APPLICANT: STINGCOMB, DAN T.
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
FILE REFERENCE: 231/175
CURRENT APPLICATION NUMBER: US/08/998,099A
CURRENT FILING DATE: 1997-12-24
EARLIER APPLICATION NUMBER: 60/037,658
EARLIER FILING DATE: 1997-01-23
EARLIER APPLICATION NUMBER: 08/373,124
EARLIER FILING DATE: 1995-01-13
EARLIER APPLICATION NUMBER: 08/245,466
EARLIER FILING DATE: 1994-05-18
NUMBER OF SEQ ID NOS: 375
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 134
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-08-998-099-134
```

```
Query Match          3.8% Score 12; DB 3; Length 17;
Best Local Similarity 75.0%; Pred. No. 9.9e+03;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      155 TCCTTCCCGCAGC 166
Db      4 UCCUCCCCCAGC 15
```

```
RESULT 40
US-09-412-289-3
Sequence 3, Application US/09412289
Patent No. 6271210
GENERAL INFORMATION:
APPLICANT: Sivaraman, Vimala S.
APPLICANT: Wang, Hsien-Yu.
APPLICANT: Malbon, Craig C.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-ACTIVATED
FILE REFERENCE: Seq. 1-4 (178-225 CIP II/CON)
CURRENT APPLICATION NUMBER: US/09/412,289
CURRENT FILING DATE: 1999-10-05
EARLIER APPLICATION NUMBER: 08/909,742
EARLIER FILING DATE: 1997-08-12
EARLIER APPLICATION NUMBER: 08/831,994
EARLIER FILING DATE: 1997-04-01
EARLIER APPLICATION NUMBER: 08/827,520
EARLIER FILING DATE: 1997-03-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 17
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthesized
US-09-412-289-3
```

```
Query Match          3.8% Score 12; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      39 CGCGCGCGCGCGC 50
Db      3 CGCGCGCGCGCGC 14
```

```
RESULT 41
US-09-412-289-4
Sequence 4, Application US/09412289
Patent No. 6271210
GENERAL INFORMATION:
```

APPLICANT: Sivaraman, Vimala S.
APPLICANT: Wang, Haien-Yu
APPLICANT: Malbon, Craig C.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-ACTIVATED
FILE OF INVENTION: PROTEIN KINASES AS THERAPY FOR CANCER
FILE REFERENCE: Seq. 1-4 (178-225 CIP II/CON)
CURRENT APPLICATION NUMBER: US/09/412,289
CURRENT FILING DATE: 1999-10-05
EARLIER APPLICATION NUMBER: 08/909,742
EARLIER FILING DATE: 1997-08-12
EARLIER APPLICATION NUMBER: 08/831,994
EARLIER FILING DATE: 1997-04-01
EARLIER APPLICATION NUMBER: 08/827,520
EARLIER FILING DATE: 1997-03-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthesized
US-09-412-289-4

Query Match 3.8%; Score 12; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCCGCCGCCGC 50
Db 3 CGCCGCCGCCGC 14

RESULT 42
US-09-431-419A-71/c
Sequence 71, Application US/09431419A
Patent No. 6458567
GENERAL INFORMATION:
APPLICANT: Barber, Jack R.
APPLICANT: Welch, Peter J.
APPLICANT: Tritz, Richard
APPLICANT: Yel, Soompin
APPLICANT: Yu, Mang
TITLE OF INVENTION: HEPATITIS C VIRUS RIBOZYMES
FILE REFERENCE: 480124.403C3
CURRENT APPLICATION NUMBER: US/09/431,419A
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 71
LENGTH: 17
TYPE: RNA
ORGANISM: Hepatitis C Virus
US-09-431-419A-71

Query Match 3.8%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 GAGGTTCGACG 152
Db 16 GAGGTTCGACG 5

RESULT 43
US-09-343-698-1/c
Sequence 1, Application US/09343698
Patent No. 6475486
GENERAL INFORMATION:
APPLICANT: Seeman, Gerhard
Boslet, Klaus
Czech, Joerg

Kolar, Cenek
Hoffman, Dieter
Sedlacek, Hans-Harald
TITLE OF INVENTION: Glycosyl-Etoposide Prodrugs, A Process For
Preparation Thereof And The Use Thereof In Combination With
Functionalized Tumor-Specific Enzyme Conjugates
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/343,698
FILING DATE: 30-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/325,955
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ogden, Scasia L.
REGISTRATION NUMBER: 36,228
REFERENCE/DOCKET NUMBER: 05552.0981-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-343-698-1

Query Match 3.8%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCCGCCGCCGC 50
Db 12 CGCCGCCGCCGC 1

RESULT 44
US-09-343-698-2
Sequence 2, Application US/09343698
Patent No. 6475486
GENERAL INFORMATION:
APPLICANT: Seeman, Gerhard
Boslet, Klaus
Czech, Joerg
Kolar, Cenek
Hoffman, Dieter
Sedlacek, Hans-Harald
TITLE OF INVENTION: Glycosyl-Etoposide Prodrugs, A Process For
Preparation Thereof And The Use Thereof In Combination With
Functionalized Tumor-Specific Enzyme Conjugates
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/343,698
FILING DATE: 30-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/325,955
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,228
REFERENCE/DOCKET NUMBER: 05552,0981-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-343-698-2

Query Match 3.8%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 39 CGCGCGCGCGC 50
Db 2 CGCGCGCGCGC 13

RESULT 45
US-09-371-772B-4397
Sequence 4397, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Becobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 4397
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-4397

Query Match 3.8%; Score 12; DB 4; Length 17;
Best Local Similarity 83.3%; Pred. No. 9.9e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 119 GAGTGACATC 130

Db 1 GAGTGACATC 12

RESULT 46
US-08-325-955-1/c
Sequence 1, Application US/08325955
Patent No. 6610299
GENERAL INFORMATION:
APPLICANT: Seeman, Gerhard
APPLICANT: Bosalec, Klaus
APPLICANT: Czech, Joerg
APPLICANT: Kolar, Cenek
APPLICANT: Hoffman, Dieter
APPLICANT: Sedlacek, Hans-Harald
TITLE OF INVENTION: Glycosyl-Etoposide Prodrugs, A Process for
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,955
FILING DATE: 19-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,228
REFERENCE/DOCKET NUMBER: 05552,0981-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-325-955-1

Query Match 3.8%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 39 CGCGCGCGCGC 50
Db 12 CGCGCGCGCGC 1

RESULT 47
US-08-325-955-2
Sequence 2, Application US/08325955
Patent No. 6610299
GENERAL INFORMATION:
APPLICANT: Seeman, Gerhard
APPLICANT: Bosalec, Klaus
APPLICANT: Czech, Joerg
APPLICANT: Kolar, Cenek
APPLICANT: Hoffman, Dieter
APPLICANT: Sedlacek, Hans-Harald
TITLE OF INVENTION: Glycosyl-Etoposide Prodrugs, A Process for
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fimnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,955
FILING DATE: 19-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,228
REFERENCE/DOCKET NUMBER: 05552.0981-04000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-325-955-2

Query Match 3.8%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 39 CGCGCGCGCGCGC 50
DB 2 CGCGCGCGCGCGC 13

RESULT 48
US-09-866-108A-8273/C
Sequence 8273, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 8273
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-8273

Query Match 3.8%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 GTCTCTGTGAGG 112
DB 17 GTCTCTGTGAGG 6

RESULT 49
US-09-866-108A-8274/C
Sequence 8274, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 8274
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-8274

Query Match 3.8%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 GTCTCTCTGAGG 112
Db 16 GTCTCTCTGAGG 5

RESULT 50

US-09-866-108A-8275/C
Sequence 8275, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wenheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 8275
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-8275

Query Match 3.8%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 GTCTCTCTGAGG 112
Db 15 GTCTCTCTGAGG 4

RESULT 51

US-09-866-108A-8276/C
Sequence 8276, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wenheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 8276
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-8276

Query Match 3.8%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 GTCTCTCTGAGG 112
Db 14 GTCTCTCTGAGG 3

RESULT 52

US-09-866-108A-8277/C
Sequence 8277, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wenheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeonica Sequence Listing Engine
SEQ ID NO 8277
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-8277

Query Match 3.8%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GTCTCTCTGAGG 112
Db 13 GTCTCTCTGAGG 2

RESULT 53
US-09-866-108A-8278/c
Sequence 8278, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AROMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeonica Sequence Listing Engine
SEQ ID NO 8278
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-8278

Query Match 3.8%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GTCTCTCTGAGG 112
Db 12 GTCTCTCTGAGG 1

RESULT 54
US-08-802-547-9/c
Sequence 9, Application US/08802547
Patent No. 5780611
GENERAL INFORMATION:
APPLICANT: Guntaka, Ramareddy V.
APPLICANT: Weber, Karl T.
APPLICANT: Kovacs, Attila
APPLICANT: Kandala, Jagannadachari
TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT EXPRESSION OF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,547
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 24129-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816-474-9050
TELEFAX: 816-474-9057
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
POSITION IN GENOME:
UNITS: Dp
US-08-802-547-9

Query Match 3.8%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 CTTTCCTTCCC 162
Db 17 CTTTCCTTCCC 6

RESULT 55
US-08-712-357-9/c
Sequence 9, Application US/08712357
Patent No. 5808037
GENERAL INFORMATION:
APPLICANT: Guntaka, Ramareddy V.
APPLICANT: Weber, Karl T.
APPLICANT: Kovacs, Attila
APPLICANT: Kandala, Jagannadachari
TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT

TITLE OF INVENTION: EXPRESSION OF COLLAGEN GENES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/712,357
APPLICATION NUMBER: US/08/712,357
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
POSITION IN GENOME:
UNITS: bp
US-08-712-357-9

Query Match 3.8%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 CCTTCCCTCCC 162
Db 17 CCTTCCCTCCC 6

RESULT 56
US-09-205-204-40/c
Sequence 40, Application US/09205204
Patent No. 5958772
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1 EXPRESSION
FILE REFERENCE: RTS-0020
CURRENT APPLICATION NUMBER: US/09/205,204
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 40
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-204-40

Query Match 3.8%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 AACAGCTGAAG 274
Db 17 AACAGCTGAAG 6

Db 17 AACAGCTGAAG 6

RESULT 57
US-09-205-860-10
Sequence 10, Application US/09205860
Patent No. 5981732
GENERAL INFORMATION:
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
FILE REFERENCE: RTS-0031
CURRENT APPLICATION NUMBER: US/09/205,860
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 10
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-860-10

Query Match 3.8%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCCGCCGCCGC 50
Db 3 CGCCGCCGCCGC 14

RESULT 58
US-08-857-946-14/c
Sequence 14, Application US/08857946
Patent No. 5994075
GENERAL INFORMATION:
APPLICANT: Goodfellow, P.N.
TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN A
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wilcoff, Inc.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,946
FILING DATE: 16-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US/60/017,824
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kathleen M. Williams
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3529/05573
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid

US-08-857-946-14

Query Match 3.8%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCG 50
DB 15 CGCGCGCGCGCG 4

RESULT 59
US-09-161-244-63/C
; Sequence 63, Application US/09161244
; Patent No. 6004814
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD71 EXPRESSION
; FILE REFERENCE: RTS-0007
; CURRENT APPLICATION NUMBER: US/09/161,244
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 63
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-161-244-63

Query Match 3.8%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 268 GCTGAGGTGT 279
DB 14 GCTGAGGTGT 3

RESULT 60
US-09-205-921-9/C
; Sequence 9, Application US/09205921A
; Patent No. 6008048
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: ex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF EGR-1 EXPRESSION
; FILE REFERENCE: RTS-0028
; CURRENT APPLICATION NUMBER: US/09/205,921A
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-921-9

Query Match 3.8%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CGCGCGCGCGAG 52
DB 13 CGCGCGCGCGAG 2

RESULT 61
US-08-970-740-14/C
; Sequence 14, Application US/08970740
; Patent No. 6015670

GENERAL INFORMATION:
; APPLICANT: Goodfellow, P.N.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN A
; TITLE OF INVENTION: GENE OF INTEREST
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Witcoff, Inc.
; STREET: 28 State Street, 28th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,740
; FILING DATE: 14-NOV-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/857,946
; FILING DATE: 16-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,824
; FILING DATE: 17-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kathleen M. Williams
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3529/59829
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-227-7111
; TELEFAX: 617-227-4399
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-970-740-14

Query Match 3.8%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCG 50
DB 15 CGCGCGCGCGCG 4

RESULT 62
US-09-143-212-44/C
; Sequence 44, Application US/09143212B
; Patent No. 6077672
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia and Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAD EXPRESSION
; FILE REFERENCE: RTS-0005
; CURRENT APPLICATION NUMBER: US/09/143,212B
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-143-212-44

Query Match 3.8%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 CGCGCGCGCGC 50
Db 12 CGCGCGCGCGC 1

RESULT 63

US-09-143-212-45/C
; Sequence 45, Application US/09143212B
; Patent No. 6077672
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia and Lex M. Cowseart
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRADD EXPRESSION
; FILE REFERENCE: RTS-0005
; CURRENT APPLICATION NUMBER: US/09/143,212B
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-143-212-45

Query Match 3.8%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 CGCGCGCGCGC 50
Db 16 CGCGCGCGCGC 5

RESULT 64
US-09-496-694B-176
; Sequence 176, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swazey
; APPLICANT: Lex M. Cowseart
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 176
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-496-694B-176

Query Match 3.8%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 GGAGGAGGCGA 93
Db 3 GGAGGAGGCGCA 14

RESULT 65
US-08-679-645-1163
; Sequence 1163, Application US/08679645
; Patent No. 6350934

GENERAL INFORMATION:

APPLICANT: Zwick, Michael G.
APPLICANT: Edington, Brent E.
APPLICANT: McSwiggen, James A.
APPLICANT: Merlo, Patricia Ann Owens
APPLICANT: Guo, Lining
APPLICANT: Skokut, Thomas A.
APPLICANT: Young, Scott A.
APPLICANT: Folkerts, Otto
APPLICANT: Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/679,645
FILING DATE: July 12, 1996
CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1500
TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 1163:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-1163

Query Match 3.8%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 CGCGCGCGCGC 50
Db 7 CGCGCGCGCGC 18

RESULT 66

US-08-679-645-1165
; Sequence 1165, Application US/08679645
; Patent No. 6350934

GENERAL INFORMATION:

APPLICANT: Zwick, Michael G.
APPLICANT: Edington, Brent E.
APPLICANT: McSwiggen, James A.
APPLICANT: Merlo, Patricia Ann Owens
APPLICANT: Guo, Lining
APPLICANT: Skokut, Thomas A.

APPLICANT: Young, Scott A.
APPLICANT: Folkerts, Otto
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: July 12, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,337
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1165:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-1165
Query Match
Best Local Similarity 3.8%; Score 12; DB 3; Length 18;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 39 CGCGCGCGCGCG 50
DB 4 CGCGCGCGCGCG 15

RESULT 67
US-09-063-733A-21
Sequence 21, Application US/09063733A
Patent No. 6372211
GENERAL INFORMATION:
APPLICANT: Isaac, Barbara G.
APPLICANT: Greenplate, John T.
APPLICANT: Purcell, John P.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: INSECTS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: PO Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA

ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/063,733A
FILING DATE: 21-APR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-787-1440
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-063-733A-21
Query Match
Best Local Similarity 3.8%; Score 12; DB 3; Length 18;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 306 CTGGGATGTCA 317
DB 5 CTGGGATGTCA 16

RESULT 68
US-09-679-298A-25
Sequence 25, Application US/09679298A
Patent No. 6566131
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD6 EXPRESSION
FILE REFERENCE: RTS-0045
CURRENT APPLICATION NUMBER: US/09/679,298A
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 25
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-679-298A-25
Query Match
Best Local Similarity 3.8%; Score 12; DB 4; Length 18;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 39 CGCGCGCGCGCG 50
DB 5 CGCGCGCGCGCG 16

RESULT 69
US-09-077-940A-8/c
Sequence 8, Application US/09077940A
Patent No. 6576441
GENERAL INFORMATION:
APPLICANT: KIMURA, Toru et al.
TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
FILE REFERENCE: 0020-4426P
CURRENT APPLICATION NUMBER: US/09/077,940A
CURRENT FILING DATE: 1998-06-05

NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derived from Homo sapiens
US-09-077-940A-8

Query Match 3.8%; Score 12; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 GACGCTCTCTGC 71
|||
Db 17 GACGCTCTCTGC 6

RESULT 70
US-09-500-700-68/c
Sequence 68, Application US/09500700
Patent No. 6790941
GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
APPLICANT: BARBAS III, Carlos F.
APPLICANT: GOTTESFELD, Joel M.
APPLICANT: WRIGHT, Peter E.
TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
FILE REFERENCE: SCRIPT160-4
CURRENT APPLICATION NUMBER: US/09/500,700
PRIORITY FILING DATE: 2003-01-10
PRIORITY FILING DATE: 1997-05-27
PRIORITY FILING DATE: 1997-05-27
PRIORITY FILING DATE: 1996-12-30
PRIORITY FILING DATE: 1996-12-30
PRIORITY FILING DATE: 1995-01-18
PRIORITY FILING DATE: 1994-09-28
PRIORITY FILING DATE: 1994-09-28
PRIORITY FILING DATE: 1994-01-18
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: (GCG) 6 probe
US-09-500-700-68

Query Match 3.8%; Score 12; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 CGCCGCGCGCGC 50
|||
Db 18 CGCCGCGCGCGC 7

RESULT 71
US-08-299-187-6
Sequence 6, Application US/08299187
Patent No. 5736325
GENERAL INFORMATION:
APPLICANT: Manowitz, Paul
APPLICANT: Poretz, Ronald D.
APPLICANT: Park, David
APPLICANT: Ricketts, Michael H.
TITLE OF INVENTION: MARKER FOR INDIVIDUALS SUSCEPTIBLE TO
TITLE OF INVENTION: ALCOHOLISM
NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,187
FILING DATE: 31-AUG-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Gieselmann, Volkmar
AUTHORS: Polten, Andreas
AUTHORS: Kreyling, Joachim
AUTHORS: von Figura, Kurt
TITLE: Arylsulfatase A pseudodeficiency: Loss of a
TITLE: polyadenylation signal and N-glycosylation site
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 86
PAGES: 9436-9440
DATE: December-1989
US-08-299-187-6

Query Match 3.8%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 AGGTGACACTGG 233
|||
Db 2 AGGTGACACTGG 13

RESULT 72
US-08-715-142-16/c
Sequence 16, Application US/08715142
Patent No. 5811244
GENERAL INFORMATION:
APPLICANT: Frankel, Wayne N.
APPLICANT: Cox, Gregory A.
APPLICANT: Lutz, Cathleen M.
APPLICANT: No 5811244bels, Jeffrey L.
TITLE OF INVENTION: CLINICAL DISORDERS ASSOCIATED WITH NHE1
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor

STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,142
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: JL-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-715-142-16

Query Match 3.8%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 CACCAGTGAAC 255
DB 15 CACCAGTGAAC 4

RESULT 73
US-08-465-485A-28/C
Sequence 28, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
FEATURE:
NAME/KEY: Modified base
LOCATION: 18..19
OTHER INFORMATION: Last two internucleoside linkages are
OTHER INFORMATION: phosphorothioates
US-08-465-485A-28

Query Match 3.8%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCGCGCGCGCG 50
DB 13 CGCGCGCGCGCG 2

RESULT 74
US-08-910-443-6
Sequence 6, Application US/08910443
Patent No. 5935790
GENERAL INFORMATION:
APPLICANT: Foretz, Ronald D.
TITLE OF INVENTION: METHOD FOR DETECTING A PREDISPOSITION TO
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,443
FILING DATE: 05-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Bsq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-056 R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: /desc = "PRIMER"
HYPOTHETICAL: NO

US-08-910-443-6

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Best Local Similarity 100.0%; Pred. No. 9.9e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 AGTGACACTGG 233

Db 2 AGTGACACTGG 13

RESULT 75

US-09-358-382-11

; Sequence 11, Application US/09358382

; Patent No. 6010806

; GENERAL INFORMATION:

; APPLICANT: Donna T. Ward

; APPLICANT: Lex M. Cowart

; TITLE OF INVENTION: ANTISENSE MODULATION OF JUN N-TERMINAL KINASE KINASE-1 EXPRESSION

; FILE REFERENCE: RPS-0071

; CURRENT APPLICATION NUMBER: US/09/358,382

; CURRENT FILING DATE: 1999-07-21

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 11

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-358-382-11

Query Match 3.8%; Score 12; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.9e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CGCCGCCGCCGC 50

Db 5 CGCCGCCGCCGC 16

Search completed: February 2, 2005, 23:37:48
Job time : 33.5987 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:07:30 : Search time 405.351 Seconds
(without alignments)
11866.381 Million cell updates/sec

Title: US-10-048-046-1_COPY_997_1128

Perfect score: 132
Sequence: 1 acatgcctcctgcgcagga.....ctactgcgcgtctcccgctg 132

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 46458

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hnc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_g861: *
9: gb_g862: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	12	9.1	27	8	AZ833326 2M0115P15
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7	11	8.3	28	8	AZ427495 1M0209A06
8	11	8.3	28	9	TAJ16B05P
9	11	8.3	29	8	AZ755923 1M0553110
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13	11	8.3	30	8	AZ610580 1M0435N21
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17	10	7.6	20	1	AJ666323 2M0093118
18	10	7.6	20	8	AZ780308 2M0017T05
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20	10	7.6	21	8	AZ421118 1M0199D16
21	10	7.6	22	1	A1035419 ub46d05.r
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C 30	10	7.6	28	1	AA636083	AA636083 nt15b06.s
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C 33	10	7.6	28	6	CF328209	CF328209 NACL--03-
C 34	10	7.6	29	9	AJ588718	AJ588718 Arabidops
C 35	10	7.6	30	2	BE385582	BE385582 601275867
C 36	10	7.6	30	8	AZ451748	AZ451748 1M0251A18
C 37	10	7.6	30	8	AZ797441	AZ797441 2M0053K07
C 38	10	7.6	30	8	AZ844017	AZ844017 2M0143001
C 39	9	6.8	9	1	CL670968	CL670968 PRI0163C-
C 40	9	6.8	11	1	AJ655553	AJ655553 AJ655553-
C 41	9	6.8	11	6	BH213431	BH213431 SALX_0092
C 42	9	6.8	16	6	CF323664	CF323664 HDN--04-H
C 43	9	6.8	19	8	AZ458806	AZ458806 1M0263012
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C 45	9	6.8	19	8	AZ794641	AZ794641 2M0048E05
C 46	9	6.8	19	8	AZ951149	AZ951149 2M0280D22
C 47	9	6.8	19	9	AJ589265	AJ589265 Arabidops
C 48	9	6.8	20	8	AZ493004	AZ493004 1M0327N06
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C 50	9	6.8	20	8	AZ817897	AZ817897 2M0087D09
C 51	9	6.8	20	1	AJ6189452	AJ6189452 Pan. trogl
C 52	9	6.8	21	9	AJ668099	AJ668099 AJ668099
C 53	9	6.8	21	8	AZ232807	AZ232807 1M0045N21
C 54	9	6.8	21	8	AZ598709	AZ598709 1M0413T08
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C 56	9	6.8	21	8	AZ796134	AZ796134 2M0051A10
C 57	9	6.8	21	8	AZ828488	AZ828488 2M0105C05
C 58	9	6.8	21	8	AZ833982	AZ833982 2M0116K23
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C 60	9	6.8	22	1	A1738818	A1738818 w139b04.x
C 61	9	6.8	22	1	AJ795973	AJ795973 AJ795973
C 62	9	6.8	22	8	AZ307716	AZ307716 1M0009N02
C 63	9	6.8	22	8	AZ416988	AZ416988 1M0192P23
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C 66	9	6.8	22	8	AZ788996	AZ788996 2M0036D22
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C 70	9	6.8	23	5	BX558114	BX558114 BX558114
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C 73	9	6.8	23	9	TAI30G06P	TAI30G06P T. brucei
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C 81	9	6.8	24	8	AZ436243	AZ436243 1M0233I20
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C 83	9	6.8	24	9	TAI20F02P	TAI20F02P T. brucei
C 84	9	6.8	25	1	TAI96B0CQ	TAI96B0CQ T. brucei
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C 86	9	6.8	25	8	AZ303786	AZ303786 1M0003G03
C 87	9	6.8	25	8	AZ498814	AZ498814 1M0336H14
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C 89	9	6.8	25	8	AZ759839	AZ759839 1M0553B02
C 90	9	6.8	25	8	AZ760021	AZ760021 1M0553P20
C 91	9	6.8	25	8	AZ776661	AZ776661 2M0010C05
C 92	9	6.8	25	8	AZ804762	AZ804762 2M0065N12
C 93	9	6.8	25	8	BH740827	BH740827 KG04506-5
C 94	9	6.8	25	8	CC060376	CC060376 EY05060-3
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C 97	9	6.8	26	1	AJ649570	AJ649570 AJ649570

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106 9 6.8 26 9 TAI68F11Q TAI68F11Q
C 107 9 6.8 26 9 CG722656 CG722656
C 108 9 6.8 26 9 AG195681 AG195681
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C 124 9 6.8 28 1 AA074506 AA074506
C 125 9 6.8 28 1 AI444428 AI444428
C 126 9 6.8 28 1 AI497442 AI497442
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C 128 9 6.8 28 1 AI785472 AI785472
129 9 6.8 28 1 AI876227 AI876227
130 9 6.8 28 1 AJ668095 AJ668095
C 131 9 6.8 28 6 BM401310 BM401310
C 132 9 6.8 28 6 CD531803 CD531803
133 9 6.8 28 7 R54679 R54679
C 134 9 6.8 28 7 W92724 W92724
C 135 9 6.8 28 8 AZ207173 AZ207173
C 136 9 6.8 28 8 AZ421028 AZ421028
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C 138 9 6.8 28 8 AZ579398 AZ579398
C 139 9 6.8 28 8 AZ618065 AZ618065
140 9 6.8 28 8 AZ836785 AZ836785
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C 143 9 6.8 28 9 TAI250H05P TAI250H05P
C 144 9 6.8 28 9 CG709153 CG709153
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C 146 9 6.8 28 9 CG733943 CG733943
C 147 9 6.8 29 1 AJ799115 AJ799115
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149 9 6.8 29 8 AZ310073 AZ310073
C 150 9 6.8 29 8 AZ391391 AZ391391

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ALIGNMENTS

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RESULT 1
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DEFINITION 20 bp DNA linear GSS 13-DEC-2000
ACCESSION AJ603262
VERSION 1
KEYWORDS 10kb plasmid UUGCM library Mus musculus genomic
SOURCE clone UUGCM0422P24 F, genomic survey sequence.
ORGANISM Mus musculus (house mouse)
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

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TITLE Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niedermaier, A. and Wright, D., Weiss, R.
JOURNAL Plasmid inserts
COMMENT Published (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0422 Row: P Column: 24
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCM library"
/note="Vector: PWD42HV; Purified genomic DNA from M.
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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ORIGIN

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Query Match 9.1%; Score 12; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 CCCTGTGTCCTA 115
Db 4 CCCTGTGTCCTA 15

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RESULT 2
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ACCESSION AZ833326
VERSION 1
KEYWORDS 10kb plasmid UUGCM library Mus musculus genomic
SOURCE clone UUGCM0115P15 F, genomic survey sequence.
ORGANISM Mus musculus (house mouse)
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

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TITLE
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

COMMENT
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0115 row: P column: 15
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
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Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U062M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 9.1%; Score 12; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION CF298174 25 bp mRNA linear EST 15-AUG-2003
758bp -01-H06.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (Japonica cultivar-group) cDNA clone 7LEAF--01-H06, mRNA
sequence.
ACCESSION CF298174
VERSION CF298174.1 GI:3366935
KEYWORDS EST.
ORGANISM Oryza sativa (Japonica cultivar-group)
SOURCE Oryza sativa (Japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 25)

AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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Location/Qualifiers

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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 CCTGCATGCAC 60
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Db 20 CCTGCATGCAC 10

RESULT 4

LOCUS A0651227 27 bp mRNA linear EST 28-JUN-2004
DEFINITION A0651227 CSEGRAN19 Sus scrofa cDNA clone C003277_L02, mRNA
sequence.
ACCESSION A0651227
VERSION A0651227.1 GI:49333672
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE
1 (bases 1 to 27)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
CONTACT Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector: pBluescript11(KS) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13P Normalised library constructed from pooled ovaries. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.ark-genomics.org.
Location/Qualifiers

FEATURES
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ORIGIN

Not: Single pass sequencing; Normalised library
constructed from pooled ovaries"

Query Match 8.3%; Score 11; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 7.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 TTCTGCGCGGC 74
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Db 26 TTCTGCGCGGC 16

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LOCUS 1M0003A09F Mouse 10kb plasmid UGCM library Mus musculus genomic

DEFINITION clone UGCM003A09 F, genomic survey sequence.

ACCESSION AZ303426
VERSION AZ303426.1 GI:10338804
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: A column: 09
Seq primer: CGTGTAAACGACGCCACG
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers

FEATURES
source 1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM003A09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G114732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

ORIGIN

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 8.3%; Score 11; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 7.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 TGTCTACTCTG 119
|||||
Db 3 TGTCTACTCTG 13

RESULT 6
AZ868893 27 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0180117R Mouse 10kb plasmid UGCM library Mus musculus genomic

DEFINITION clone UGCM0180117 R, genomic survey sequence.

ACCESSION AZ868893
VERSION AZ868893.1 GI:13072662
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0180 row: I column: 17
Seq primer: CACACAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers

FEATURES
source 1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0180117"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G114732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

ORIGIN

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 8.3%; Score 11; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 7.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 CTGTCTCTCTAC 116
|||||
DB 7 CTGTCTCTCTAC 17

RESULT 7

AZ427495 28 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0209A06R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0209A06 R, genomic survey sequence.

ACCESSION AZ427495
VERSION AZ427495.1 GI:10551508
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiser, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0209 row: A column: 06
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers

FEATURES
source

1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0209A06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: pMD29v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD29 (g14732114[g14732114]Af129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into

ORIGIN

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 8.3%; Score 11; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 AGTTTGACGCC 50
|||||
DB 8 AGTTTGACGCC 18

RESULT 8

TA316B05P/c 28 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 316b05, forward sequence,
genomic survey sequence.

ACCESSION AL491155
VERSION AL491155.1 GI:11866878
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei

REFERENCE 1 (bases 1 to 28)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

FEATURES
source

1..28
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="316b05"
Location/Qualifiers
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

ORIGIN

Query Match 8.3%; Score 11; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 CATTGACACG 64
|||||
DB 25 CATTGACACG 15

RESULT 9

AZ759923/c 29 bp DNA linear GSS 16-FEB-2001
LOCUS 1M055311F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M055311 F, genomic survey sequence.

ACCESSION AZ759923
VERSION AZ759923.1 GI:12867209
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)

REFERENCE 1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R. Niederahausen, A. and Wright, D., Weis, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss

COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0553 row: 1 column: 10
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES
 source location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UTGCM0553110"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 8.3%; Score 11; DB 8; Length 29;
 Best Local Similarity 100.0%; Pred. No. 7.7e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 GTTGCAGCCC 51
 |||||
 Db 26 GTTGCAGCCC 16

RESULT 10
 AZ827011 29 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0103112F Mouse 10kb plasmid UGCM library Mus musculus genomic
 DEFINITION clone UGCM2M0103112 F, genomic survey sequence.
 ACCESSION AZ827011
 VERSION A2827011.1 GI:12996919
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)

REFERENCE 1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R. Niederahausen, A. and Wright, D., Weis, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss

COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0103 row: 1 column: 12
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES
 source location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UTGCM0103112"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 8.3%; Score 11; DB 8; Length 29;
 Best Local Similarity 100.0%; Pred. No. 7.7e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 CCTGTGTCTTA 115
 |||||
 Db 19 CCTGTGTCTTA 29

RESULT 11
 CL438501 29 bp DNA linear GSS 18-MAR-2004
 LOCUS PS7630-NL.Seg MCB1 Mus musculus genomic clone PS7630-NL.Seg,
 DEFINITION genomic survey sequence.
 ACCESSION CL438501
 VERSION CL438501.1 GI:45575115
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
Hicks, G.G.
www.Escells.ca
Unpublished (2002)
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksagg@cc.umanitoba.ca
Unneostyl gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST7630-NL.Se
q

FEATURES
source
Class: Gene Trap.
Location/Qualifiers
1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST7630-NL.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MIBC1"
/note="Vector: U3NeosV1"

ORIGIN
Query Match 8.3%; Score 11; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGCCAGACCT 23
|||||
3 TGCCAGACCT 13

Db 3 TGCCAGACCT 13

RESULT 12
AZ389514/c 30 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0150108F Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION clone UUCGM0150108 F, genomic survey sequence.
ACCESSION AZ389514
VERSION AZ389514.1 GI:10503222
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

JOURNAL
COMMENT

Plate: 0150 row: 1 column: 08
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0150108"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGM library"
/note="Vector: PWD42hv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g1473214[gblAF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 8.3%; Score 11; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 CCTGTGTCTTA 115
|||||
16 CCTGTGTCTTA 6

Db 16 CCTGTGTCTTA 6

RESULT 13
AZ610580 30 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0435N21R Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION clone UUCGM0435N21 R, genomic survey sequence.
ACCESSION AZ610580
VERSION AZ610580.1 GI:11732770
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

JOURNAL
COMMENT

Plate: 0435 row: N column: 21
Seq primer: CACACAGGAAACAGCTATGAC
Clase: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers

FEATURES

source

1..30

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="TUGC1M0435N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid TUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 7.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

111 TCTACTCTGCC 121

Db

13 TCTACTCTGCC 23

RESULT 14

TA240F05P/c

LOCUS

30 bp DNA linear GSS 13-DEC-2000

DEFINITION

T. brucei sheared genomic DNA clone 240F05, forward sequence,
genomic survey sequence.

ACCESSION

AL481612.1 GI:11847838

KEYWORDS

GSS.

SOURCE

Trypanosoma brucei

ORGANISM

Trypanosoma brucei
Eukaryote; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE

1 (bases 1 to 30)

AUTHORS

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Ackin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE

Direct Submission

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
nhi@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).
Email: nleay@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers

FEATURES

source

1..30

/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="240F05"

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 7.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

59 ACACGTTCTGC 69

Db

13 ACACGTTCTGC 3

RESULT 15

AA916934/c

LOCUS

19 bp mRNA linear EST 17-JUN-1998

DEFINITION

on14a09.s1 NCI CGAP LUS Homo sapiens CDNA clone IMAGE:155632.3'
similar to SW-B13.MOUSE P28662 BRAIN PROTEIN I3 ;, mRNA sequence.

ACCESSION

AA916934.1 GI:3056326

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 19)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cga@bcr-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library

CDNA Library Prepared by: Greg Lennon, Ph.D.

DNA Sequencing

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html

Trace

Trace considered overall poor quality
Insert Length: 444 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham

High quality

High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1..19

ORGANISM

Homo sapiens
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:155632"
/issue_type="carnoid"
/lab_host="DH10B"
/clone_1lb="NCI-CGAP LUS"
/note="Organ: Lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoma, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 7.6%; Score 10; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.6e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 GAGTTTGACG 48
 |||||
 12 GAGTTTGACG 3

RESULT 16
 A2820818 19 bp DNA linear GSS 20-FEB-2001

LOCUS 2M0093118F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCG2M0093118 F, genomic survey sequence.

ACCESSION A2820818
 VERSION A2820818.1 GI:12990726

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weisse, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA

FEATURES
 source
 1. 19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0093118"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_11b="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/mares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g14732114[gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 7.6%; Score 10; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.6e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 GCCTTGCTAC 81
 |||||
 2 GCCTTGCTAC 11

RESULT 17
 AJ666323 20 bp mRNA linear EST 28-JUN-2004

LOCUS AJ666323 CSEGRAN09 Sus scrofa cDNA clone C0000033_j06, mRNA
 sequence.

ACCESSION AJ666323
 VERSION AJ666323.1 GI:49350774

KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 1 (bases 1 to 20)

AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
 TITLE Development of cDNA and EST resources for studying reproduction and
 embryo development in pigs and cattle
 JOURNAL Unpublished (2004)
 COMMENT Contact: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

FEATURES
 source
 1. 20
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="C0000033_j06"
 /issue_type="placenta"
 /clone_11b="CSEGRAN09"
 /note="Vector: pBluescriptII(ks+); site 1: EcoRI; site 2:
 NotI; Single pass sequencing. Normalised library
 constructed from pooled tissue from day 30 placentas."

ORIGIN
 Query Match 7.6%; Score 10; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.6e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 CCTGTGCTCT 114
 |||||
 11 CCTGTGCTCT 2

RESULT 18
 A2780308 20 bp DNA linear GSS 16-FEB-2001

LOCUS 2M001J05R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCG2M001J05 R, genomic survey sequence.

ACCESSION A2780308
 VERSION A2780308.1 GI:12911838

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weis
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0017 row: 5 column: 05
 Seq primer: CACACAGAAACACGTATGAC
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES

Source

1. .20
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC2M0017J05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_id="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g1473214|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 7.6%; Score 10; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.6e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 TGCATGCACA 61
 |||||
 Db 10 TGCATGCACA 1

RESULT 19
 AZ333915 21 bp DNA linear GSS 29-SEP-2000
 LOCUS
 DEFINITION 1M0063002F Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0063002 F, genomic survey sequence.
 ACCESSION
 VERSION AZ333915
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Haml, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weis
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0063 row: 0 column: 02
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

Source

1. .21
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0063002"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_id="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g1473214|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 7.6%; Score 10; DB 8; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.6e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATGCATCAT 11
 |||||
 Db 3 CATGCATCAT 12

RESULT 20
 AZ421118 21 bp DNA linear GSS 03-OCT-2000
 LOCUS
 DEFINITION 1M0199D16F Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0199D16 F, genomic survey sequence.
 ACCESSION
 VERSION AZ421118
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Haml, C.,

TITLE
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
unpublished (2000)

JOURNAL
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0199 row: D column: 16
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

SOURCE

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0199D16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb]|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 7.6%; Score 10; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GGACTGCTG 27
|||||||
5 GGACTGCTG 14

RESULT 21
LOCUS AI035419/c 22 bp mRNA linear EST 26-JUN-1998
DEFINITION ub46d05.r1 Soares_mammary_gland NbMWG Mus musculus cDNA clone
IMAGE:1380777 5' similar to TR:Q16247 Q16247 HISTONE H1
TRANSCRIPTION FACTOR LARGE SUBUNIT 2A. ; mRNA sequence.

ACCESSION AI035419
VERSION AI035419.1 GI:3259129
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steproe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE
The WashU-HMI Mouse EST Project
JOURNAL
unpublished (1996)
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu

This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:903245

Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -28nt3 rev2 ET from Amersham
High quality sequence stop: 1.

FEATURES

SOURCE

1..22
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1380777"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_id="Soares_mammary_gland_NbMWG"
/note="Organ: mammary gland; Vector: pRTT3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
TGTTACCAATCTGAGAGGAGGCGCCGCAATGTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRTT3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

ORIGIN

Query Match 7.6%; Score 10; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 GGCTGATGG 94
|||||||
18 GGCTGATGG 9

RESULT 22
LOCUS AZ810074/c 23 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0074J19P Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0074J19 F, genomic survey sequence.

ACCESSION AZ810074
VERSION AZ810074.1 GI:12976974
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT

Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00
Plate: 0074 row: J column: 19
Seq primer: CGTGTGAAACGACGCGACAT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
SOURCE

Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M074J19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g[14732114]gb[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 7.6%; Score 10; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGACCTGC 25
|||||
Db 18 CAGGACCTGC 9

RESULT 23
AZ586137/c 24 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
1M0391M1R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0391M17 R, genomic survey sequence.
ACCESSION
AZ586137
VERSION
AZ586137.1 GI:11708315
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beecorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT

Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00
Plate: 0391 row: M column: 17
Seq primer: CACACAGAAACGATATAGCC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
SOURCE

Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0391M17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g[14732114]gb[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 7.6%; Score 10; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 TGCATGCACA 61
|||||
Db 24 TGCATGCACA 15

RESULT 24
AZ829971 24 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION
2M0107K20R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0107K20 R, genomic survey sequence.
ACCESSION
AZ829971
VERSION
AZ829971.1 GI:12999879
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beecorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT
plasmid inserts
unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0107 row: K column: 20
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES
source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="TUCG2M0107K20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid TUCG1M library"
/note="Vector: PMD24nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb]|AF19072.1)' a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 7.6%; Score 10; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 CCTACCTGCC 121
|||||
Db 11 CCTACCTGCC 20

RESULT 25
TA201F10P/c 24 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 201f10, forward sequence,
genomic survey sequence.
ACCESSION AL476254
VERSION AL476254.1 GI:11842994
KEYWORDS
SOURCE
ORGANISM
Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 24)
Hail, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrall, B.G.
TITLE
Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

JOURNAL
COMMENT
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrall@sanger.ac.uk and
nhs@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrall, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="201f10"

ORIGIN

Query Match 7.6%; Score 10; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CGTTCGTGGC 71
|||||
Db 16 CGTTCGTGGC 7

RESULT 26
CG722681 25 bp DNA linear GSS 20-OCT-2003
LOCUS
DEFINITION 1119073A10.1BL.x1 1119 - RescuenM Grid AA Zea mays genomic, genomic
survey sequence.
ACCESSION CG722681
VERSION CG722681.1 GI:37757777
KEYWORDS
SOURCE
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 25)
Walbot, V.
Maize genomic sequences found using engineered RescuenM transposon
unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119073 row: A column: 10
Class: transposon-tagged.
Location/Qualifiers

FEATURES
source
1..25
/organism="Zea mays"
/mol_type="genomic DNA"
/culivars="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/cissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescuenM Grid AA"
/note="Organ: leaf; Vector: RescuenM (engineered from
pBluescript backbone); Site_1: BamHI; Site_2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmld.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 7.6%; Score 10; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATGATCA 10
Db 23 ACATGATCA 14

RESULT 27
AZ623015 26 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0460F14F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0460F14 F, genomic survey sequence.
ACCESSION AZ623015
VERSION AZ623015.1 GI:11745205
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: F column: 14
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES
source 1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0460F14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 7.6%; Score 10; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 GCACGACTGC 36
Db 20 GCACGACTGC 11

RESULT 28
AZ825865 26 bp DNA linear GSS 20-FEB-2001
LOCUS 2M010J14F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM010J14 F, genomic survey sequence.
ACCESSION AZ825865
VERSION AZ825865.1 GI:12995773
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0101 row: J column: 14
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES
source 1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM010J14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapored mouse DNA was annealed to adapored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 7.6%; Score 10; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 88 TGGATGGAGC 97
|||||
Db 17 TGGATGGAGC 8

RESULT 29
CG723368 27 bp DNA linear GSS 20-OCT-2003
LOCUS 119076A11.1EL.Y1.1119 - Rescuemu Grid AA Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION CG723368
VERSION CG723368.1 GI:37759145
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 27)
Walbot, V.
Maize genomic sequences found using engineered Rescuemu transposon unpublished (2001)
JOURNAL Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 119076 row: A column: 11
Class: transposon-tagged.

FEATURES

Source

1..27
/organism="Zea mays"
/mol_type="genomic DNA"
/cultiar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="1119 - Rescuemu Grid AA"
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site 1: BamHI, Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu'. Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 7.6%; Score 10; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 CCTGTGATGC 58
|||||
Db 12 CCTGTGATGC 3

RESULT 30
AA636083 28 bp mRNA linear EST 31-OCT-1997
LOCUS nt15b06.s1 NCI CGAP Ew1 Homo sapiens cDNA clone IMAGE:1168019
DEFINITION similar to Wf:W02B12.10 CE03770 ;, mRNA sequence.
ACCESSION AA636083
VERSION AA636083.1 GI:2559022
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 28)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Kitzman, Ph.D.
cDNA Library Arrayed by: Greg Lemmon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1170 Std Error: 0.00
Seq primer: -40m13 fwd. EF from Amersham
High quality sequence stop: 1.

FEATURES

Source

1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1168019"
/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
/clone_id="NCI-CGAP Ew1"
/note="Vector: PAMP10; mRNA made from Ewing's sarcoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Kitzman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 7.6%; Score 10; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 GAGTTTGACG 48
|||||
Db 5 GAGTTTGACG 14

RESULT 31
A1930845/c 28 bp mRNA linear EST 12-JUN-2004
LOCUS gb43b01.y1 Gm-c1015 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-c1015-2.5' similar to TR:022999 022999 PUTATIVE NAM/NO APICAL MERISTEM PROTEIN.;, mRNA sequence.
ACCESSION A1930845

VERSION A1930845.1 GI:566809
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max (soybean)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 28)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, J., Pearson, B., Swaller, T., Gibbons, M., Page, D., Harey, N., Schurr, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. Trace considered overall poor quality possible reversed clone; similarity on wrong strand. This clone is available through: Biogenetic Services, 801 32nd Ave, Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1..28
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams 82"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl015-2"
 /tissue_type="Mature flowers, field grown plants"
 /lab_host="X110-Gold"
 /clone_id="Gm-cl015"
 /note="Vector: Bluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene Bluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the Bluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."

ORIGIN

Query Match 7.6%; Score 10; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.6e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCATCAT 11
 |||||
 Db 24 CATGCATCAT 15

RESULT 32
 AJ807731/c 28 bp mRNA linear EST 11-AUG-2004
 LOCUS AJ807731 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
 DEFINITION 018_6_07_114, mRNA sequence.
 ACCESSION AJ807731

VERSION AJ807731.1 GI:51123059
 KEYWORDS EST.
 SOURCE Antirrhinum majus (snapdragon)
 ORGANISM Antirrhinum majus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.

REFERENCE 1 (bases 1 to 28)
 Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
 Antirrhinum EST collection
 Unpublished (2003)
 Contact: Schwarz-Sommer Z.
 Molekulare Pflanzen-genetik
 MPI fuer Zuechtungsforshung
 Carl-von-Linne Weg 10, D-50829, Germany.
 Location/Qualifiers
 1..28
 /organism="Antirrhinum majus"
 /mol_type="mRNA"
 /db_xref="taxon:4151"
 /clone="018_6_07_114"
 /tissue_type="whole plant"
 /clone_id="Antirrhinum majus whole plant"

FEATURES
 source

ORIGIN

Query Match 7.6%; Score 10; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.6e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 GAGTTTGACG 48
 |||||
 Db 17 GAGTTTGACG 8

RESULT 33
 CF328209 28 bp mRNA linear EST 18-AUG-2003
 LOCUS CF328209
 DEFINITION NACL-03-A03.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa [japonica cultivar-group] cDNA clone NACL-03-A03, mRNA sequence.
 ACCESSION CF328209
 VERSION CF328209
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 28)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nam, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nam B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of BioScience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..28
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL-03-A03"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_id="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO, Site_1: EcoRI; mRNA was capped

ORIGIN with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 7.6%; Score 10; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 TGGTCGACGA 32
|||||
4 TGGTCGACGA 13

RESULT 34
AJ588718/c 29 bp DNA linear GSS 15-JAN-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 356H08, genomic survey sequence.
ACCESSION AJ588718.1 GI:37938342
VERSION GSS: left border: T-DNA flanking sequence.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 29)
AUTHORS Balzerque, S.
TITLE Direct Submision
JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment (s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.intobio.gen.fr>).
Location/Qualifiers

FEATURES
source
1..29
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/culivar="Wassiliwskija"
/db_xref="taxon:3702"
/clone="356H08"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
1..29
/note="T-DNA flanking sequence
left border"

ORIGIN

Query Match 7.6%; Score 10; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 ATGCACACGT 64
|||||
10 ATGCACACGT 1

RESULT 35
BE385582/c 30 bp mRNA linear EST 21-JUL-2000
LOCUS 601275867F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616888 5',
DEFINITION mRNA sequence.
ACCESSION BE385582
VERSION BE385582.1 GI:9330947
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 30)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTP/DRP

CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMU at: image.llnl.gov
Plate: LUCM283 row: e column: 17.
Location/Qualifiers

FEATURES

source
1..30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3616888"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_20"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
Location/Qualifiers

ORIGIN

Query Match 7.6%; Score 10; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 CTACCTGCGG 122
|||||
16 CTACCTGCGG 7

RESULT 36
A2451718/c 30 bp DNA linear GSS 04-OCT-2000
LOCUS A2451718
DEFINITION IM0251A18F Mouse 10kb plasmid UDCGM library Mus musculus genomic
clone UDCGM0251A18 F, genomic survey sequence.
ACCESSION A2451718
VERSION A2451718.1 GI:10607803
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 30)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0251 row: A column: 18
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0251A18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 7.6%; Score 10; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GACCTGCTGC 28
|||||
Db 28 GACCTGCTGC 19

RESULT 37
LOCUS A2797441 30 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0053K07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0053K07 R, genomic survey sequence.
ACCESSION A2797441
VERSION A2797441.1 GI:12946521
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duvall, B., Hamill, C.,
Isalam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0053 row: K column: 07
Seq primer: CACACGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0053K07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 7.6%; Score 10; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 TGCAGCCCTG 53
|||||
Db 19 TGCAGCCCTG 28

RESULT 38
LOCUS AZ844017 30 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0133001F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0143001 F, genomic survey sequence.
ACCESSION AZ844017
VERSION AZ844017.1 GI:13013925
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duvall, B., Hamill, C.,
Isalam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0143 row: 0 column: 01
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers

FEATURES

source

1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0143001"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb Plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[g14732114]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptor and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 7.6%; Score 10; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 GACCTGCTGC 28
|||||||
Db 8 GACCTGCTGC 17

RESULT 39
CL670968
LOCUS
DEFINITION
pacificus var. California *Pristionchus pacificus* genomic, genomic
survey sequence.
CL670968
PR10163C.B10 - PR10163C.B21 (9) Mixed stage fosmid library of *P.*
CL670968.1 GI:50169457
GSS.
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 9)
Strinvaasen, J., Otto, G.W., Kahlow, U., Geisler, R., and Sommer, R.J.
Apbada: an Acedb database for the nematode satellite organism
Nucleic Acids Res. 32 (1), D421-D422 (2004)
JOURNAL
Contact: Sommer RJ
Evolutionary Biology

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Evolutionary Biology

FEATURES

source

Max Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..9
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of *P. pacificus*
var. California"
/note="Vector: pBf10s-5 Fosmid vector"

ORIGIN

Query Match 6.8%; Score 9; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 4e+09;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 GCGTTGCTA 80
|||||||
Db 1 GCGTTGCTA 9

RESULT 40
AJ655553
LOCUS
DEFINITION
AJ655553 KN277 Sus scrofa cDNA clone C0005190_F15, mRNA sequence.
ACCESSION
AJ655553.1 GI:49339585
EST.
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 11)
Anderson, S.I., Finlayson, H.A., and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector: pBluescriptII (SK+) R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pooled early embryos, from 8-cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
www.arkgenomics.org.

JOURNAL
COMMENT

FEATURES

source

1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005190_F15"
/issue_type="embryo"
/note="Vector: pBluescriptII (SK+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
to blastocysts."

ORIGIN

Query Match 6.8%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGACCTG 24
|||||
1 CAGACCTG 9

Db

RESULT 41
BH213431 11 bp DNA linear GSS 24-OCT-2001
LOCUS
DEFINITION
SALK_009214 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_009214, genomic survey sequence.
ACCESSION
BH213431
VERSION
BH213431.1 GI:16395344
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
1 (bases 1 to 11)
Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shim,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
JOURNAL
Contact: Joseph R. Ecker
COMMENT
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
FEATURES
source
1..11
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_009214"
/clone_1ib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 6.8%; Score 9; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 TTGCAGCC 51
|||||
3 TTGCAGCC 11

Db

RESULT 42
CF323664 16 bp mRNA linear EST 18-AUG-2003
LOCUS
DEFINITION
HNN-04-H04.g1 OSHDAC1-overexpressing rice lambda phage clone library II (HNN) Oryza sativa (japonica cultivar-group) cDNA
clone HNN-04-H04, mRNA sequence.
ACCESSION
CF323664
VERSION
CF323664.1 GI:33795589
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
Contact: Nahm B.H.
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
FEATURES
source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HNN-04-H04"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_1ib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library II (HNN)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 6.8%; Score 9; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGACCTGCT 26
|||||
8 GGACCTGCT 16

Db

RESULT 43
AZ458806 19 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION
1M0263012F Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM0263012 F, genomic survey sequence.
ACCESSION
AZ458806
VERSION
AZ458806.1 GI:10616531
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL
Contact: Robert B. Weiss
COMMENT
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0263 row: 0 column: 12

Seq primer: GGTGTAAACAGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

SOURCE

1.19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0521C15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 6.8%; Score 9; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CAGCCCTGC 54
|||||||

Db 11 CAGCCCTGC 19

RESULT 44

A2651177/c

LOCUS 19 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0521C15R Mouse 10kb plasmid UGC1M library Mus musculus genomic
clone UGC1M0521C15 R, genomic survey sequence.

ACCESSION

A2651177

VERSION

A2651177.1 GI:11786406

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0521 row: C column: 15

Seq primer: CACACAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

SOURCE

1.19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0521C15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 6.8%; Score 9; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CAGCCCTGC 54
|||||||

Db 18 CAGCCCTGC 10

RESULT 45

A2794641

LOCUS 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0048E05R Mouse 10kb plasmid UGC1M library Mus musculus genomic
clone UGC2M0048E05 R, genomic survey sequence.

ACCESSION

A2794641

VERSION

A2794641.1 GI:12940815

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0048 row: E column: 05

Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source

1.19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGC2M0048E05"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UGC2M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 6.8%; Score 9; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.9e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GACCTGCTG 27
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 Db 7 GACCTGCTG 15

RESULT 46
 AZ995149 19 bp DNA linear GSS 27-APR-2001
 LOCUS 2M0280D2R Mouse 10kb plasmid UGC2M library Mus musculus genomic
 DEFINITION clone UGC2M0280D22 R, genomic survey sequence.
 ACCESSION AZ995149
 VERSION AZ995149.1 GI:13866376
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
 TITLE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Isalam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 COMMENT Unpublished (2000)
 CONTACT: Robert B. Weiss
 UNIVERSITY of Utah Genome Center
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 TEL: 801 585 5606
 FAX: 801 585 7177
 EMAIL: ddunn@genetics.utah.edu
 INSERT LENGTH: 10000 Std Error: 0.00
 Plate: 0280 row: D column: 22

Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source

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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGC2M0280D22"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UGC2M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 6.8%; Score 9; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.9e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCTGCTGC 28
 |||||
 Db 2 ACCTGCTGC 10

RESULT 47
 AJ589265 19 bp DNA linear GSS 15-JUN-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, right border, clone 547806, genomic survey sequence.
 DEFINITION AJ589265
 ACCESSION AJ589265.1 GI:37938889
 VERSION AJ589265.1
 KEYWORDS GSS; right border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 REFERENCE
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids. 1
 TITLE Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.
 JOURNAL T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
 COMMENT EMBO Rep. 3 (12), 1152-1157 (2002)
 MEDLINE 22363535
 PUBLISHED 12446565
 REFERENCE
 AUTHORS Balzerque, S.
 JOURNAL Direct Submision
 COMMENT Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program "Genoplante" (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES

source

1. .19

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/cultivar="Wassiljewskija"

/db_xref="taxon:3702"

/clone="547E06"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

1. .19
/note="T-DNA flanking sequence
right border"

ORIGIN

Query Match

Best Local Similarity 6.8%; Score 9; DB 9; Length 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 TACCTGCCG 122

Db 3 TACCTGCCG 11

RESULT 48

AZ493004

LOCUS A2493004 20 bp DNA linear GSS 05-OCT-2000

DEFINITION clone UUGC1M0327N06 R, genomic survey sequence.

ACCESSION A2493004

VERSION A2493004.1 GI:10666449

KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)

SOURCE

REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D., Weiss,R.TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0327 row: N column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

1. .20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0327N06"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match

Best Local Similarity 6.8%; Score 9; DB 8; Length 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 CTGCATGCA 59

Db 12 CTGCATGCA 20

RESULT 49

A2780308

LOCUS A2780308 20 bp DNA linear GSS 16-FEB-2001

DEFINITION clone UUGC2M0017J05 R, genomic survey sequence.

ACCESSION A2780308

VERSION A2780308.1 GI:12911838

KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)

SOURCE

REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D., Weiss,R.TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0017 row: J column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

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/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0017J05"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g[4732114]gb[AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 6.8%; Score 9; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCATCA 10
|||||
Db 5 CATGCATCA 13

RESULT 50

LOCUS AZ817897 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0087D09R Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCG2M0087D09 R, genomic survey sequence.

ACCESSION AZ817897
VERSION AZ817897.1 GI:12987805
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

TITLE Contact: Robert B. Weiss
JOURNAL University of Utah Genome Center
COMMENT Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0087 row: D column: 09
Seq primer: CACACAGAAACAGCATATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source 1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0087D09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g[4732114]gb[AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 6.8%; Score 9; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 CCTGTGTC 113
|||||
Db 20 CCTGTGTC 12

RESULT 51

LOCUS AG189452 20 bp DNA linear GSS 06-MAR-2004
DEFINITION Pan troglodytes DNA, clone: RP43-063P18.TU, genomic survey
sequence.

ACCESSION AG189452
VERSION AG189452.1 GI:45221628
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan. 1

AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
BAC end sequences of Library RP-43
Unpublished
2 (bases 1 to 20)

TITLE Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
JOURNAL Direct Submission
COMMENT Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail: redstone@mail.krrib.re.kr. URL: <http://pbs.grc.krrib.re.kr/>, Tel: 82-42-866-7181, Fax: 82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: TU
LIBRARY
Vector : pBACe3.6
R.site 1 : EcoRI
R.site 2 : EcoRI.
Location/Qualifiers

FEATURES
source 1..20
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-063P18.TU"
/sex="male"
/cell_type="Lymphocytes"

ORIGIN /clone_11b="RP-43 Chimpanzee Male BAC library"

Query Match 6.8%; Score 9; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CTGCTGCAC 30
|||||
7 CTGCTGCAC 15

Db 7 CTGCTGCAC 15

RESULT 52
LOCUS A1668099 21 bp mRNA linear EST 28-JUN-2004
DEFINITION A1668099 CSEORAN09 Sus scrofa cDNA clone C000004_113, mRNA
sequence.
ACCESSION A1668099
VERSION A1668099.1 GI:49352550
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 21)
REFERENCE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
UNPUBLISHED (2004)
CONTACT: Anderson SI
JOURNAL Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pluescriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
location/Qualifiers
1. 21
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C000004_113"
/issue_type="Placenta"
/clone_lib="CSEORAN09"
/note="Vector: pluescriptII(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

ORIGIN

Query Match 6.8%; Score 9; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 CTGCCGCTG 125
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7 CTGCCGCTG 15

Db 7 CTGCCGCTG 15

RESULT 53
LOCUS A2323807 21 bp DNA linear GSS 29-SEP-2000
DEFINITION A2323807 Mouse 10kb plasmid UNGCM1 library Mus musculus genomic
clone UNGCM0045N21 F, genomic survey sequence.
ACCESSION A2323807
VERSION A2323807.1 GI:10378892
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
UNPUBLISHED (2000)
CONTACT: Robert B. Weiss
JOURNAL University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: N column: 21
Seq primer: CGTTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 21.
location/Qualifiers
1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNGCM0045N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid UNGCM1 library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (G1473214[g5]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 6.8%; Score 9; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 CTCCGGCTG 89
|||||
Db 18 CTCCGGCTG 10

RESULT 54
LOCUS A2598709 21 bp DNA linear GSS 13-DEC-2000
DEFINITION A2598709 Mouse 10kb plasmid UNGCM1 library Mus musculus genomic
clone UNGCM0413J08 R, genomic survey sequence.
ACCESSION A2598709
VERSION A2598709.1 GI:11720899
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0413 row: J column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0413J08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1[4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 6.8%; Score 9; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 84 GGGCTGGAT 92
|||||
Db 8 GGGCTGGAT 16

RESULT 55
A2794048 21 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0047H07R Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION clone UUCGM0047H07 R, genomic survey sequence.
ACCESSION A2794048
VERSION A2794048.1 GI:12939619
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0047 row: H column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM047H07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1[4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 6.8%; Score 9; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86 GCTGGATGG 94
|||||
Db 13 GCTGGATGG 21

RESULT 56
A2796134 21 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0051A10R Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION clone UUCGM0051A10 R, genomic survey sequence.
ACCESSION A2796134
VERSION A2796134.1 GI:12943710
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0051 row: A column: 10
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0051A10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1/4732114[gbl/AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 6.8%; Score 9; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 GGATGAGC 97
|||||
Db 6 GGATGAGC 14

RESULT 57
A2828488/c
LOCUS A2828488 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0105C05R Mouse 10kb plasmid UUGCM library Mus musculus genomic
clone UUC2M0105C05 R, genomic survey sequence.
ACCESSION A2828488
VERSION A2828488.1 GI:12998396
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0105 row: C column: 05
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0105C05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1/4732114[gbl/AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 6.8%; Score 9; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 CATGACAC 62
|||||
Db 10 CATGACAC 2

RESULT 58
A2833982/c
LOCUS A2833982 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0116K23F Mouse 10kb plasmid UUGCM library Mus musculus genomic
clone UUC2M0116K23 F, genomic survey sequence.
ACCESSION A2833982
VERSION A2833982.1 GI:13003890
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 21)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Dunn, D., Aoyagi, A., Barber, M., Beccorn, T., Duval, B., Hamil, C.,
 Isalam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 016 Row: K Column: 23
 Seq primer: CGTGTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC2M0116K23"
 /sex="male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 digested DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 6.8%; Score 9; DB 8; Length 21;
 Best Local Similarity 100.0%; Pred. No. 8.9e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 34 TGGCTGAGT 42
 |||||
 16 TGGCTGAGT 8

RESULT 59
 AG189469/c 21 bp DNA linear GSS 06-MAR-2004
 LOCUS AG189469
 DEFINITION Pan troglodytes DNA, clone: RP43-064A05.TU, genomic survey
 sequence.
 ACCESSION AG189469
 VERSION AG189469.1 GI:45221645
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
 Hoon, S.T., Chu, W., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 BAC end sequences of Library RP-43
 Unpublished
 2 (bases 1 to 21)
 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
 Hoon, S.T., Chu, W., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 Direct Submission
 Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
 Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
 52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
 (E-mail: redstone@mail.krrib.re.kr; URL: http://pns.grc.krrib.re.kr/;
 Tel: 82-42-866-7181, Fax: 82-42-860-4409)
 Clones are derived from the chimpanzee BAC library RP-43 This BAC
 end was generated during the RAD process and may have higher chance
 of clone tracking errors.
 PRIMERS
 Sequencing: T7
 LIBRARY
 Vector : pBac3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
 Location/Qualifiers
 1..21
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-064A05.TU"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_1lb="RP-43 Chimpanzee Male BAC Library"

ORIGIN
 Query Match 6.8%; Score 9; DB 9; Length 21;
 Best Local Similarity 100.0%; Pred. No. 8.9e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 92 TGGACGCT 100
 |||||
 15 TGGACGCT 7

RESULT 60
 A1738818 22 bp mRNA linear EST 21-DEC-1999
 LOCUS A1738818
 DEFINITION w13b04.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2392591 3'
 similar to TR:002393 002393 HUMAN PAPILLOMAVIRUS 18 ES CENTRAL
 SEQUENCE MOTIF PROTEIN 1; mRNA sequence.
 A1738818
 A1738818.1 GI:5100799
 EST.
 Homo sapiens (human)
 SOURCE Homo sapiens
 KEYWORDS
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 22)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 522 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

SOURCE

```

1. .22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2392591"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/clone_lib="NCI CGAP Col6"
/note="Organ: colon; Vector: pRT3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI.
Plasmid DNA from the normalized library NCI CGAP Col6 was
prepared, and 88 circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo.

```

ORIGIN

Query Match 6.8%; Score 9; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 CATGCACAC 62
|||||||
Db 4 CATGCACAC 12

RESULT 61

LOCUS

AJ795973 22 bp mRNA linear EST 11-AUG-2004
DEFINITION AJ795973 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018.3.09.122, mRNA sequence.

ACCESSION

AJ795973
AJ795973.1 GI:5111301

VERSION

KEYWORDS

SOURCE

ORGANISM

```

EST.
Antirrhinum majus (snapdragon)
Antirrhinum majus
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; lamiales; Plantaginaceae; Antirrhinae;
Antirrhinum.

```

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 22)
Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
Antirrhinum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers

FEATURES

SOURCE

```

1. .22
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018.3.09.122"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

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ORIGIN

Query Match 6.8%; Score 9; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 TTTCGACGC 50
|||||||
Db 7 TTTCGACGC 15

RESULT 62

LOCUS

AZ307716 22 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0009N02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0009N02 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

```

GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: N column: 02
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

```

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

```

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0009N02"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g114732114[gblAF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

ORIGIN

Query Match 6.8%; Score 9; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 CCTGCATGC 58
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Db 12 CCTGCATGC 20

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RESULT 63
AZ616988
LOCUS      22 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION 1M0192P23F Mouse 10kb plasmid UGCGM library Mus musculus genomic
            clone UGCGM0192P23 F, genomic survey sequence.
ACCESSION  AZ616988
VERSION     AZ616988
KEYWORDS   GI:10541001
SOURCE     GSS.
ORGANISM   Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 22)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
TITLE     Unpublished (2000)
JOURNAL   Contact: Robert B. Weiss
COMMENT   University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0192 row: P column: 23
            Seq primer: CGTTGTAAACGACGCCACGT
            Class: plasmid ends
            High quality sequence stop: 22.
            Location/Qualifiers
                source          1..22
                                /organism="Mus musculus"
                                /mol_type="genomic DNA"
                                /strain="C57BL/6J"
                                /db_xref="taxon:10090"
                                /clone="UGCGM0192P23"
                                /sex="Male"
                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                /clone_1lb="Mouse 10kb plasmid UGCGM library"
                                /note="Vector: PMD42nv; Purified genomic DNA from M.
                                musculus C57BL/6J (male) was obtained from the Jackson
                                Laboratory Mouse DNA Resource
                                (http://www.jax.org/resources/documents/dnares/). The DNA
                                was hydrodynamically sheared by repeated passage through a
                                0.005 inch orifice at constant velocity. The sheared DNA
                                was blunt end-repaired with T4 DNA polymerase and T4
                                polynucleotide kinase. Adaptor oligonucleotides were
                                ligated to the blunt ends in high molar excess. The
                                adapted DNA was purified and size-selected for a 9.5 to
                                10.5 kb range using preparative agarose gel
                                electrophoresis. Vector DNA was prepared from a derivative
                                of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
                                inducible derivative of plasmid R1. The vector was ligated
                                with adaptors complementary to the insert adaptors and
                                purified. The sheared, adaptor mouse DNA was annealed to
                                adaptor vector DNA, and transformed into
                                chemically-competent E. coli XL10-Gold (Stratagene) cells
                                and selected for ampicillin resistance."
ORIGIN
Query Match      6.8%; Score 9; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 CAGGACCTG 24
DB 14 CAGGACCTG 22

```

```

RESULT 64
AZ610074/c
LOCUS      22 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION 1M0435J11F Mouse 10kb plasmid UGCGM library Mus musculus genomic
            clone UGCGM0435J11 F, genomic survey sequence.
ACCESSION  AZ610074
VERSION     AZ610074
KEYWORDS   GI:11732264
SOURCE     GSS.
ORGANISM   Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 22)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
TITLE     Unpublished (2000)
JOURNAL   Contact: Robert B. Weiss
COMMENT   University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0435 row: J column: 11
            Seq primer: CGTTGTAAACGACGCCACGT
            Class: plasmid ends
            High quality sequence stop: 22.
            Location/Qualifiers
                source          1..22
                                /organism="Mus musculus"
                                /mol_type="genomic DNA"
                                /strain="C57BL/6J"
                                /db_xref="taxon:10090"
                                /clone="UGCGM0435J11"
                                /sex="Male"
                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                /clone_1lb="Mouse 10kb plasmid UGCGM library"
                                /note="Vector: PMD42nv; Purified genomic DNA from M.
                                musculus C57BL/6J (male) was obtained from the Jackson
                                Laboratory Mouse DNA Resource
                                (http://www.jax.org/resources/documents/dnares/). The DNA
                                was hydrodynamically sheared by repeated passage through a
                                0.005 inch orifice at constant velocity. The sheared DNA
                                was blunt end-repaired with T4 DNA polymerase and T4
                                polynucleotide kinase. Adaptor oligonucleotides were
                                ligated to the blunt ends in high molar excess. The
                                adapted DNA was purified and size-selected for a 9.5 to
                                10.5 kb range using preparative agarose gel
                                electrophoresis. Vector DNA was prepared from a derivative
                                of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
                                inducible derivative of plasmid R1. The vector was ligated
                                with adaptors complementary to the insert adaptors and
                                purified. The sheared, adaptor mouse DNA was annealed to
                                adaptor vector DNA, and transformed into
                                chemically-competent E. coli XL10-Gold (Stratagene) cells
                                and selected for ampicillin resistance."
ORIGIN
Query Match      6.8%; Score 9; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 AGGACCTGC 25
DB 21 AGGACCTGC 13

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RESULT 65
 A2775047 22 bp DNA linear GSS 16-FEB-2001
 LOCUS A2775047
 DEFINITION 2M0007D04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0007D04 F, genomic survey sequence.
 ACCESSION A2775047
 VERSION A2775047.1 GI:12901134
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0007 row: D column: 04
 Seq primer: CGTTGTAACAGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES

1. .22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0007D04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD2 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 6.8%; Score 9; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.9e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 8 TCATCTGCC 16
 |||||
 Db 6 TCATCTGCC 14

RESULT 66
 A2788996 22 bp DNA linear GSS 16-FEB-2001
 LOCUS A2788996
 DEFINITION 2M0036O22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0036O22 F, genomic survey sequence.
 ACCESSION A2788996
 VERSION A2788996.1 GI:12929358
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0036 row: O column: 22
 Seq primer: CGTTGTAACAGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES

1. .22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0036O22"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD2 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 6.8%; Score 9; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.9e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 10 ATCTGCCAG 18
 |||||
 Db 8 ATCTGCCAG 16

RESULT	67		
AZ990555			
LOCUS			
DEFINITION	AZ990555	22 bp	DNA
ACCESSION	2M0274N14F		linear
VERSION	clone UUGC2M0274N14 F, genomic		GSS 27-APR-2001
KEYWORDS	AZ990555		library Mus musculus genomic
SOURCE	AZ990555.1	GI:13861782	sequence.
ORGANISM	GSS		
	Mus musculus (house mouse)		
	Mus musculus		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 22)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C., Islam, H., Lagrange, S., Mahmoud, M., Mennen, E., Pedersen, T., Rellmy, M., Rose, M., Rose, R., Stokes, R., Tilgley, A., von Niederhausern, A., and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss

ORIGIN

```
Query Match      6.8%; Score 9; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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RESULT	68
AM249584/c	
LOCUS	AM249584
DEFINITION	2821490..3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821490 3'
ACCESSION	AM249584
VERSION	AM249584.1 GI:5592577
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

FEATURES	Location/Qualifiers
source	1. .23

ORIGIN

Query Match	6.8%	Score 9;	DB 2;	Length 23;
Best Local Similarity	100.0%;	Pred. No. 8.9e+06;		
Matches	9;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0

RESULT 69				
BM396286/c				
LOCUS	23 bp	mrna	linear	EST 17-JAN-2001
DEFINITION	BM396286	5009-0-2-A10.c.2	Chilcoat/Turkewitz CDNA (large fraction)	
ACCESSION			Tetrahymena thermophila cdna, mRNA sequence.	
	BM396286			

```

VERSION      BM396286.1  GI:18196339
KEYWORDS     EST.
SOURCE       Tetrahymena thermophila
ORGANISM     Tetrahymena thermophila
              Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
              Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE    1 (bases 1 to 23)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
              Frankel,J. and Klobutcher,L.
              EST from Tetrahymena thermophila, strain CU428.1, growing cells
              Unpublished (2002)
JOURNAL      Contact: Turkewitz AP
              Molecular Genetics and Cell Biology
              University of Chicago
              920 E. 58th Street, Chicago, IL 60637, USA
              Tel: 773 702 4374
              Fax: 773 702 3172
              Email: apturkew@midway.uchicago.edu
COMMENT      Seq primer: T3.
FEATURES
  source      Location/Qualifiers
              1..23
              /organism="Tetrahymena thermophila"
              /mol_type="mRNA"
              /strain="CU428.1"
              /db_xref="taxon:5911"
              /clone_lib="Chlicoat/Turkewitz cDNA (large fraction)"
              /note="Vector: Bluescript 2 SK+ Details on library
              preparation can be found in Chlicoat and Turkewitz (2001)
              Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
Query Match      6.8%; Score 9; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 GCGTGAGTT 43
      |||||
      19 GCGTGAGTT 11
RESULT 70
BX558114      23 bp  mRNA  linear  EST 10-OCT-2003
LOCUS         BX558114 Glossina morsitans morsitans adult infected gut Glossina
              morsitans morsitans cDNA tse36902_q1c, mRNA sequence.
ACCESSION     BX558114
VERSION       BX558114.1  GI:33429261
KEYWORDS      EST.
SOURCE        Glossina morsitans morsitans
              Glossina morsitans morsitans
              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Hippoboscidae; Glossinidae; Glossina.
              1 (bases 1 to 23)
              1 (bases 1 to 23)
REFERENCE     Lehane,M.J., Akcoy,S., Gibson,W., Keshornou,A., Berriman,M.,
              Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
              Adult midgut expressed sequence tags from the tsetse fly Glossina
              morsitans morsitans and expression analysis of putative immune
              response genes
JOURNAL      Genome Biol. 4 (10), R63 (2003)
MEDLINE      22881942
PUBMED       14519198
COMMENT      Contact: Hall N
              Pathogen Sequencing Unit
              The Sanger Institute The Wellcome Trust Genome Campus
              Hinxton, Cambridge, CB10 1SA, UK
              Request for clones, please contact: Mike Lehane
              Prof. M.J. Lehane
              School of Biological Sciences,
              University of Wales,
              Bangor LL57 2UW
              All clones with suffix q1c are reverse primer reads starting at 5'
              end of the cDNA all p1c reads are from

```

```

FEATURES      the 3' end.
              Location/Qualifiers
  source      1..23
              /organism="Glossina morsitans morsitans"
              /mol_type="mRNA"
              /sub_species="morsitans"
              /db_xref="taxon:37546"
              /clone="Tse36902 q1c"
              /tissue_type="adult infected gut"
              /clone_lib="Glossina morsitans morsitans adult infected
              gut"
              /note="country: Zimbabwe; EST from adult gut infected with
              T.brucei"
ORIGIN
Query Match      6.8%; Score 9; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 ACGACTGCG 37
      |||||
      9 ACGACTGCG 17
RESULT 71
A0934937      23 bp  DNA  linear  GSS 28-DEC-1999
LOCUS         A0934937 D11BC68 RPCT-23 Mus musculus genomic clone 443J16-T7, genomic
              survey sequence.
DEFINITION    A0934937
ACCESSION     A0934937
VERSION       A0934937.1  GI:6636903
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
              Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 23)
              1 (bases 1 to 23)
REFERENCE     Bradley,A., Li,J., Cai,W., Pershous,M.A., Biggs,P.J., Su,H. and
              Chinault,A.C.
              BAC End Sequences from Mouse Chromosome 11 (Bradley,A. et al.)
              Unpublished (1999)
JOURNAL      Contact: Li, Jiewen
              Department of Molecular and Human Genetics
              Baylor College of Medicine
              7326, One Baylor Plaza, Houston, TX 77030, USA
              Tel: 713 798 6514
              Fax: 713 798 8142
              Email: jliwen1@bcm.tmc.edu
              Plate: 443 row: J column: 16
              Seq primer: T7
              Class: BAC ends.
FEATURES      Location/Qualifiers
  source      1..23
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /strain="C57Bl/6J"
              /db_xref="taxon:10090"
              /clone="443J16-T7"
              /sex="Female"
              /lab_host="DH10B"
              /clone_lib="RPCT-23"
              /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
              EcorI; Site 2: EcorI; Female C57Bl/6J mouse kidney and/or
              brain genomic DNA was isolated and partially digested
              with a combination of EcorI and EcorI Methylase. Size
              selected DNA was cloned into the pBACe3.6 vector at the
              EcorI sites. The ligation products were transformed into
              DH10B electrocompetent cells (BRL Life Technologies)."
ORIGIN
Query Match      6.8%; Score 9; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


QY 102 GTCCCTGTG 110
 Db 5 GTCCCTGTG 13

RESULT 72
 A2849204 23 bp DNA linear GSS 21-FEB-2001
 LOCUS A2849204
 DEFINITION clone UUCGCM0150J02 R, genomic survey sequence.
 ACCESSION A2849204
 VERSION A2849204.1 GI:13033040
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 1 (bases 1 to 23)
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Nedderhansen, A., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Mouse whole genome scaffolding with paired end reads from 10kb
 Plasmid inserts
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT University of Utah Genome Center
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0150 row: J column: 02
 Seq primer: CACACAGAAACACGATATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES

source

1..23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGCM0150J02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCGCM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid RL. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 6.8%; Score 9; DB 8; Length 23;
 Best Local Similarity 100.0%; Pred. No. 8.9e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATGCATCAT 11
 Db 5 ATGCATCAT 13

RESULT 73
 TA130G06P/C 23 bp DNA linear GSS 13-DEC-2000
 LOCUS TA130G06P/C
 DEFINITION T. Brucei sheared genomic DNA clone 130G06, forward sequence,
 genomic survey sequence.
 ACCESSION AL465454
 VERSION AL465454.1 GI:11834863
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nhls@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1..23
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="130G06"

ORIGIN

Query Match 6.8%; Score 9; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 8.9e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 TGCACACGT 64
 Db 15 TGCACACGT 7

RESULT 74
 TA143D12P/C 23 bp DNA linear GSS 13-DEC-2000
 LOCUS TA143D12P/C
 DEFINITION T. brucei sheared genomic DNA clone 143d12, forward sequence,
 genomic survey sequence.
 ACCESSION AL466773
 VERSION AL466773.1 GI:11836128
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE
JOURNAL

Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The V + I method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES

SOURCE

1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="143d12"

ORIGIN

Query Match 6.8%; Score 9; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 CCTGCATG 57
|||||||

Db 17 CCTGCATG 9

RESULT 75

TA269E10P

LOCUS

DEFINITION

TA269E10P 23 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 269e10, forward sequence,

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE

AUTHORS

1 (bases 1 to 23)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

TITLE

JOURNAL

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The V + I method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES

SOURCE

1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"

/db_xref="taxon:5691"
/clone="269e10"

ORIGIN

Query Match 6.8%; Score 9; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 CTGATGGA 95
|||||||

Db 3 CTGATGGA 11

Search completed: February 2, 2005, 23:32:05
Job time : 412.351 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:06:25 ; Search time 62.0342 Seconds
(without alignments)
11170.029 Million cell updates/sec

Title: US-10-048-046-1_COPY_997_1128

Perfect score: 132
Sequence: 1 acatgcctatctcgcagga.....ctactcgcgcgtcccgctg 132

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3366436

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

Database:

N_Geneseq_23Sep04:.*
1: Geneseq19980s:.*
2: Geneseq19908s:.*
3: Geneseq12000s:.*
4: Geneseq12001as:.*
5: Geneseq12001bs:.*
6: Geneseq12002as:.*
7: Geneseq12002bs:.*
8: Geneseq12003as:.*
9: Geneseq12003bs:.*
10: Geneseq12003cs:.*
11: Geneseq12003ds:.*
12: Geneseq12004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	17	12.9	28 5 AAF30356	Aaf30356 Human che
2	15	11.4	28 5 AAK55933	AAk55933 Human CLC
3	15	11.4	17 6 AAK56533	AAk56533 Human CLC
4	15	11.4	17 6 AAK56534	AAk56534 Human CLC
5	14	10.6	17 6 AAK56532	AAk56532 Human CLC
6	14	10.6	17 8 ACC68011	ACC68011 Murine o1
7	14	10.6	18 10 ADC59459	ADC59459 Human epl
8	14	10.6	20 2 AAV64426	AAv64426 Plecterri
9	14	10.6	20 10 ADF74517	ADf74517 Forward p
10	14	10.6	26 6 AAS98254	AAs98254 Human pla
11	13	9.8	26 6 AAQ95923	AAq95923 Primer A
12	13	9.8	17 6 AAK55934	AAk55934 Human CLC
13	13	9.8	17 8 AAB265159	ABb265159 Human HER
14	13	9.8	19 4 AAB27321	ABh27321 Human TSG
15	13	9.8	19 4 AAB27375	ABh27375 PCR prime
16	13	9.8	19 4 AAB27320	ABh27320 Human TSG
17	13	9.8	19 11 ADL78982	ADl78982 Human HER
18	13	9.8	19 11 ADL79231	ADl79231 Human HER
19	13	9.8	20 2 AAQ34360	AAq34360 PACK Prim
20	13	9.8	20 2 AAY08740	AAy08740 PCR prime
21	13	9.8	20 6 ABA81765	ABa81765 PCR prime

22	13	9.8	20 6 AAD30197	AAd30197 Human UGT
23	13	9.8	20 6 ABX97303	ABx97303 Human NOV
24	13	9.8	20 6 ABX97309	ABx97309 Human NOV
25	13	9.8	20 12 ADH13368	ADh13368 Human mal
26	13	9.8	20 12 ADN62206	ADn62206 Human NOV
27	13	9.8	20 12 ADN62212	ADn62212 Human NOV
28	13	9.8	23 12 ADQ76915	ADq76915 Escherich
29	13	9.8	24 3 AAA29645	AAa29645 Hybrid to
30	13	9.8	24 3 AAA29653	AAa29653 Hybrid to
31	13	9.8	24 4 AAS11903	AAs11903 DNA encod
32	13	9.8	24 4 AAS11899	AAs11899 DNA encod
33	13	9.8	25 6 ABO75751	ABo75751 Cloning v
34	13	9.8	25 9 ACI42579	ACi42579 Human mic
35	13	9.8	25 12 ADL33473	ADl33473 HIV gag-p
36	13	9.8	26 2 AAQ70579	AAq70579 Mutagenic
37	13	9.8	28 2 AAX19285	AAx19285 HIV-1 gag
38	13	9.8	28 6 ABK51801	ABk51801 Human UGT
39	13	9.8	29 2 AAV21245	AAv21245 Homo sap1
40	13	9.8	29 2 AAX77337	AAx77337 Human sec
41	13	9.8	29 10 ADC38944	ADc38944 Human sec
42	12	9.1	15 12 ADH69868	ADh69868 Human Ybe
43	12	9.1	17 6 ABN02189	ABn02189 Human GDM
44	12	9.1	17 6 ABN02191	ABn02191 Human GDM
45	12	9.1	17 6 ABN02194	ABn02194 Human GDM
46	12	9.1	17 6 ABN02193	ABn02193 Human GDM
47	12	9.1	17 6 ABN02192	ABn02192 Human GDM
48	12	9.1	17 6 ABR02192	ABr02192 Human GDM
49	12	9.1	17 6 ABK56932	ABk56932 Human CLC
50	12	9.1	17 8 ABK56535	ABk56535 Human CLC
51	12	9.1	17 8 ABT37731	ABt37731 Tumour su
52	12	9.1	17 8 ABZ65160	ABz65160 Human HER
53	12	9.1	17 8 ACD63405	ACd63405 HCV minue
54	12	9.1	17 8 ACD59264	ACd59264 HCV DNAY
55	12	9.1	17 11 ADM11727	ADM11727 Amplifica
56	12	9.1	17 12 ADK94931	ADk94931 Primer of
57	12	9.1	17 12 ADI86075	ADI86075 HCV DNAY
58	12	9.1	17 12 ADI83988	ADi83988 HCV DNAY
59	12	9.1	18 3 AAZ95457	AAz95457 TEIL rand
60	12	9.1	18 4 AAF75988	AAf75988 Human fra
61	12	9.1	18 12 ADK97335	ADk97335 Primer of
62	12	9.1	18 12 ADL95352	ADl95352 Rat P2X3
63	12	9.1	18 12 ADL95356	ADl95356 Rat P2X3
64	12	9.1	19 2 AAO47546	AAo47546 Rat Gs RA
65	12	9.1	19 2 AAV17327	AAv17327 Primer us
66	12	9.1	19 2 AAV41791	AAv41791 Human pan
67	12	9.1	19 10 ADF84430	ADf84430 Human ABL
68	12	9.1	19 10 ADF84749	ADf84749 Human ABL
69	12	9.1	20 2 AAZ05043	AAz05043 PCR prime
70	12	9.1	20 2 AAX95935	AAx95935 PCR prime
71	12	9.1	20 2 AAX95827	AAx95827 PCR prime
72	12	9.1	20 3 AAC79573	AAc79573 Human p38
73	12	9.1	20 5 AAF80036	AAf80036 PCR prime
74	12	9.1	20 5 AAH42633	AAh42633 PCR prime
75	12	9.1	20 6 AAB487895	ABb487895 Synthetic
76	12	9.1	20 8 ABX78173	ABx78173 Human p38
77	12	9.1	20 10 ADF87753	ADf87753 Single nu
78	12	9.1	20 10 ADI61594	ADi61594 Human SAP
79	12	9.1	20 10 ABZ29201	ABz29201 Human o11
80	12	9.1	20 10 ABE299201	ABe299201 Human PDE
81	12	9.1	20 10 ADL25202	ADl25202 Intesclina
82	12	9.1	20 11 ADM34310	ADM34310 Human p38
83	12	9.1	20 11 ABD29202	ABd29202 A150500-
84	12	9.1	20 11 ABD32232	ABd32232 Human PDE
85	12	9.1	20 11 ADP75386	ADp75386 Human NRG
86	12	9.1	20 12 ADG72086	ADg72086 Human SRE
87	12	9.1	20 12 ADI61086	ADi61086 Oligonuc1
88	12	9.1	20 12 ADU37622	ADu37622 Human pro
89	12	9.1	20 12 ADU37659	ADu37659 Human pro
90	12	9.1	20 12 ADOS1074	ADo51074 Human BCL
91	12	9.1	21 4 AAF96648	AAf96648 Human gen
92	12	9.1	21 4 AAH20433	AAh20433 PCR prime
93	12	9.1	21 4 AAC84823	AAc84823 Human TLR
94	12	9.1		

C 95	12	9.1	21	6	AAI40247	Isoprenol
C 96	12	9.1	21	10	ADBO3337	Human tmm
C 97	12	9.1	21	12	ADJ95469	Mouse Ubs
C 98	12	9.1	21	12	ADL95361	Adl95361 Oligoribb
C 99	12	9.1	21	12	ADL95359	Adl95359 Oligoribb
100	12	9.1	21	12	ADL95358	Adl95358 Oligoribb
101	12	9.1	21	12	ADL95360	Adl95360 Oligoribb
C 102	12	9.1	21	12	ADPE21223	ADp21223 Kappa 1-ga
C 103	12	9.1	22	3	AAAI5505	AAAI5505 Human G-a
C 104	12	9.1	22	6	ABK93310	ABK93310 PCR prime
C 105	12	9.1	22	10	ADd47282	Ad47282 Human RT
C 106	12	9.1	22	12	ADG77102	Adg77102 V-gene pr
C 107	12	9.1	22	12	ADNI1934	ADni1934 t cucumete
C 108	12	9.1	23	2	AAQ32318	AAq32318 HUV5SABAC
C 109	12	9.1	23	2	AAQ23795	AAq23795 Primer Hu
C 110	12	9.1	23	2	AAQ39379	AAq39379 Kappa-cha
C 111	12	9.1	23	2	AAI29187	AAi29187 HUVK5a ka
C 112	12	9.1	23	2	AAQ86318	AAq86318 Wilson di
C 113	12	9.1	23	2	AAV41807	AAv41807 Human pan
C 114	12	9.1	23	2	AAV41190	AAv41190 Human pan
C 115	12	9.1	23	2	AAZ32542	AAz32542 PCR prime
C 116	12	9.1	23	2	AAK76633	AAk76633 Human sfv
C 117	12	9.1	23	4	ABAO3087	ABa3087 PCR prime
C 118	12	9.1	23	4	AAD20034	AAd20034 Human ant
C 119	12	9.1	23	4	AAI13315	AAi13315 Human VL
C 120	12	9.1	23	4	AAI13214	AAi13214 Human VL
C 121	12	9.1	23	4	ABN87318	ABn87318 Human VL
C 122	12	9.1	23	5	AAEC8365	AAec8365 VKappa ba
C 123	12	9.1	23	6	ABEK5186	ABe5186 PCR prime
C 124	12	9.1	23	6	ABF76660	ABf76660 Novel met
C 125	12	9.1	23	6	AAD28830	AAd28830 Human ant
C 126	12	9.1	23	6	ABO82776	ABo82776 K-betaM3
C 127	12	9.1	23	6	ABE68586	ABe68586 Human Imm
C 128	12	9.1	23	6	ABO83158	ABo83158 Human HGP
C 129	12	9.1	23	6	ABT09837	ABt09837 K+beta M6
C 130	12	9.1	23	6	AAD42442	AAd42442 Human HDG
C 131	12	9.1	23	6	AAD46094	AAd46094 Human K+b
C 132	12	9.1	23	6	AAD30863	AAI49682 PCR prime
C 133	12	9.1	23	6	AAI49682	AAI49682 Anti-HGPR
C 134	12	9.1	23	6	AAK98436	AAK98436 Human V g
C 135	12	9.1	23	6	ADJ33366	ADj33366 Human VL
C 136	12	9.1	23	6	ADT42693	ADt42693 Human GPC
C 137	12	9.1	23	8	AAI59954	AAI59954 Human ant
C 138	12	9.1	23	8	ABQ77009	ABq77009 Human ant
C 139	12	9.1	23	8	ACA94795	ACa94795 Human sin
C 140	12	9.1	23	8	ABX08586	ABx08586 Human ant
C 141	12	9.1	23	8	AAD49565	AAd49565 Human VL
C 142	12	9.1	23	8	ABX92250	ABx92250 Anti-CAN-
C 143	12	9.1	23	8	ACC48666	ACC48666 Human ant
C 144	12	9.1	23	8	AAAD54826	AAAd54826 Human TR4
C 145	12	9.1	23	9	AAI62812	AAI62812 Human VL
C 146	12	9.1	23	9	ACD91458	ACd91458 Human lig
C 147	12	9.1	23	9	ABT43639	ABt43639 PCR prime
C 148	12	9.1	23	9	ADA09686	ADa09686 Human ant
C 149	12	9.1	23	9	ACF05362	ACf05362 Human HGP
C 150	12	9.1	23	10	AAAD59753	AAAd59753 Human HGP

ALIGNMENTS

RESULT 1
 AAF30356/C
 ID AAF30356 standard; DNA; 28 BP.
 XX
 AC AAF30356;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Human checkpoint gene chr 3' PCR primer.
 DE
 XX
 XX
 KW Checkpoint with forkhead associated domain and ring finger; Chr; human
 KW microst; cell cycle; tumour; diagnosis; antitumour; drug screening;

KW	ubiquitin-protein ligase; PCR primer; ss.
XX	Homo sapiens.
OS	
XX	MO200109150-A2.
PN	
XX	
PD	08-FEB-2001.
XX	
PF	14-JUN-2000; 2000MO-US016391.
XX	
PR	29-JUL-1999; 99US-0146194P.
XX	
PA	(WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX	
PI	Halazonetis T, Scolnick D;
XX	WPI; 2001-182927/18.
DR	
XX	
PT	Novel nucleic acid sequence of mitotic checkpoint gene encoding a
XX	checkpoint with forkhead-associated domain and ring finger protein, for
PR	diagnosing tumorigenic cells and in screening for anticancer drugs.
XX	
PS	Example 3; Page 38; 85pp; English.
XX	
CC	The present sequence is that of a 3' PCR primer, used with the 5' primer
CC	given in AAF30355, to amplify a cDNA fragment corresponding to
CC	nucleotides 352-1055 of the human chr gene sequence given in AAF30352. The
CC	chr gene encodes the human mitotic checkpoint protein Chfr (see
CC	AA02019), which is required for regulation of the transition of cells
CC	from prophase to metaphase during mitosis. Loss of expression of Chfr is
CC	associated with a predisposition to tumourigenesis upon exposure to
CC	mitotic stress. A set of primers (see AAF30353-76) was used to amplify
CC	regions spanning the entire chr coding region in order to determine
CC	whether the chr gene is mutated in any of the human cancer cell lines
CC	SW480, DLD1, H129, HCT116, SAOS2, U2OS, IMR5 and NGP. A mutation leading
CC	to a Val-580 to Met amino acid substitution was identified in the chr
CC	gene of U2OS cells. Chfr polypeptides and chr nucleic acids are used in
CC	methods of diagnosing tumorigenic cells and chfr screening for drugs which
CC	can inhibit the activity of Chfr in a cancer cell, rendering it more
CC	sensitive to additional antitumour therapies
SQ	
Sequence	28 BP; 10 A; 4 C; 8 G; 6 T; 0 U; 0 Other;
Query Match	12.9%; Score 17; DB 5; Length 28;
Best Local Similarity	100.0%; Pred. No. 1.2e+02;
Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	1 ACATGCATCATCTGCCA 17
Dd	25 ACATGCATCATCTGCCA 9
RESULT 2	
ID	ABK55933/c
ID	ABK55933 standard; RNA; 17 BP.
XX	
AC	ABK55933;
XX	
DT	02-JUL-2002 (first entry)
DE	
XX	
XX	Human CLCA1 gene enzymatic nucleic acid #304.
KW	Humann; chloride channel activated 1; CLCA1; ss; antiasthmatic;
KW	antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW	chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW	oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW	acetylcytosteine.
XX	
OS	Homo sapiens.
XX	
XX	MO200211674-A2.
XX	
XD	14-FEB-2002.

XX 09-AUG-2001; 2001WO-US024970.
PF
XX
PR 09-AUG-2000; 2000US-0224383P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTAX USA LLC.
PA (THOM/) THOMPSON J.
XX
PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE,
PI Grube A;
XX
DR WPI; 2002-217145/27.
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS Claim 4; Page 58; 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 8 C; 3 G; 0 T; 3 U; 0 Other;
XX
Query Match 11.4%; Score 15; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86 GCTGATGAGCGCT 100
DB 17 GCTGATGAGCGCT 3
RESULT 3
ABK56533/c
ID ABK56533 standard; RNA; 17 BP.
XX
AC ABK56533;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human CLCA1 gene enzymatic nucleic acid #904.
XX
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
OS Homo sapiens.
XX
PN WO200211674-A2.
XX
PD 14-FEB-2002.
XX
PR 09-AUG-2001; 2001WO-US024970.
XX

PR 09-AUG-2000; 2000US-0224383P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTAX USA LLC.
PA (THOM/) THOMPSON J.
XX
PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE,
PI Grube A;
XX
DR WPI; 2002-217145/27.
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
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XX
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CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 8 C; 3 G; 0 T; 3 U; 0 Other;
XX
Query Match 11.4%; Score 15; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86 GCTGATGAGCGCT 100
DB 16 GCTGATGAGCGCT 2
RESULT 4
ABK56534/c
ID ABK56534 standard; RNA; 17 BP.
XX
AC ABK56534;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human CLCA1 gene enzymatic nucleic acid #905.
XX
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
OS Homo sapiens.
XX
PN WO200211674-A2.
XX
PD 14-FEB-2002.
XX
PR 09-AUG-2001; 2001WO-US024970.
XX
PR 09-AUG-2000; 2000US-0224383P.
XX
PA (RIBO-) RIBOZYME PHARM INC.

PA (SYNTEK USA LLC.
 PA (THOM/) THOMPSON J.
 XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE,
 P1 Gruppe A;
 XX WPJ, 2002-217145/27.
 DR Enzymatic polynucleotide that down regulates expression of chloride
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 XX pulmonary disease (COPD), chronic bronchitis and asthma.
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 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention
 XX
 XX Sequence 17 BP; 3 A; 7 C; 3 G; 0 T; 4 U; 0 Other;

Query Match	11.4%	Score 15;	DB 6;	Length 17;
Best Local Similarity	100.0%	Pred. No. 1.3e+03;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	86	GCTGATGAGCGCT	100	
Db	15	GCTGATGAGCGCT	1	
RESULT 5				
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XX	AC	ABK56532;		
XX	DT	02-JUL-2002 (first entry)		
XX	DE	Human CLCA1 gene enzymatic nucleic acid #903.		
XX	Human; chloride channel activated 1; CLCA1; ss; antiasthmatic;			
XX	Human; chlonide channel calcium activated 1; CLCA1; ss; antiasthmatic;			
XX	antihflammatory; chronic obstructive pulmonary disease; COPD; asthma;			
XX	chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;			
XX	oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;			
XX	acetylcyseine.			
XX	Homo sapiens.			
XX	OS			
XX	PN	MO200211674-A2.		
XX	PD	14-FEB-2002.		
XX	PF	09-AUG-2001; 2001WO-US024970.		
XX	PR	09-AUG-2000; 2000US-0224383P.		
XX	PA	(RIBO-) RIBOZYME PHARM INC.		
XX	PA	(SYNT) SYNTX USA LLC.		
XX	PA	(THOM) THOMPSON J.		
XX				

Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
 Gruppe A;
 WPI, 2002-217145/27.
 Enzymatic polynucleotide that down regulates expression of chloride
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 Claim 4, Page 73; 152pp; English.
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 by cleaving RNA derived from the genes. The nucleic acid sequences are
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 enzymatic nucleic acid molecule of the invention
 Sequence 17 BP; 3 A; 8 C; 3 G; 0 T; 3 U; 0 Other;

```

Query Match 10.6%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY      87 CTGATGAGACGCT 100
      |||||
DB      17 CTGATGAGACGCT 4

RESULT 6
ACCG8011
ID      ACC68011 standard; DNA; 17 BP.
AC
XX      ACC68011;
XX
DT      01-JUL-2003 (first entry)
XX
DE      Murine oligonucleotide associated with tumour suppression, SEQ ID 5258.
XX
KW      Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW      tumour suppression; tumour reversion; apoptosis; virus resistance;
KW      viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW      schizophrenia; ss.
XX
OS      Mus musculus.
XX
PN      M02003025176-A2.
XX
PD      27-MAR-2003.
XX
PF      17-SEP-2002; 2002MO-IB04210.
XX
PR      17-SEP-2001; 2001PR-00011979.
XX
PA      (MOL-E-) MOLECULAR ENGINES LAB.
XX
PI      Teleman A, Amson R, Tuijnder M;
XX
DR      WPI; 2003-333167/31.
XX
PT      New isolated nucleic acid, useful for treating viral diseases associated
PT      with tumors and cell degeneration also related polypeptides, antibodies

```

PT and transfected cells.
 XX
 PS Disclosure; Page 645; 738pp; French.
 XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 10.6%; Score 14; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 113 CTACCTGCCGCTGT 126
 DB 4 CTACCTGCCGCTGT 17
 RESULT 7
 ADCS9459
 ID ADCS9459 standard; DNA; 18 BP.
 XX
 AC ADCS9459;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human epiplakin PCR primer, SEQ ID NO:13, used in expression analysis.
 XX
 KW Human: epiplakin; epidermal autoantigen; autoimmune disease;
 KW skin disease; transgenic animals; diagnosis; drug screening; pemphigoid;
 KW pemphigus; dermatological; immunosuppressive; expression analysis; PCR;
 KW primer; 88.
 XX
 OS Homo sapiens.
 XX
 PN JP2003047469-A.
 XX
 PD 18-FEB-2003.
 XX
 PF 16-JUL-2001; 2001JP-00216025.
 XX
 PR 16-JUL-2001; 2001JP-00216025.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2003-508702/48.
 XX
 PT Novel protein having epiplakin activity, useful for screening agents
 PT which inhibit and activate epiplakin activity, and for treating
 PT autoimmune skin disease such as pemphigoid or pemphigus.
 XX
 PS Example 4; SEQ ID NO 13; 55pp; Japanese.
 XX
 CC The invention relates to a 450 kd human epidermal autoantigen, epiplakin
 CC (ADCS9448), and nucleic acids encoding it (ADCS9447). The invention also
 CC encompasses an epiplakin antigenic epitope (ADCS9449) which is reactive
 CC with serum from patients with autoimmune disease, fusion polypeptides
 CC containing epiplakin or its epitope, an antibody against epiplakin, host
 CC cells comprising human epiplakin nucleic acids, transgenic animals which
 CC under- or over-express epiplakin, epiplakin nucleic acid probes for
 CC diagnosis of autoimmune disease, and methods of screening for agents
 CC which modulate epiplakin activity. Epiplakin polypeptides and
 CC polynucleotides are useful in drug screening for agents which promote or
 CC inhibit the activity of epiplakin which can be used in the treatment of
 CC autoimmune disease, particularly those of the skin such as pemphigoid or

CC pemphigus; Epiplakin antibodies and nucleic acid probes are useful for
 CC diagnosis of these diseases. Sequences ADCS9459-ADCS9460 represent human
 CC epiplakin PCR primers used to generate a probe used in expression
 CC analysis in an example of the invention.
 XX
 SQ Sequence 18 BP; 3 A; 6 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 10.6%; Score 14; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 GCCAGACCTGCTG 27
 DB 4 GCCAGACCTGCTG 17
 RESULT 8
 AAV64426/C
 ID AAV64426 standard; DNA; 20 BP.
 XX
 AC AAV64426;
 XX
 DT 01-MAR-1999 (first entry)
 XX
 DE Pleckstrin homology domain PCR primer.
 XX
 KW Praja-1; mouse; liver development; haematopoiesis; iron transport;
 KW hepatocyte; liver disease; anidrotic ectoderm dysplasia;
 KW hepatocellular carcinoma; colon cancer; spinocerebellar ataxia;
 KW sideroblastic anaemia; haemochromatosis; Ito cell; fibrosis; PCR; primer;
 KW signal transduction; therapy; gene 59; pleckstrin homology; 88.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN M09848827-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 30-APR-1998; 98WO-US008656.
 XX
 PR 30-APR-1997; 97US-00841349.
 XX
 PA (MISH/) MISHRA L.
 XX
 PI Mishra L;
 XX
 DR WPI; 1999-009382/01.
 XX
 PT New isolated early liver development genes - used to develop products for
 PT treating, e.g. liver disease, hepatocellular carcinoma, degenerative
 PT neurological disorders, anaemia, ataxia or haemochromatosis.
 XX
 PS Example 1; Page 28; 92pp; English.
 XX
 CC This oligonucleotide primer was designed to amplify a conserved region of
 CC the pleckstrin homology domain of clone 145/PH. It was used with a
 CC reverse primer (see AAV64425) in the PCR amplification of the cDNA
 CC derived from mouse embryo (11 day post-coitus) liver. A PCR product,
 CC termed CH7, was subsequently used as a probe to screen the embryonic
 CC liver library. 2 Overlapping clones were obtained and used to produce a
 CC nucleotide sequence (see AAV64414) coding for a novel protein, termed
 CC praia-1 (see AAW81641), of the mouse early developing liver. The
 CC invention provides proteins and genes of the murine early developing
 CC liver. These can be used in the treatment and diagnosis of liver disease
 CC and other disorders, including those relating to oncogenesis and tissue
 CC repair
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 10.6%; Score 14; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 13 TGGCAGGACCTGCT 26
Db 18 TGGCAGGACCTGCT 5

RESULT 9
ADF74517/c
ID ADF74517 standard; DNA; 20 BP.

XX ADF74517;
XX
XX 26-FEB-2004 (first entry)
XX

DE Forward PCR primer used to amplify murine clone 145/PH.

XX murine; mouse; PCR; ss; early liver development; end stage liver disease;
KW elf 1-3; 11yor-1 (145); pk; protein 106; praja-1; hepatocyte lineage;
KW cholestasis; biliary stons; hepatic obstruction; stricture;
KW primary biliary cirrhosis; primary sclerosing cholangitis; gene therapy;
KW anhidrotic ectoderm dysplasia; hepatocellular carcinoma; anaemia; ataxia;
KW neurological disorder; haemochromatosis; hepatotropic; cytostatic;
KW neuroprotective; anti-naemic; cardiant.

XX Mus musculus.

OS US6642362-B1.

PN 04-NOV-2003.

XX 01-NOV-1999; 99US-00431184.

XX 30-APR-1997; 97US-00841349.

PR 30-APR-1998; 98MO-US008656.

PA (MISH/) MISHRA L.

XX Mishra L;

PI WPI; 2003-851362/79.

XX New antibodies recognizing early liver development proteins, useful as
PT markers, in identifying peptides and proteins having early liver
PT development characteristics, tracing hepatocyte lineage or treating liver
PT disease.

PS Example 1; Col 18; 82pp; English.

XX This invention relates to novel genes and encoded proteins thereof,
CC isolated during early liver development that are useful in the diagnosis
CC and treatment of end stage liver disease and other disorders.
CC Specifically, it refers to genes that encode proteins such as elf 1-3,
CC 11yor-1 (145), pk, protein 106 and praja-1. The present invention
CC describes the characterisation of these early liver development proteins,
CC and also methods to raise peptide specific antibodies that are useful as
CC markers, as well as for tracing hepatocyte lineage. Furthermore, elf
CC proteins 1-3 are useful in treating hepatocyte lineage disorders, elf
CC biliary stones, hepatic obstruction, stricture, primary biliary cirrhosis
CC or primary sclerosing cholangitis. In addition, through using gene
CC therapy, praja-1, 11yor-1 (145) and pk can be used to treat anhidrotic
CC ectoderm dysplasia, hepatocellular carcinoma and other diseases including
CC anaemia, ataxia, degenerative neurological disorders and
CC haemochromatosis. Accordingly, these proteins can be described as
CC hepatotropic, cytostatic, neuroprotective, anti-naemic and cardiant. This
CC oligonucleotide sequence is the forward PCR primer used to amplify murine
CC clone 145/PH of the invention.

XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 10.6%; Score 14; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 TGGCAGGACCTGCT 26
Db 18 TGGCAGGACCTGCT 5

RESULT 10
AAS98254/c
ID AAS98254 standard; DNA; 26 BP.

XX AAS98254;
XX

XX 12-MAR-2002 (first entry)
XX

DE Human plakoglobin interacting protein PLA_2H12 PCR primer #50.

XX Human; plakoglobin; cytostatic; osteopathic; dermatological; cardiant;
KW plakoglobin related disease; skin carcinoma; acantholytic disease;
KW basal cell carcinoma; squamous cell carcinoma; Naxos disease; PCR primer;
KW extramammary Paget's disease; heart disease; skin blistering;
KW subcorneal acantholysis; Grover's disease; Halley-Halley's disease;
KW Darier's disease; ectodermal dysplasia; skin fragility syndrome; ss.
XX Homo sapiens.

OS MO200185933-A2.

PN 15-NOV-2001.

XX 02-MAY-2001; 2001WO-EP004872.

PR 09-MAY-2000; 2000EP-00201668.

PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

XX Van Roy F, Bonne S, Vanlandschoot A;

PI WPI; 2002-062246/08.

XX New polypeptide, useful for treating skin carcinoma or acantholytic
PT disease such as Grover's and Darier's disease, comprises a protein
PT interacting with human plakoglobin and involved in transduction of
PT plakoglobin related signal to nucleus.

PS Disclosure; Page 28; 98pp; English.

XX The invention relates to an isolated plakoglobin interacting polypeptide
CC (I). (I) is useful as a medicament and in the manufacture of a medicament
CC for treating plakoglobin related diseases, such as skin carcinoma or an
CC acantholytic disease, and to screen compounds that interfere with the
CC interaction of the polypeptide with plakoglobin The plakoglobin related
CC diseases include basal cell carcinoma, squamous cell carcinoma,
CC extramammary Paget's disease, Naxos disease, heart diseases, skin
CC blistering and acantholytic diseases such as subcorneal acantholysis,
CC Grover's disease, Halley-Halley's disease or Darier's disease, and
CC ectodermal dysplasia/skin fragility syndrome. AAS98201 - AAS98288
CC represent novel human plakoglobin interacting protein coding sequences
CC and PCR primers of the invention

XX Sequence 26 BP; 4 A; 4 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 10.6%; Score 14; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 TCATCTGCCAGGAC 21
Db 19 TCATCTGCCAGGAC 6

RESULT 11
AAQ95923/c
ID AAQ95923 standard; DNA; 16 BP.

XX	AAQ95923;
AC	
XX	21-FEB-1996 (first entry)
DT	
XX	
DE	Primer A (Group 13, set A) for marker D1S413, chromosome 16.
XX	
XX	primer1: polymerase chain reaction; PCR; linkage study; locus;
KM	microsatellite marker sequence; automated genotyping; allele;
KW	polymorphism; detection; Homo sapiens; ss.
XX	
OS	Synthetic.
XX	
PN	W09515400-A1.
PD	08-JUN-1995.
XX	
PF	05-DEC-1994; 94WO-US013945.
XX	
PR	03-DEC-1993; 93US-00160837.
XX	
PA	(UYJO) UNIV JOHNS HOPKINS.
XX	
PI	LevyIt RC;
XX	
DR	WPI, 1995-215278/28.
XX	
XX	
PT	Kit for automated genotyping contg. pairs of PCR primers - designed to
PT	amplify polymorphic nucleotide repeat sequences, arranged in sets each
PT	with a characteristic fluorescence label, useful e.g. in detection of
PT	disease related genetic rearrangement.
XX	
PS	Disclosure; Fig 7M-2; 104pp; English.
XX	
CC	The method aims to provide a collection of highly reproducible
CC	microsatellite marker sequences (MMS) at approx. 10-50 cM intervals
CC	throughout the human genome which can be detectably labelled. The MMS are
CC	polymorphic, simple sequence repeats and can be used in automated
CC	genotyping, esp. fluorescence-based. The primers correspond to the unique
CC	DNA sequence surrounding each marker, and PCR is used to detect each
CC	polymorphism. When the MMS show considerable polymorphism (ie. a
CC	difference in the number of repeats) between individuals, the markers can
CC	be particularly informative. The MMS can be ideal for linkage studies.
CC	Kits comprise at least 4 groups, of at least 3 sets, each comprising
CC	labelled primers for PCR amplification of the DNA. Group 13 primer pairs
CC	are shown in AAQ95915-46. The published size range of the D1S413 allele
CC	is 131-149 bp, and the degree of heterozygosity in the population is
CC	about 83%
CC	
XX	
SO	Sequence 16 BP; 5 A; 6 C; 3 G; 2 T; 0 U; 0 Other;
XX	
Qy	
DB	79 TACTGGGCGCTGGA 91
	15 TACTGGGCGCTGGA 3
XX	
RESULT 12	
ABK55934/C	
ID	ABK55934 standard; RNA; 17 BP.
XX	
AC	ABK55934;
XX	
DT	02-JUL-2002 (first entry)
XX	
XX	
XX	Human CLCA1 gene enzymatic nucleic acid #305.
KX	
KW	Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW	antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW	chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; .

KM	oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KM	acetylcysteine.
XX	
OS	Homo sapiens.
XX	
PN	MO200211674-A2.
XX	
PD	14-FEB-2002.
XX	
PF	09-AUG-2001; 2001WO-US024970.
XX	
PR	09-AUG-2000; 2000US-0224383P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
PA	(SYNT) SYNTAX USA LLC.
XX	(THOM)/ THOMPSON J.
PJ	Thompson J, Mcswiggen J., McKenzie T, Ayers D, Szymkowski DE,
PI	Gruppe A;
DR	WPI, 2002-217145/27.
XX	
PT	Enzymatic polynucleotide that down regulates expression of chloride
PT	channel calcium activated gene, useful for treating Chronic obstructive
PT	pulmonary disease (COPD), chronic bronchitis and asthma.
XX	
PS	Claim 4; Page 58; 152pp; English.
XX	
CC	The invention relates to enzymatic nucleic acid molecules that down
CC	regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC	by cleaving RNA derived from the genes. The nucleic acid sequences are
CC	useful as pharmaceutical agents for treating conditions such as chronic
CC	obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC	fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC	that are related to or will respond to the levels of CLCA1 in a cell or
CC	tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC	hence, are useful for treatment of a patient having a condition
CC	associated with the level of CLCA1, where the invention further comprises
CC	the use of one or more therapies under conditions suitable for the
CC	treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC	antibacterials, vaccinations, acetylcysteine and mukcinetic agents. The
CC	nucleic acids of the invention are also used as diagnostic tools to
CC	examine genetic drift and mutations within diseased cells or to detect
CC	the presence of CLCA1 RNA in a cell. This sequence represents an
CC	enzymatic nucleic acid molecule of the invention
XX	
SQ	Sequence 17 BP; 3 A; 7 C; 3 G; 0 T; 4 U; 0 Other;
Query Match	9.8%; Score 13; DB 6; Length 17;
Best Local Similarity	100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	86 GCTGATCGAGCG 98
Db	13 GCTGGATCGAGCG 1
RESULT 13	
ABZ65159	
ID	ABZ65159 standard; RNA; 17 BP.
XX	
AC	ABZ65159;
XX	
DT	21-MAR-2003 (first entry)
DE	Human HER2 DNAzyme substrate #61c.
XX	
KV	Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KV	enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KW	anti-rheumatic; cancer; AIDS; ss.
XX	
OS	Homo sapiens.
XX	

PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 23-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
XX
PR 06-JUN-2001; 2001US-0296249P.
XX
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer; modulates the expression of a nucleic acid encoding
PT HRR2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 4; Page 144; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HRR2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HRR2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in AB259889 - AB262216, AB264544 - AB265531, AB265520 - AB265524,
CC AB266530 - AB266585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 0 T; 3 U; 0 Other;
XX
Query Match 9.8%; Score 13; DB 8; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
QY 15 CCAGACCTGCTG 27
DB 4 CCAGACCTGCTG 16
XX
RESULT 14
AAH27321/c
ID AAH27321 standard; DNA; 19 BP.
XX
XX AAH27321;
XX
AC 08-AUG-2001 (first entry)
XX
DT 08-AUG-2001 (first entry)
XX
DE Human TSG16 PCR primer #21.
XX
XX Tumour suppressor gene 16; TSG16; human; immune response modulator;
KM inflammatory response modulator; signal transduction activator;
KM cytokine inhibitor; gene therapy; anticancer; anti-inflammatory;
KM autoimmune disorder; infection; chromosome 16q24.3;
XX cellular proliferation suppressor; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200132861-A1.
XX
XX 10-MAY-2001.
XX
XX 30-OCT-2000; 2000WO-AU001329.
XX
XX 29-OCT-1999; 99AU-00003771.
XX
PA (WOMEN-) WOMEN'S & CHILDREN'S HOSPITAL.

XX
PI Callen DF, Whitmore SA, Kremmidiotis G, Kochetkova M, Crawford J;
XX
DR WPI; 2001-316439/33.
XX
XX New nucleic acid representing the human tumor suppressor gene TSG16,
PT useful e.g. for diagnosis and treatment of tumors, inflammatory and
PT immunological disorders.
XX
XX Claim 84; Page 185; 215pp; English.
XX
XX The present invention relates to human tumour suppressor gene 16 (TSG16;
CC see AAH23688). TSG16 was isolated from chromosome 16q24.3. TSG16
CC suppresses cellular proliferation. TSG16 is useful for treating disorders
CC associated with decreased expression or activity of TSG16, e.g. cancers,
CC (auto)immune disorders, inflammation, complications of wound healing and
CC infections (by viruses, bacteria, fungi, parasites, protozoa or
CC helminths). The present sequence is a PCR primer, which was used in the
CC present invention
XX
SQ Sequence 19 BP; 4 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match 9.8%; Score 13; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 98 GCTCGTCCCTG 110
DB 14 GCTCGTCCCTG 2
XX
RESULT 15
AAH27375
ID AAH27375 standard; DNA; 19 BP.
XX
XX AAH27375;
XX
DT 08-AUG-2001 (first entry)
XX
DE PCR primer #44.
XX
XX Tumour suppressor gene 16; TSG16; immune response modulator;
KM inflammatory response modulator; signal transduction activator;
KM cytokine inhibitor; gene therapy; anticancer; anti-inflammatory;
KM autoimmune disorder; infection; chromosome 16q24.3; human;
XX cellular proliferation suppressor; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200132861-A1.
XX
XX 10-MAY-2001.
XX
XX 30-OCT-2000; 2000WO-AU001329.
XX
XX 29-OCT-1999; 99AU-00003771.
XX
XX (WOMEN-) WOMEN'S & CHILDREN'S HOSPITAL.
XX
XX Callen DF, Whitmore SA, Kremmidiotis G, Kochetkova M, Crawford J;
XX
XX WPI; 2001-316439/33.
XX
XX New nucleic acid representing the human tumor suppressor gene TSG16,
PT useful e.g. for diagnosis and treatment of tumors, inflammatory and
PT immunological disorders.
XX
XX Disclosure; Page 195; 215pp; English.
XX
XX The present invention relates to human tumour suppressor gene 16 (TSG16;
CC see AAH23688). TSG16 was isolated from chromosome 16q24.3. TSG16
CC suppresses cellular proliferation. TSG16 is useful for treating disorders
CC associated with decreased expression or activity of TSG16, e.g. cancers,

CC (auto)immune disorders, inflammation, complications of wound healing and
CC infections (by viruses, bacteria, fungi, parasites, protozoa or
CC helminths). The present sequence is a PCR primer, which was used in the
CC present invention

XX Sequence 19 BP; 1 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Query Match

9.8%; Score 13; DB 4; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 98 GCTGCTCCCTGTG 110

Db 4 GCTGCTCCCTGTG 16

AAH27320

ID AAH27320 standard; DNA; 19 BP.

XX AAH27320;

XX 08-AUG-2001 (first entry)

XX Human TSG16 PCR primer #20.

XX Tumour suppressor gene 16; TSG16; human; immune response modulator;
XX inflammatory response modulator; signal transduction activator;
XX cyclokinin inhibitor; gene therapy; anticancer; anti-inflammatory;
XX autoimmune disorder; infection; chromosome 16q24.3;
XX cellular proliferation suppressor; PCR primer; ss.

XX Homo sapiens.

XX MO200132861-A1.

XX 10-MAY-2001.

XX 30-OCT-2000; 2000WO-AU001329.

XX 29-OCT-1999; 99AU-00003771.

XX (WOMEN-) WOMEN'S & CHILDREN'S HOSPITAL.

XX Callen DF, Whitmore SA, Kremmidiotis G, Kocheckova M, Crawford J,

XX WPI; 2001-316439/33.

XX New nucleic acid representing the human tumor suppressor gene TSG16,
XX useful e.g. for diagnosis and treatment of tumors, inflammatory and
XX immunological disorders.

XX Claim 84; Page 185; 215pp; English.

XX The present invention relates to human tumour suppressor gene 16 (TSG16;
XX see AAH23886). TSG16 was isolated from chromosome 16q24.3. TSG16
XX suppresses cellular proliferation. TSG16 is useful for treating disorders
XX associated with decreased expression or activity of TSG16, e.g. cancers,
XX (auto)immune disorders, inflammation, complications of wound healing and
XX infections (by viruses, bacteria, fungi, parasites, protozoa or
XX helminths). The present sequence is a PCR primer, which was used in the
XX present invention

XX Sequence 19 BP; 1 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Query Match

9.8%; Score 13; DB 4; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 98 GCTGCTCCCTGTG 110

Db 4 GCTGCTCCCTGTG 16

RESULT 17

ID ADL78982 standard; RNA; 19 BP.

XX ADL78982;

XX 20-MAY-2004 (first entry)

XX Human HER2 (EGFR2) transcript target sequence/siNA upper strand, SEQ:147.

XX RNA interference; short interfering nucleic acid; siNA;
XX short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
XX short hairpin RNA; shRNA; expression modulation; gene therapy;
XX drug screening; diagnosis; therapeutic target identification;
XX pharmacogenomics; gene function analysis; gene mapping; cancer;
XX cytostatic; human; oncogene; epidermal growth factor receptor; EGFR;
XX HER2; EGFR2; neu; erbB2; c-erb-B-2; target sequence; ss.

XX Homo sapiens.

XX MO2003070912-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005045.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 29-MAY-2002; 2002WO-US016640.

XX 06-JUN-2002; 2002US-00163552.

XX 06-JUN-2002; 2002US-0386782P.

XX 03-JUL-2002; 2002US-0393924P.

XX 29-AUG-2002; 2002US-0406378P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 19-SEP-2002; 2002US-00251117.

XX 21-OCT-2002; 2002US-00277494.

XX 15-JAN-2003; 2003US-0440129P.

XX (RIBO-) RIBOZYME PHARM INC.

XX McWiggen J, Pavco P, Beigelman L, Fossnaugh K, Jamison S;

XX WPI; 2003-697612/66.

XX New short interfering nucleic acid, useful e.g. for treatment and
XX diagnosis of cancer, downregulates expression of the epidermal growth
XX factor receptor gene.

XX Example 3; SEQ ID NO 147; 171pp; English.

XX The invention relates to short interfering nucleic acids (siNA) which
XX downregulate expression of one or more human epidermal growth factor
XX receptor (EGFR) genes (including HER1, HER2, HER3 and HER4) by RNA
XX interference. The siNAs may or may not comprise ribonucleotides and may
XX be double or single stranded. They further comprise sense and antisense
XX regions, or alternatively are assembled from a sense oligonucleotide and
XX an antisense oligonucleotide. Specifically, the siNAs include short
XX interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
XX hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
XX can contain deoxyribonucleotides, and can be chemically synthesised,
XX expressed from a vector or enzymatically synthesised. The invention also
XX relates to kits for the in vitro or in vivo delivery of siNA; conjugates
XX and/or complexes of siNA; and vectors that express siNA. The siNAs are
XX used to modulate expression of EGFR genes in cells, tissue explants or
XX organisms (e.g., by ex vivo gene therapy), or in grats and transplants
XX for the treatment of a variety of conditions. They may be used for
XX treating a wide range of cancers such as breast and ovarian cancer. The
XX siNAs are also useful for drug screening, diagnosis, pharmacogenomics,
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function, and gene mapping (e.g., of single nucleotide
XX polymorphisms). The present sequence represents the upper strand of a

CC human HER2 (EGFR2)-targeted double-stranded siNA, which is identical to
 CC the HER2 transcript target sequence.
 XX
 SQ Sequence 19 BP; 4 A; 7 C; 4 G; 0 T; 4 U; 0 Other;
 Query Match 9.8%; Score 13; DB 11; Length 19;
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 15 CCAGGACCTGCTG 27
 |||||
 3 CCAGGACCTGCTG 15
 Db
 RESULT 18
 ADL79231/C
 ID ADL79231 standard; RNA; 19 BP.
 XX
 AC ADL79231;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human HER2 (EGFR2) siNA lower strand, SEQ ID NO:396.
 XX
 KW RNA interference; short interfering nucleic acid; siNA;
 KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
 KW short hairpin RNA; shRNA; expression modulation; gene therapy;
 KW drug screening; diagnosis; therapeutic target identification;
 KW pharmacogenomics; gene function analysis; gene mapping; cancer;
 KW cytostatic; human; oncogene; epidermal growth factor receptor; EGFR;
 KW HER2; EGFR2; neu; erbB2; c-erb-B-2; ss.
 XX
 OS Homo sapiens.
 XX
 PN W02003070912-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 20-FEB-2003; 2003WO-US005045.
 XX
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 29-MAY-2002; 2002WO-US016840.
 PR 06-JUN-2002; 2002US-00163552.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 03-JUL-2002; 2002US-0393974P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 19-SEP-2002; 2002US-00251117.
 PR 21-OCT-2002; 2002US-00277494.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mswiigen J, Pavco P, Beigelman L, Fosnaugh K, Jamison S;
 XX
 DR WPI; 2003-697612/66.
 XX
 PT New short interfering nucleic acid, useful e.g. for treatment and
 XX
 PT diagnosis of cancer, downregulates expression of the epidermal growth
 XX
 PT factor receptor gene.
 XX
 PS Example 3; SEQ ID NO 396; 171pp; English.
 XX
 SS
 CC The invention relates to short interfering nucleic acids (siNA) which
 CC downregulate expression of one or more human epidermal growth factor
 CC receptor (EGFR) genes (including HER1, HER2, HER3 and HER4) by RNA
 CC interference. The siNAs may or may not comprise ribonucleotides and may
 CC be double or single stranded. They further comprise sense and antisense
 CC regions, or alternatively are assembled from a sense oligonucleotide and
 CC an antisense oligonucleotide. Specifically, the siNAs include short
 CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short

CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
 CC can contain deoxyribonucleotides, and can be chemically synthesized,
 CC expressed from a vector or enzymatically synthesized. The invention also
 CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
 CC and/or complexes of siNA, and vectors that express siNA. The siNAs are
 CC used to modulate expression of EGFR genes in cells, tissue explants or
 CC organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
 CC for the treatment of a variety of conditions. They may be used for
 CC treating a wide range of cancers such as breast and ovarian cancer. The
 CC siNAs are also useful for drug screening, diagnosis, therapeutic target
 CC identification and validation, genetic engineering, pharmacogenomics,
 CC studying gene function, and gene mapping (e.g., of single nucleotide
 CC polymorphisms). The present sequence represents the lower strand of a
 CC HER2 (EGFR2)-targeted double-stranded siNA.
 XX
 SQ Sequence 19 BP; 4 A; 4 C; 7 G; 0 T; 4 U; 0 Other;
 Query Match 9.8%; Score 13; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 CCAGGACCTGCTG 27
 |||||
 17 CCAGGACCTGCTG 5
 Db
 RESULT 19
 AAQ33460
 ID AAQ33460 standard; DNA; 20 BP.
 XX
 AC AAQ33460;
 XX
 DT 17-DEC-2001 (revised)
 XX
 DT 11-MAY-1993 (first entry)
 XX
 DE PACK Primer #2.
 XX
 KW HIV; env; nef; LTR; polyA site; SV40; late gene; packaging; provirus;
 KW particle; pNL4-3; ss.
 XX
 OS Synthetic.
 XX
 PN USN7751830-N.
 XX
 PD 01-DEC-1992.
 XX
 PF 30-AUG-1991; 91US-00751830.
 XX
 PR 30-AUG-1991; 91US-00751830.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
 XX
 PI Schubert M, Harnison GG, Chen CJ, Banerjee A;
 XX
 DR WPI; 1993-017808/02.
 XX
 PT Defective interfering HIV particles - effecting in-vivo down-regulation
 XX
 PT of the env. of HIV envelope protein on surface of host cell.
 XX
 PS Example VIII; Page 52; 110pp; English.
 XX
 SS
 CC HDPACK1 is identical to HIV with 3 important deletions which eliminate an
 CC essential packaging signal, part of the env region and the nef and 3' LTR
 CC region which is replaced by the polyA site of the SV40 late genes. This
 CC construct when coexpressed with the defective RNAs provide proteins for
 CC the assembly of new defective virus particles. Example VIII describes the
 CC construction of the packaging provirus DNA construct HDPACK1 which
 CC requires a number of deletions and the addition of a polyA site. The
 CC primers of AAQ33459-66 were used. Primers PACK primer #1 and #2 were used
 CC in PCR with pNL4-3 as template. Primer #1 is a deletion primer which
 CC removes part of the essential packaging signal. (Note: Revised entry
 CC submitted to correct the patent number format of US Government-owned NTIS
 CC applications to prevent clashes with ongoing US granted patent numbers.

PF 02-JUL-2001; 2001WO-EP007524.
XX
PR 14-JUL-2000; 2000EP-00115353.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Acuna G, Foernzler D, Leong DU;
XX WPI; 2002-179803/23.
DR
XX
XX
PT Detecting predisposition to hepatotoxic reaction of human being caused by
PT administration of a compound, by determining single nucleotide
PT polymorphism in UDP-glucuronosyl transferase gene in sample of human
PT being.
XX
XX
PS Example; Page 22; 62pp; English.
XX
XX The invention relates to a method for diagnosing a pre-disposition to
CC drug induced liverotoxicity which involves determining at least one single
CC nucleotide polymorphism (SNP) in the UDP-glucuronosyl transferase (UGT1)
CC gene. The method is useful for detecting a predisposition to a
CC hepatotoxic reaction of a human being caused by administration of a
CC pharmaceutical active compound based on determination of a SNP in UGT1
CC gene in a sample of the human being. Nucleic acids containing
CC polymorphism are useful for performing sequence identification. They are
CC also useful in screening assays to establish animal, cell and in vitro
CC models for drug metabolism and for genotyping individuals. The present
CC sequence is a common PCR primer used to detect human UGT1 gene
CC polymorphism
XX
SQ Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 9.8%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 CCCTGTGTCTTAC 116
17 CCCTGTGTCTTAC 5
Db
RESULT 23
ABX97303
ID ABX97303 standard; DNA; 20 BP.
XX
AC ABX97303;
XX
XX 20-MAY-2003 (first entry)
DT
XX
DE Human NOV-associated forward primer from primer-probe set Ag3952.
XX
KM NOVX; cytoskeletal; cardiac; antiarteriosclerotic; antiasthmatic; cancer;
KM hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
KM human; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX W0200272757-A2.
PN
XX 19-SEP-2002.
PD
XX
PF 08-MAR-2002; 2002WO-US006908.
XX
PR 08-MAR-2001; 2001US-0274101P.
PR 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.

PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277833P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0277338P.
PR 30-MAR-2001; 2001US-0279959P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 04-APR-2001; 2001US-0281194P.
PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.
PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294889P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.
PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.
PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318462P.
PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325430P.
PR 27-SEP-2001; 2001US-0325681P.
PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332271P.
PR 14-NOV-2001; 2001US-0332372P.
PR 14-NOV-2001; 2001US-0333184P.
PR 14-NOV-2001; 2001US-0333722P.
PR 21-NOV-2001; 2001US-0337094P.
PR 03-DEC-2001; 2001US-0337426P.
PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
PR 07-MAR-2002; 2002US-00092900.
(CURA-) CURAGEN CORP.
XX
XX Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CBA, Li L;
PI Zernhagen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
PI Patlurajan M, Gangoli E, Vermet CAM, Guo X, Tchiernev V;
PI Fernandes ER, Caeman SV, Malyankar UM, Gerlach V, Liu Y, Anderson D;
PI Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JF;
PI Lepley DM, Rieger DK;
XX
XX WPI; 2002-723332/78.
DR
XX
XX NOVX polypeptides and polynucleotides, useful for preventing or treating
XX a disorder associated with aberrant NOVX expression or activity e.g.,
XX cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
XX asthma.
XX Example C; Page 641; 1103pp; English.
XX
XX This invention describes novel human NOVX polypeptides which have

CC cytosolic, cardiac, antiarteriosclerotic, antiasthmatic and hypotensive
CC activity. Pharmaceutical compositions comprising the NOVX proteins or
CC nucleic acid molecules or NOVX antibodies are useful for preventing or
CC treating a disorder associated with aberrant NOVX expression or activity
CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
CC asthma. The products of the invention can be used for gene therapy or in
CC a vaccine. ABX13460-ABX13462 and ABX97186-ABX97593 represent PCR primers
CC and probes used in the amplification and isolation of the NOVX
CC polynucleotides represented in ABX97008-ABX97185 which encode the
CC polypeptides represented in ABU65041-ABU65218

SQ Sequence 20 BP; 2 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 9.8%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 GTCCCTGTCTCT 114
DB 5 GTCCCTGTCTCT 17

RESULT 24
ABX97309
ID ABX97309 standard; DNA; 20 BP.
XX
AC ABX97309;
XX
DT 20-MAY-2003 (first entry)
XX
DE Human NOV-associated forward primer from primer-probe set Ag3952 #2.
XX
KM NOVX; cytosolic; cardiac; antiarteriosclerotic; antiasthmatic; cancer;
KM hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
KM human; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200272757-A2.
XX
PD 19-SEP-2002.
XX
PF 08-MAR-2002; 2002WO-US006908.
XX
PR 08-MAR-2001; 2001US-0274101P.
PR 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276999P.
PR 20-MAR-2001; 2001US-0277237P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0278333P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278899P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0279388P.
PR 30-MAR-2001; 2001US-0279955P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 02-APR-2001; 2001US-0280900P.
PR 04-APR-2001; 2001US-0281194P.
PR

PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.
PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294899P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.
PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.
PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318462P.
PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325430P.
PR 27-SEP-2001; 2001US-0325681P.
PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332271P.
PR 14-NOV-2001; 2001US-0332272P.
PR 14-NOV-2001; 2001US-0333184P.
PR 14-NOV-2001; 2001US-0333272P.
PR 21-NOV-2001; 2001US-0332094P.
PR 03-DEC-2001; 2001US-0337426P.
PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
PR 07-MAR-2002; 2002US-00092900.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CE, Li L;
PI Zernhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
PI Paturajan M, Gangoli E, Vernet CAM, Guo X, Tchernev V;
PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
PI Spaderna SK, Catterton E, Burgess C, Lette M, Zhong H, Alebrook JP;
PI Lepley DM, Rieger DK;
XX
XX WPI; 2002-723332/78.
XX
XX NOVX polypeptides and polynucleotides, useful for preventing or treating
XX a disorder associated with aberrant NOVX expression or activity e.g.,
XX cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
XX asthma.
XX
XX Example C; Page 646; 1103pp; English.
XX
XX This invention describes novel human NOVX polypeptides which have
XX cytosolic, cardiac, antiarteriosclerotic, antiasthmatic and hypotensive
XX activity. Pharmaceutical compositions comprising the NOVX proteins or
XX nucleic acid molecules or NOVX antibodies are useful for preventing or
XX treating a disorder associated with aberrant NOVX expression or activity
XX e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
XX asthma. The products of the invention can be used for gene therapy or in
XX a vaccine. ABX13460-ABX13462 and ABX97186-ABX97593 represent PCR primers
XX and probes used in the amplification and isolation of the NOVX
XX polynucleotides represented in ABX97008-ABX97185 which encode the
XX polypeptides represented in ABU65041-ABU65218

SQ Sequence 20 BP; 2 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 9.8%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 GTCCCTGTCTCT 114
|||||

Db 5 GTCCCTGTGTCT 17

RESULT 25
ADH13368
ID ADH13368 standard; DNA; 20 BP.
XX
AC ADH13368;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human malignant neoplasia-related PCR primer SeqID217.
XX
KM malignant neoplasia; cytostatic; breast cancer; ovarian cancer;
KM gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;
KM bladder cancer; non-small cell lung cancer; human; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN EPI365034-A2.
XX
PD 26-NOV-2003.
XX
PF 09-MAY-2003; 2003EP-00010447.
XX
PR 21-MAY-2002; 2002EP-00010291.
PR 13-FEB-2003; 2003EP-00003112.
XX
PA (PARB) BAYER AG.
XX
PI Wirtz R, Munnes M, Kallabis H;
XX
DR WPI; 2004-073279/08.
XX
PT Predicting, diagnosing or prognosing malignant neoplasia by detecting at
PT least two markers, where the markers are genes from one or more
PT chromosomal regions altered in malignant neoplasia.
XX
PS Example 1; SEQ ID NO 217; 267bp; English.
XX
CC This invention relates to a novel method for the prediction, diagnosis,
CC or prognosis of malignant neoplasia by the detection of at least two
CC markers. The invention may also be useful for the development of
CC cytostatic compounds through the regulation of the expression of a gene
CC or activity of a protein associated with malignant neoplasia. The method
CC is useful for prediction, diagnosis or prognosis of malignant neoplasia
CC such as breast cancer, ovarian cancer, gastric cancer, colon cancer,
CC oesophageal cancer, mesenchymal cancer, bladder cancer or non-small cell
CC lung cancer. The polynucleotides and polypeptides defined in the
CC specification, antisense polynucleotides targeting the polynucleotides,
CC antibodies targeting either one of the polynucleotides or polypeptides,
CC and compounds identified by the screening methods are useful for
CC preventing or treating malignant neoplasia. The disease treated is
CC preferably breast cancer. The present sequence is that of a PCR primer
CC which was used in the exemplification of the invention.
XX
SQ Sequence 20 BP; 0 A; 7 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 9.8%; Score 13; DB 12; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GTCCCTGTGTCT 114
Db 4 GTCCCTGTGTCT 16

RESULT 26
ADN62206
ID ADN62206 standard; DNA; 20 BP.
XX
AC ADN62206;
XX

DT 01-JUL-2004 (first entry)
XX
DE Human NOV24a/c RTQ-PCR forward primer #1.
XX
KM Human; ss; PCR; NOV; diabetes; obesity; infectious disease; anorexia;
KM cancer-associated cachexia; cancer; neurodegenerative disorder;
KM Alzheimer's disease; Parkinson's disease; immune disorder;
KM haematopoietic disorder; dyslipidaemia; chronic disease; primer; RTQ-PCR;
KM real time quantitative PCR.
XX
OS Homo sapiens.
XX
PN US2004043382-A1.
XX
PD 04-MAR-2004.
XX
PF 07-MAR-2002; 2002US-00092900.
XX
PR 08-MAR-2001; 2001US-0274191P.
PR 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275335P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277339P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 20-MAR-2001; 2001US-0277338P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277833P.
PR 23-MAR-2001; 2001US-0278152P.
PR 25-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0279959P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 02-APR-2001; 2001US-0280900P.
PR 04-APR-2001; 2001US-0281444P.
PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.
PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294899P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.
PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.
PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318770P.
PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325430P.
PR 27-SEP-2001; 2001US-0325681P.
PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332371P.
PR 14-NOV-2001; 2001US-0332272P.

PR 14-NOV-2001; 2001US-0333184P.
 PR 14-NOV-2001; 2001US-0333272P.
 PR 21-NOV-2001; 2001US-0332094P.
 PR 03-DEC-2001; 2001US-0337426P.
 PR 03-DEC-2001; 2001US-0338092P.
 PR 04-DEC-2001; 2001US-0337185P.
 PR 03-JAN-2002; 2002US-0345705P.
 XX
 PA (PADL/) PADIGARU M.
 PA (SPYT/) SPYTEK K A.
 PA (SHEN/) SHENOY S G.
 PA (TAUP/) TAUPIER R J.
 PA (PENNA/) PENNA C E A.
 PA (LILL/) LI L.
 PA (ZERH/) ZERHUSEN B D.
 PA (GUSE/) GUSEV V Y.
 PA (JIMW/) JI W.
 PA (GORM/) GORMAN L.
 PA (MILL/) MILLER C E.
 PA (KEKU/) KEKUDA R.
 PA (PART/) PARTURAJAN M.
 PA (GANG/) GANGOLLI E A.
 PA (VERN/) VERNER C A M.
 PA (GUOX/) GUO X S.
 PA (TCHE/) TCHERNEV V T.
 PA (FERN/) FERNANDES E R.
 PA (CASM/) CASMAN S J.
 PA (MALY/) MALYANKAR U M.
 PA (GERL/) GERLACH V.
 PA (LIUY/) LIU Y.
 PA (ANDE/) ANDERSON D W.
 PA (SPAD/) SPADERNA S K.
 PA (CART/) CARTERTON E.
 PA (LEIT/) LEITE M W.
 PA (ZHON/) ZHONG H.
 PA (ALSO/) ALSOBROOK J P.
 PA (LEPL/) LEPLLEY D M.
 PA (RIEG/) RIEGER D K.
 PA (BURG/) BURGESS C E.
 XX
 PI Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CE, Li L,
 PI Zehusen BD, Gusev VY, Ji W, Gorman L, Miller CE, Kekuda R,
 PI Parturajan M, Gangolli EA, Vernet CAM, Guo XS, Tchernev VT;
 PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y,
 PI Anderson DW, Spaderna SK, Carterton E, Leite MW, Zhong H;
 PI Alsbrook JP, Lepley DM, Rieger DK, Burgess CE;
 XX
 DR WPI; 2004-225693/21.
 XX
 FT New NOVX polypeptides and nucleic acid molecules useful for diagnosing,
 FT preventing or treating NOVX-associated disorders, e.g. cancer, diabetes,
 FT infection or obesity, and in chromosome mapping, tissue typing or
 FT pharmacogenomics.
 PT
 XX
 PS Example C; SEQ ID NO 475; 786pp; English.
 XX
 CC The invention relates to an isolated polypeptide (designated NOVX, or
 CC NOV1-NOV127) comprising a sequence selected from 178 fully defined amino
 CC acid sequences (and their mature forms, variants and fragments). Also
 CC included are an isolated nucleic acid molecule encoding NOVX, a vector
 CC comprising the nucleic acid, a cell comprising the vector, methods for
 CC determining the presence or amount of the polypeptide or the nucleic acid
 CC molecule in a sample, methods for determining the presence of or
 CC predisposition to a disease associated with altered levels of expression
 CC of the above polypeptide or nucleic acid molecule in a first mammalian
 CC subject, a method for identifying an agent that binds to the above
 CC polypeptide, a method for identifying a potential therapeutic agent for
 CC use in the treatment of a pathology that is related to aberrant
 CC expression or physiological interactions of the polypeptide, a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide and a method for modulating
 CC the activity of the polypeptide cited above. The composition and methods
 CC are useful for diagnosing, preventing or treating diseases such as

CC diabetes, obesity, infectious diseases, anorexia, cancer-associated
 CC cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or
 CC Parkinson's disease, immune disorders, haematopoietic disorders, and
 CC dyslipidaemias, and other chronic diseases. These may also be used in
 CC chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The polypeptides are also useful as vaccines. The
 CC present sequence is an RTQ-PCR (real time quantitative PCR) primer used
 CC to assay tissue specific expression of a NOVX mRNA.
 XX
 SQ Sequence 20 BP, 2 A, 6 C, 5 G, 7 T, 0 U, 0 Other;
 XX
 Query Match 9.8%; Score 13; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 102 GTCCCTGTGTCTCT 114
 Db 5 GTCCCTGTGTCTCT 17
 XX
 RESULT 27
 ADN62212
 ID ADN62212 standard; DNA; 20 BP.
 XX
 AC ADN62212;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human NOV24b RTQ-PCR forward primer.
 XX
 KW Human; sex: PCR; NOVX; diabetes; obesity; infectious disease; anorexia;
 KW cancer-associated cachexia; cancer; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; chronic disease; primer; RTQ-PCR;
 KW real time quantitative PCR.
 XX
 OS Homo sapiens.
 XX
 FN US2004043382-A1.
 XX
 PD 04-MAR-2004.
 XX
 PF 07-MAR-2002; 2002US-00092900.
 XX
 PR 08-MAR-2001; 2001US-0274191P.
 PR 08-MAR-2001; 2001US-0274194P.
 PR 08-MAR-2001; 2001US-0274281P.
 PR 08-MAR-2001; 2001US-0274332P.
 PR 09-MAR-2001; 2001US-0274849P.
 PR 12-MAR-2001; 2001US-0275235P.
 PR 13-MAR-2001; 2001US-0275578P.
 PR 13-MAR-2001; 2001US-0275579P.
 PR 13-MAR-2001; 2001US-0275601P.
 PR 14-MAR-2001; 2001US-0276000P.
 PR 16-MAR-2001; 2001US-0276776P.
 PR 19-MAR-2001; 2001US-0276994P.
 PR 20-MAR-2001; 2001US-0277239P.
 PR 20-MAR-2001; 2001US-0277321P.
 PR 20-MAR-2001; 2001US-0277337P.
 PR 20-MAR-2001; 2001US-0277338P.
 PR 21-MAR-2001; 2001US-0277791P.
 PR 22-MAR-2001; 2001US-0277833P.
 PR 23-MAR-2001; 2001US-0278152P.
 PR 26-MAR-2001; 2001US-0278894P.
 PR 27-MAR-2001; 2001US-0278999P.
 PR 27-MAR-2001; 2001US-0279036P.
 PR 28-MAR-2001; 2001US-0279344P.
 PR 30-MAR-2001; 2001US-0279959P.
 PR 30-MAR-2001; 2001US-0280233P.
 PR 02-APR-2001; 2001US-0280802P.
 PR 02-APR-2001; 2001US-0280822P.
 PR 02-APR-2001; 2001US-0280900P.
 PR 04-APR-2001; 2001US-0281444P.
 PR

PR 13-APR-2001; 2001US-0283675P.
 PR 30-APR-2001; 2001US-0287424P.
 PR 02-MAY-2001; 2001US-0288066P.
 PR 03-MAY-2001; 2001US-0288342P.
 PR 03-MAY-2001; 2001US-0288528P.
 PR 15-MAY-2001; 2001US-0291190P.
 PR 16-MAY-2001; 2001US-0291099P.
 PR 16-MAY-2001; 2001US-0291240P.
 PR 30-MAY-2001; 2001US-0294485P.
 PR 31-MAY-2001; 2001US-0294889P.
 PR 31-MAY-2001; 2001US-0294899P.
 PR 18-JUN-2001; 2001US-0299027P.
 PR 19-JUN-2001; 2001US-0299303P.
 PR 19-JUN-2001; 2001US-0299310P.
 PR 10-JUL-2001; 2001US-0304354P.
 PR 31-JUL-2001; 2001US-0309188P.
 PR 16-AUG-2001; 2001US-0312903P.
 PR 10-SEP-2001; 2001US-0318462P.
 PR 12-SEP-2001; 2001US-0318770P.
 PR 27-SEP-2001; 2001US-0325430P.
 PR 27-SEP-2001; 2001US-0325681P.
 PR 18-OCT-2001; 2001US-0330380P.
 PR 31-OCT-2001; 2001US-0335301P.
 PR 14-NOV-2001; 2001US-0332172P.
 PR 14-NOV-2001; 2001US-0332271P.
 PR 14-NOV-2001; 2001US-0332272P.
 PR 14-NOV-2001; 2001US-0333184P.
 PR 14-NOV-2001; 2001US-0333272P.
 PR 21-NOV-2001; 2001US-0332094P.
 PR 03-DEC-2001; 2001US-0337456P.
 PR 03-DEC-2001; 2001US-0338092P.
 PR 04-DEC-2001; 2001US-0337185P.
 PR 03-JAN-2002; 2002US-0345705P.
 XX
 PA (PADJ/) PADIGARU M.
 PA (SPYT/) SPYTEK K A.
 PA (SHEN/) SHENY S G.
 PA (TAUP/) TAUPIER R J.
 PA (PENNA/) PENNA C E A.
 PA (LIIL/) LI L.
 PA (ZERH/) ZERHUSEN B D.
 PA (GUSE/) GUSEV V Y.
 PA (JIMW/) JI W.
 PA (GORM/) GORMAN L.
 PA (MILL/) MILLER C E.
 PA (KEKU/) KEKUDA R.
 PA (PATT/) PATTURAJAN M.
 PA (GANG/) GANGOLLI E A.
 PA (VERN/) VERNET C A M.
 PA (GUOX/) GUO X S.
 PA (TCHE/) TCHERNEV V T.
 PA (PERN/) FERNANDES E R.
 PA (CASM/) CASKMAN S J.
 PA (MALY/) MALYANKAR U M.
 PA (GERL/) GERLACH V.
 PA (LIUY/) LIU Y.
 PA (ANDE/) ANDERSON D W.
 PA (SPAD/) SPADERNA S K.
 PA (CATT/) CATTERTON E.
 PA (LEIT/) LEITE M W.
 PA (ZHON/) ZHONG H.
 PA (ALSO/) ALSOBROOK J P.
 PA (LEPL/) LEPLEY D M.
 PA (RIEG/) RIEGER D K.
 PA (BURG/) BURGESS C E.
 XX
 PI Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L,
 PI Zehrusen BD, Gusev VY, Ji W, Gorman L, Miller CE, Kekuda R,
 PI Patturajan M, Gangoli EA, Vernet CM, Guo XS, Tcherny VT,
 PI Fernandes ER, Caskan SJ, Malynkar UM, Gerlach V, Liu Y,
 PI Anderson DW, Spaderna SK, Catterton E, Leite MW, Zhong H,
 PI Alsobrook JP, Lepley DM, Rieger DK, Burgess CE,
 XX

DR WPI; 2004-225693/21.
 XX
 PT New NOVA polypeptides and nucleic acid molecules useful for diagnosing,
 PT preventing or treating NOVA-associated disorder, e.g. cancer, diabetes,
 PT infection or obesity, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 XX Example C; SEQ ID NO 481, 786pp; English.
 XX
 CC The invention relates to an isolated polypeptide (designated NOVA, or
 CC NOVA1127) comprising a sequence selected from 178 fully defined amino
 CC acid sequences (and their mature forms, variants and fragments). Also
 CC included are an isolated nucleic acid molecule encoding NOVA, a vector
 CC comprising the nucleic acid, a cell comprising the vector, methods for
 CC determining the presence or amount of the polypeptide or the nucleic acid
 CC molecule in a sample, methods for determining the presence of or
 CC predisposition to a disease associated with altered levels of expression
 CC of the above polypeptide or nucleic acid molecule in a first mammalian
 CC subject, a method for identifying an agent that binds to the above
 CC polypeptide, a method for identifying a potential therapeutic agent for
 CC use in the treatment of a pathology that is related to aberrant
 CC expression or physiological interactions of the polypeptide, a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide and a method for modulating
 CC the activity of the polypeptide cited above. The composition and methods
 CC are useful for diagnosing, preventing or treating diseases such as
 CC diabetes, obesity, infectious diseases, anorexia, cancer-associated
 CC cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or
 CC Parkinson's disease, immune disorders, hematopoietic disorders,
 CC dyslipidaemias, and other chronic diseases. These may also be used in
 CC chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The polypeptides are also useful as vaccines. The
 CC present sequence is an RTQ-PCR (real time quantitative PCR) primer used
 CC to assay tissue specific expression of a NOVA mRNA.
 XX
 SQ Sequence 20 BP; 2 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
 XX
 Query Match 9.8%; Score 13; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 1.3e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 102 GTCCCTGTGTCTCT 114
 Db 5 GTCCCTGTGTCTCT 17
 XX
 RESULT 28
 ID ADQ76915
 ID ADQ76915 standard; DNA; 23 BP.
 XX
 AC ADQ76915;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Escherichia coli csrc gene PCR primer Dlsrb.
 XX
 KW Biofilm; infection; Csrc; antibacterial; PCR; primer; ss.
 XX
 OS Escherichia coli.
 XX
 PN CA2450504-A1.
 XX
 PD 26-MAY-2004.
 XX
 PF 22-DEC-2003; 2003CA-02450504.
 XX
 PR 20-DEC-2002; 2002US-0434779P.
 XX
 PA (KANB-) KANB BIOTEC INC.
 XX
 PI Wang X, Weibacher T, Romeo T, Suzuki K,
 PI WPI; 2004-481158/46.
 XX

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XX  Csrc polynucleotide, used in reducing the symptoms of a bacterial
PT  infection by biofilm producing bacteria in a mammalian patient.
XX
XX  Example; SEQ ID NO 11; 57pp; English.
XX
CC  The present sequence is that of PCR primer Diserb for the csrc gene
CC  AD07696 of Baccherichia coli strain K-12. Diserb was used with primer
CC  D1cheet1 AD076916 in an example from the invention for the construction
CC  of a csrc null mutant. Csrc interacts with the RNA-binding protein CsrcA,
CC  and antagonizes the regulatory effects of CsrcA. The invention relates to
CC  the csrc gene and RNA, and methods of using these to modulate biofilm
CC  formation. A claimed method of altering the metabolism or structural or
CC  functional properties of a bacterial cell comprises altering the genetic
CC  expression of csrc or the Csrc binding activity of csrc. A result of
CC  altered genetic expression of csrc may be a change in glycogen
CC  biosynthesis or gluconeogenesis. A claimed method of reducing biofilm
CC  formation involves decreasing csrc transcription in a biofilm-forming
CC  cell. A claimed method of inhibiting motility of biofilm-producing
CC  bacteria comprises increasing csrc expression. A claimed method of
CC  reducing the symptoms of a bacterial infection by biofilm-producing
CC  bacteria in a mammalian patient involves administering an antibacterial
CC  agent and decreasing biofilm formation through modulation of csrc.
XX
XX  Sequence 23 BP; 5 A; 2 C; 9 G; 7 T; 0 U; 0 Other;
XX
Query Match          9.8%; Score 13; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  33  CTGCGTGAAGTTTG 45
    |||||
Db  2  CTGCGTGAAGTTTG 14
XX
RESULT 29
ID  AAA29645/c
XX  AAA29645 standard; DNA; 24 BP.
XX
AC  AAA29645;
XX
DT  11-AUG-2000 (first entry)
XX
DE  Hybrid toxin construction adapter #1.
XX
KW  Half-length hybrid toxin; quarter-length hybrid toxin; pesticide;
KW  Bacillus thuringiensis HD-73; Diphtheria toxin; fusion protein; chimeric;
KW  insecticide; adapter; ds.
XX
OS  Bacillus thuringiensis.
OS  Corynebacterium diphtheriae.
OS  Synthetic.
OS  Chimeric.
XX
XX  US6051556-A.
XX
XX  18-APR-2000.
XX
XX  10-MAY-1995; 95US-00438465.
XX
XX  28-APR-1988; 88US-00187167.
XX  30-NOV-1992; 92US-00983344.
XX
XX  (MYCO ) MYCOGEN CORP.
XX
XX  Culver P, Schwab GE, Edwards DL, Wilcox ER, Thompson M;
XX  WPI; 2000-316974/27.
XX
XX  Increasing host range or toxicity of an insecticidal protein used as
XX  microbial insecticide by fusion of pesticidal toxin to a cytotoxic agent.
XX  Example 1; Col 11; 27pp; English.

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```

XX  A method has been developed of increasing the host range or toxicity of
CC  an insecticidal protein by delivering an insecticidal protein or protein
CC  domain to the gut epithelium of a target insect using a targeting protein
CC  capable of binding to the gut epithelium. Insecticidal and targeting
CC  protein do not both originate from Bacillus thuringiensis (B.t.). The
CC  hybrid proteins are used as insecticides. The hybrid proteins have
CC  increased toxicity against target pests. The present sequence represents
CC  an adapter sequence which is used in the construction of hybrid toxins in
CC  an example from the present invention
XX
XX  Sequence 24 BP; 3 A; 5 C; 8 G; 8 T; 0 U; 0 Other;
XX
Query Match          9.8%; Score 13; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  50  CCTGCATGCACAC 62
    |||||
Db  14  CCTGCATGCACAC 2
XX
RESULT 30
ID  AAA29653/c
XX  AAA29653 standard; DNA; 24 BP.
XX
AC  AAA29653;
XX
DT  11-AUG-2000 (first entry)
XX
DE  Hybrid toxin construction adapter #9.
XX
KW  Half-length hybrid toxin; quarter-length hybrid toxin; pesticide;
KW  Bacillus thuringiensis HD-73; Diphtheria toxin; fusion protein; chimeric;
KW  insecticide; adapter; ds.
XX
OS  Bacillus thuringiensis.
OS  Corynebacterium diphtheriae.
OS  Synthetic.
OS  Chimeric.
XX
XX  US6051556-A.
XX
XX  18-APR-2000.
XX
XX  10-MAY-1995; 95US-00438465.
XX
XX  28-APR-1988; 88US-00187167.
XX  30-NOV-1992; 92US-00983344.
XX
XX  (MYCO ) MYCOGEN CORP.
XX
XX  Culver P, Schwab GE, Edwards DL, Wilcox ER, Thompson M;
XX  WPI; 2000-316974/27.
XX
XX  Increasing host range or toxicity of an insecticidal protein used as
XX  microbial insecticide by fusion of pesticidal toxin to a cytotoxic agent.
XX  Example 2; Col 13; 27pp; English.
XX
CC  A method has been developed of increasing the host range or toxicity of
CC  an insecticidal protein by delivering an insecticidal protein or protein
CC  domain to the gut epithelium of a target insect using a targeting protein
CC  capable of binding to the gut epithelium. Insecticidal and targeting
CC  protein do not both originate from Bacillus thuringiensis (B.t.). The
CC  hybrid proteins are used as insecticides. The hybrid proteins have
CC  increased toxicity against target pests. The present sequence represents
CC  an adapter sequence which is used in the construction of hybrid toxins in
CC  an example from the present invention
XX
XX  Sequence 24 BP; 3 A; 6 C; 9 G; 6 T; 0 U; 0 Other;
XX

```

Query Match 9.8%; Score 13; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

50 CCTGCATGCACAC 62
 |||||
 14 CCTGCATGCACAC 2

RESULT 31
 AAS11903/c
 ID AAS11903 standard; DNA; 24 Bp.

AC AAS11903;
 DT 07-NOV-2001 (first entry)

DE DNA encoding Diphtheria toxin B-chain/B.t toxin HD-73 fusion junction #3.
 XX Hybrid toxin; B.t toxin; diphtheria toxin; cytosstatic; pesticide;
 KW Insecticide; ds.

OS Corynebacterium diphtheriae.
 OS Bacillus thuringiensis serovar kurstaki; HD73.
 OS Synthetic.
 OS Chimeric.

XX Location/Qualifiers

FT 1..24
 CDS /*tag= a
 /product= "Fusion protein junction #3"
 /partial
 /note= "No stop or start codon"

XX US2001014469-A1.

XX 16-AUG-2001.

XX 26-JAN-2000; 2000US-00491320.

XX 28-APR-1988; 88US-00187167.

XX 30-NOV-1992; 92US-00983344.

XX 10-MAY-1995; 95US-00438465.

XX (WILC/) WILCOX E R.
 XX (EDWA/) EDWARDS D L.
 XX (SCHW/) SCHWAB G E.
 XX (THOM/) THOMPSON M.
 XX (CULV/) CULVER P.

XX WILCOX ER, Edwards DL, Schwab GE, Thompson M, Culver P,

XX WPI; 2001-529105/58.

XX P-PSDB; AAU07529.

XX Novel hybrid pesticidal toxin useful as insecticide, comprises cytotoxic
 PT agent, preferably diphtheria toxin and pest gut epithelial cell
 PT recognition portion of protein linked by a peptide linker.

XX Example 2; Page 7; 28pp; English.

XX The invention relates to a hybrid pesticidal protein toxin comprising a
 CC cytotoxic agent and a pest gut epithelial cell recognition portion of a
 CC protein, where the cytotoxic agent and the recognition portion are not
 CC naturally contiguous. The hybrid toxin is expressed by the gene fragment
 CC from B.thuringiensis (B.t) var. kurstaki HD-73 which is transformed into
 CC a suitable host for use as an insecticide. Expression of the toxin gene
 CC results, directly or indirectly in the intracellular production and
 CC maintenance of the pesticide. The microbe hosting the toxin gene can be
 CC treated under conditions that prolong the activity of the toxin produced
 CC in the cell and the treated cell can then be applied to the environment
 CC of target pest(s). The resulting product retains the toxicity of the B.t
 CC toxin. The present sequence encodes the amino acid sequence of the

CC junction between diphtheria toxin B chain His 484 and B.t HD-73 Arg 258.
 CC in a fusion protein between these two proteins. The fusion protein is the
 CC "quarter-length" hybrid toxin, Diphtheria toxin B chain 484/B.t HD-73 Ala
 CC 450-Glu 613
 XX

50 CCTGCATGCACAC 62
 |||||
 14 CCTGCATGCACAC 2

Query Match 9.8%; Score 13; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

50 CCTGCATGCACAC 62
 |||||
 14 CCTGCATGCACAC 2

RESULT 32
 AAS11899/c
 ID AAS11899 standard; DNA; 24 Bp.

AC AAS11899;
 DT 07-NOV-2001 (first entry)

DE DNA encoding Diphtheria toxin B-chain/B.t toxin HD-73 fusion junction #1.
 XX Hybrid toxin; B.t toxin; diphtheria toxin; cytosstatic; pesticide;
 KW Insecticide; ds.

OS Corynebacterium diphtheriae.
 OS Bacillus thuringiensis serovar kurstaki; HD73.
 OS Synthetic.
 OS Chimeric.

XX Location/Qualifiers

FT 1..24
 CDS /*tag= a
 /product= "Fusion protein junction #1"
 /partial
 /note= "No start or stop codons"

XX US2001014469-A1.

XX 16-AUG-2001.

XX 26-JAN-2000; 2000US-00491320.

XX 28-APR-1988; 88US-00187167.

XX 30-NOV-1992; 92US-00983344.

XX 10-MAY-1995; 95US-00438465.

XX (WILC/) WILCOX E R.
 XX (EDWA/) EDWARDS D L.
 XX (SCHW/) SCHWAB G E.
 XX (THOM/) THOMPSON M.
 XX (CULV/) CULVER P.

XX WILCOX ER, Edwards DL, Schwab GE, Thompson M, Culver P,

XX WPI; 2001-529105/58.

XX P-PSDB; AAU07529.

XX Novel hybrid pesticidal toxin useful as insecticide, comprises cytotoxic
 PT agent, preferably diphtheria toxin and pest gut epithelial cell
 PT recognition portion of protein linked by a peptide linker.

XX Example 1; Page 6; 28pp; English.

XX The invention relates to a hybrid pesticidal protein toxin comprising a
 CC cytotoxic agent and a pest gut epithelial cell recognition portion of a
 CC protein, where the cytotoxic agent and the recognition portion are not
 CC naturally contiguous. The hybrid toxin is expressed by the gene fragment
 CC from B.thuringiensis (B.t) var. kurstaki HD-73 which is transformed into

CC a suitable host for use as an insecticide. Expression of the toxin gene
CC results, directly or indirectly in the intracellular production and
CC maintenance of the pesticide. The microbe hosting the toxin gene can be
CC treated under conditions that prolong the activity of the toxin produced
CC in the cell and the treated cell can then be applied to the environment
CC of target pest(s). The resulting product retains the toxicity of the B.t
CC toxin. The present sequence encodes the amino acid sequence of the B.t
CC junction between diptheria toxin B chain His 484 and B.t Hd-73 Cys 10,
CC in a fusion protein between these two proteins
CC
XX
SQ Sequence 24 BP; 3 A; 5 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 9.8%; Score 13; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 CCTGCATGCACAC 62
Db 14 CCTGCATGCACAC 2

RESULT 33
AB075751/c
ID AB075751 standard; DNA; 25 BP.
XX
AC AB075751;
XX
DT 12-NOV-2002 (first entry)
XX
DE Cloning vector DNA construction related PCR primer lacMCR-R.
XX
KM Cloning vector; molecular cloning; molecular biology; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO20026658-A2.
XX
PD 29-AUG-2002.
XX
PF 20-FEB-2002; 2002WO-CA000215.
XX
PR 22-FEB-2001; 2001CA-02335412.
XX
PA (BIOS-) BIO S & T.
XX
PI Cat Q, Idu J;
XX
DR WPI; 2002-674951/72.
XX
PT Modified cloning vector with a system for direct selection of
PT recombinants through activation of the antibiotic resistance gene, useful
PT for molecular DNA cloning for use in molecular biology.
XX
PS Example 2; Page 21; 46pp; English.
XX
CC The present invention represents a vector (1) for cloning a DNA molecule
CC comprising a ColEI replication origin, a lacI repressor gene, a lac
CC operon-amp^r cassette (lac-ABR operon), or an fl origin, all in the same
CC orientation. Also described is a vector for cloning a DNA molecule
CC comprising: (a) a TAC promoter sequence; (b) a T7 primer sequence; (c) a
CC transcription terminator sequence; (d) a sequence for an operon with an
CC antibiotic resistance marker (ABR); (e) a repressor sequence coding for an
CC inhibitor that is capable of regulating the operon of (d); and (f) a
CC cloning site comprising at least one restriction enzyme site within the
CC repressor sequence that does not change the amino acid sequence of the
CC inhibitor, where the structural genes of the operon are replaced by at
CC least one antibiotic resistance marker and are linked in an upstream
CC manner to the ColEI sequence in the reverse orientation, and where the
CC repressor sequence is operatively linked to the TAC promoter sequence and
CC between them the T7 primer is introduced for the purpose of sequencing
CC from a forward orientation. Methods and compositions from the present
CC invention can be used for molecular cloning and for use in molecular
CC biology. The present sequence represents a PCR primer which is used in an

CC example from the present invention
XX
SQ Sequence 25 BP; 5 A; 6 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 9.8%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 GCCCTGCATGCAC 60
Db 14 GCCCTGCATGCAC 2

RESULT 34
AC142579
ID AC142579 standard; DNA; 25 BP.
XX
AC AC142579;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 42570.
XX
KM EST; ss; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; diallelic marker; polymorphism; human,
KM cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Miltmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 42570; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

AAK19285
ID AAK19285 standard; DNA; 28 BP.
XX
AC AAK19285;
XX
DT 17-MAY-1999 (first entry)
XX
DE HIV-1 gag PCR primer Gag3'.
XX
KW HIV-1; LTR; long terminal repeat; human immunodeficiency virus;
KW lentiviral vector; gene therapy; replication-competent virus; anaemia;
KW diabetes; viral infection; cancer; immune response; autoimmune disease;
KW vaccine; PCR primer; ss.
XX
OS Synthetic.
OS Human immunodeficiency virus 1.
XX
PN WO9904026-A2.
XX
PD 28-JAN-1999.
XX
PF 20-JUL-1998; 98WO-US014996.
XX
PR 18-JUL-1997; 97US-0053066P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chen S, Gasmel M, Yee JK, Jolly DJ;
XX
DR WPI; 1999-132267/11.
XX
PT New lentiviral vector and related expression cassettes, and packaging
PT cells - useful in gene therapy, can be produced free of replication-
PT competent virus.
XX
PS Example 2; Page 60; 83pp; English.
XX
CC The present invention describes a lentiviral vector (A) comprising a 5'-
CC lentiviral long terminal repeat (LTR), RNA binding site, packaging
CC signal, promoter linked to at least one gene of interest (I), and an
CC origin of second strand DNA synthesis and a 3'-lentiviral LTR. It
CC includes a nuclear transport element (NTE) that is not an RRE (Rev
CC responsive element). The vectors are used in gene therapy to express a
CC wide range of (I) products including, e.g. antibodies, immunogens,
CC toxins, antisense sequences, hormones, and enzymes, for the treatment of
CC e.g. anaemia, diabetes, viral, other infections, and cancer. It is also
CC used in vaccines to generate an immune response or for treating
CC autoimmune diseases by down regulating such a response. The vectors may
CC also be used to produce the expression products of (I), particularly in
CC insect cell cultures. The present sequence represents a PCR primer which
CC is used in an example from the present invention
XX
SQ Sequence 28 BP; 7 A; 8 C; 8 G; 5 T; 0 U; 0 Other;
XX
Query Match 9.8%; Score 13; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 48 GCCCTGCATGCAC 60
DB 14 GCCCTGCATGCAC 26
XX
RESULT 38
ABK51801
ID ABK51801 standard; DNA; 28 BP.
XX
AC ABK51801;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human UGT1 gene region 560-587.
XX

KW Human; enzyme classification; enzyme quantitative determination;
KW glucuronic acid conjugation; UDP-glucuronosyltransferase; UGT1; ds.
XX
OS Homo sapiens.
XX
PN JP2002085066-A.
XX
PD 26-MAR-2002.
XX
PF 07-SEP-2000; 2000JP-00272228.
XX
PR 07-SEP-2000; 2000JP-00272228.
XX
PA (SAKA) OTSUKA SEIYAKU KOGYO KK.
XX
DR WPI; 2002-378271/41.
XX
PT Determination of enzymes participating in glucuronic acid conjugation in
PT human being, comprises use of oligonucleotide probes.
XX
PS Claim 4; Page 9; 13pp; Japanese.
XX
CC The present invention relates to a method for classification and
CC quantitative determination of enzymes participating in glucuronic acid
CC conjugation. The method involves the use of oligonucleotide probes
CC hybridising to regions of the human UDP-glucuronosyltransferase (UGT)
CC genes (e.g. UGT1, UGT1A7, UGT1A9, UGT1A10, UGT2A1, UGT2B7, UGT2B10,
CC UGT2B11, UGT2B15, UGT2B17, UGT8), and the DOST gene. The method and
CC probes are useful for the genetic determination of enzymes participating
CC in glucuronic acid conjugation with catalysed UGT. The method is both
CC rapid and accurate. ABK51801-ABK51812 represent regions of the human UGT
CC or DOST genes
XX
SQ Sequence 28 BP; 5 A; 10 C; 5 G; 8 T; 0 U; 0 Other;
XX
Query Match 9.8%; Score 13; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 104 CCTGTGTCTCTAC 116
DB 2 CCTGTGTCTCTAC 14
XX
RESULT 39
AAV21245/C
ID AAV21245 standard; DNA; 29 BP.
XX
AC AAV21245;
XX
DT 25-MAR-2003 (revised)
DT 03-AUG-1998 (first entry)
XX
DE Homo sapiens clone CC365_40 probe.
XX
KW secreted protein; human; probe; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9807859-A2.
XX
PD 26-FEB-1998.
XX
PF 22-AUG-1997; 97WO-US014874.
XX
PR 23-AUG-1996; 96US-00702344.
XX
PA (GEMV) GENETICS INST INC.
XX
PI Merberg D, McCoy JM, Lavallie ER, Racine LA, Treacy M;
PI Spaulding V, Jacobs K;
XX

DR WPI; 1998-169163/15.

XX New nucleic acid encoding secreted proteins from human cells - useful

PT e.g. as immuno-modulators, antitumour agents, promoters of tissue growth,

PT haemostatic and thrombolytic agents etc.

XX

PS Disclosure; Page 66; 79pp; English.

XX

CC The sequence is that of a probe used in the isolation of clone CC365_40.

CC (updated on 25-MAR-2003 to correct PI field.)

CC

XX

Sequence 29 BP; 7 A; 8 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 9.8%; Score 13; DB 2; Length 29;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CAGCCTGCATGC 58

DB 25 CAGCCTGCATGC 13

RESULT 40

AA77337/C

ID AA77337 standard; DNA; 29 BP.

XX

AC AA77337;

XX

DT 04-AUG-1999 (first entry)

XX

DE Human secreted protein DNA isolating probe.

XX

KW Secreted protein; retina; brain; blood; testis; nutritional activity;

KW cell proliferation; differentiation; immune stimulation; human; probe;

KW hematopoiesis regulation; tissue growth; chemotactic; thrombolytic;

KW anti-inflammatory; tumour invasion suppression; gene therapy; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN W09926973-A1.

XX

PD 03-JUN-1999.

XX

PF 20-NOV-1998; 98MO-US024944.

XX

PR 21-NOV-1997; 97US-00976112.

PR 19-NOV-1998; 98US-00196027.

XX

PA (GENMY) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Spaulding V,

XX

DR WPI; 1999-357814/30.

XX

PT New polynucleotides encoding secreted human proteins.

PS

XX Disclosure; Page 100; 106pp; English.

XX

CC The invention relates to human secreted proteins (AA721588-597) encoded

CC by polynucleotides obtained from adult retina, adult brain, adult blood

CC or adult testes cDNA libraries. The nucleic acid sequences encoding the

CC secreted proteins correspond to clones AY421-2, BV278-2, C344-1, CC332-

CC 33, CC365-40, C68-4, D329-1, H698-2 and H963-20, (all clones are

CC deposited as ATCC 98145). The PNs and proteins are predicted to have

CC biological activities which would make them suitable for treating,

CC preventing or ameliorating medical conditions in humans and animals,

CC although no supporting data is given. Suggested activities include

CC nutritional activity, cytokine and cell proliferation/differentiation

CC activity, immune stimulating (e.g. as vaccines) or suppressing activity,

CC hematopoiesis regulating activity, tissue growth activity, activin/

CC inhibin activity, chemotactic/chemokinetic activity, hemostatic and

CC thrombolytic activity, receptor/ligand activity, anti-inflammatory

CC activity, cadherin/tumour invasion suppressor activity and tumor

CC inhibition activity. The PNs are also stated to be useful for gene

CC therapy

XX

Sequence 29 BP; 7 A; 8 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 9.8%; Score 13; DB 2; Length 29;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CAGCCTGCATGC 58

DB 25 CAGCCTGCATGC 13

RESULT 41

ADC38944/C

ID ADC38944 standard; DNA; 29 BP.

XX

AC ADC38944;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human secreted protein cDNA oligonucleotide probe #86.

XX

KW ss; probe; immune disorder; severe combined immunodeficiency; SCID;

KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;

KW rheumatoid arthritis; allergic reaction; asthma; myeloid cell deficiency;

KW lymphoid cell deficiency; osteoporosis; osteoarthritis;

KW peripheral nervous system disease; peripheral neuropathy;

KW Alzheimer's disease; Parkinson's disease; coagulation disorder;

KW inflammatory disease; systemic inflammatory response syndrome; SIRS;

KW ischemia-reperfusion injury; Crohn's disease; anaphylaxis;

KW hypersensitivity; regeneration; neural cell proliferation; fertility;

KW tumour; chemokine; human; secreted protein.

XX

OS Homo sapiens.

XX

PN US2002193567-A1.

XX

PD 19-DEC-2002.

XX

PF 02-APR-2002; 2002US-00114893.

XX

PR 11-AUG-1995; 95US-00514014.

PR 05-APR-1996; 96US-00628364.

PR 19-APR-1996; 96US-00635311.

PR 07-JUN-1996; 96US-00659224.

PR 17-JUN-1996; 96US-00664596.

PR 09-JUL-1996; 96US-00677231.

PR 26-JUL-1996; 96US-00686878.

PR 23-AUG-1996; 96US-00701819.

PR 27-SEP-1996; 96US-00721488.

PR 27-SEP-1996; 96US-00721798.

PR 27-SEP-1996; 96US-00721923.

PR 27-SEP-1996; 96US-00721926.

PR 25-OCT-1996; 96US-00738367.

PR 30-OCT-1996; 96US-00739775.

PR 13-JAN-1997; 97US-00783395.

PR 10-APR-1997; 97US-00833823.

PR 02-JUN-1997; 97US-00866677.

PR 05-SEP-1997; 97US-00924838.

PR 06-OCT-1997; 99US-00413232.

XX

PA (GENMY) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Bowman WR, Spaulding V, Carlin-Duckett M,

PI Kelleher K;

XX

DR WPI; 2003-657236/62.

PT Proteins A23021 encoded by clone A23021 from human adult colon, and
PT BD12716 encoded by clone BD12716 from human fetal kidney cDNA library,
XX useful for treating e.g. multiple sclerosis and rheumatoid arthritis.
PS
XX Disclosure; SEQ ID NO 302; 412pp; English.
XX
CC The invention relates to a protein comprising fully defined A2302 1
CC protein or BD127 1 6 protein. The polynucleotides are useful for
CC expressing recombinant proteins for analysis and are also useful as
CC chromosome markers or tags to identify chromosomes or to map related gene
CC positions. The proteins are useful as amino acid supplement, carbon
CC source, nitrogen source and carbohydrate source. The proteins are useful
CC for treating various immune deficiencies and disorders (e.g. severe
CC combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis), allergic
CC reactions (e.g. asthma), myeloid or lymphoid cell deficiencies,
CC osteoporosis or osteoarthritis, peripheral nervous system diseases (e.g.
CC peripheral neuropathy, Alzheimer's disease, Parkinson's disease),
CC coagulation disorders, inflammatory diseases (e.g. systemic inflammatory
CC response syndrome (SIRS), ischaemia-reperfusion injury, Crohn's disease),
CC anaphylaxis and hypersensitivity. Proteins are also useful for inducing
CC tumour immunity, for inducing bone, cartilage, tendon, ligament and/or
CC nerve growth or regeneration, for proliferating neural cells and for
CC regenerating nerve and brain tissue, for inducing fertility and for
CC inhibiting tumour growth. Proteins are also useful as chemokine for
CC mammalian cells (e.g., monocytes, fibroblasts, neutrophils), and also
CC useful as inhibitors of receptor/ligand interactions. The present
CC sequence represents a oligonucleotide probe for a cDNA encoding a human
CC secreted protein.
XX
SQ Sequence 29 BP; 7 A; 8 C; 8 G; 5 T; 0 U; 1 Other;
XX
Query Match 9.8%; Score 13; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 46 CAGCCCTGCATGC 58
Db 25 CAGCCCTGCATGC 13
XX
RESULT 42
ADH69868/c
ID ADH69868 standard; DNA; 15 BP.
XX
AC
XX ADH69868;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta genes Intron 1 3' splice site #8.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosomiasis;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
XX Homo sapiens.
XX OS
XX US2002150891-A1.
XX PV
XX 17-OCT-2002.
XX PD
XX 05-MAR-1999; 99US-00263959.
XX PF
XX 19-SEP-1994; 94US-00309335.
XX PR

PR 19-SEP-1995; 95US-00531241.
XX
XX (HOOD/J) HOOD L E.
XX PA (ROME/J) ROMEN L.
XX
XX Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
XX Kit for diagnosing and treating T-cell associated diseases e.g.
XX autoimmune, degenerative nervous system and infectious disease, comprises
XX nucleic acid primers specifically priming and allowing amplification of a
XX Vbeta gene.
XX
PS Disclosure; SEQ ID NO 62; 164pp; English.
XX
XX The invention relates to a kit for diagnosing and treating T-cell
XX associated diseases which comprises a panel of nucleic acid primers
XX specifically priming and allowing amplification of each Vbeta gene,
XX VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
XX rejection and diagnosing and treating T-cell associated diseases
XX including autoimmune diseases, degenerative nervous system diseases,
XX graft versus host disease, hypersensitivity diseases, infectious diseases
XX and neoplastic diseases. Autoimmune diseases include Addison's disease,
XX atrophic gastritis. Degenerative nervous system diseases include multiple
XX sclerosis and Alzheimer's disease. Hypersensitivity diseases include type
XX I hypersensitivities such as contact with allergens that lead to
XX allergies, type II hypersensitivities such as those present in
XX Goodpasture's syndrome and type IV hypersensitivities such as those
XX manifested in leprosy. Infectious diseases include viral infections
XX caused by viruses such as HIV, fungal infections such as those caused by
XX the yeast genus Candida, parasitic infections such as those caused by
XX schistosomes, filaria and bacterial infections such as those caused by
XX Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
XX such as leukemias, lymphomas and cancers such as cancer of the brain.
XX breast. The present sequence represents a Vbeta gene intron splice site.
XX
SQ Sequence 15 BP; 6 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
XX
Query Match 9.1%; Score 12; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 103 TCCTGTGTCTCT 114
Db 14 TCCTGTGTCTCT 3
XX
RESULT 43
ABN02189/c
ID ABN02189 standard; DNA; 17 BP.
XX
XX ABN02189;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMMP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2181.
XX
KW Human; genome-derived myosin-like protein 1; GDMMP-1; hGDMMP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX OS
XX WO200192524-A2.
XX PN
XX 06-DEC-2001.
XX PD
XX 25-MAY-2001; 2001WO-US016981.
XX PF
XX 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX PR

PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PA (AEOM-) AEOMICA INC.
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
DR
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption/ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 2181; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognize hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionization, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CCAGAGACTGCT 26
Db 17 CCAGAGACTGCT 6
XX
RESULT 44
ABN02191/c
ID ABN02191 standard; DNA; 17 BP.
XX
AC ABN02191;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2183.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX

OS Homo sapiens.
XX
XX WO200192524-A2.
PN
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
PA (AEOM-) AEOMICA INC.
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
DR
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption/ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 2183; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognize hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionization, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 4 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CCAGAGACTGCT 26
Db 15 CCAGAGACTGCT 4
XX
RESULT 45
ABN02194/c
ID ABN02194 standard; DNA; 17 BP.

XX AC ABN02194;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2186.
XX KM Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX OS skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN W0200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US016981.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX DR WPI; 2002-179446/23.
XX PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
XX PT or as specific biomolecule capture probes for surface-enhanced laser
XX PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX PS Disclosure; SEQ ID NO 2186; 214pp; English.
XX PS
XX CC The present invention describes a human genome-derived myosin-like
XX CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
XX CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
XX CC nucleic acids can be used as probes to detect, characterise and quantify
XX CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
XX CC provide initial substrates for the recombinant engineering of hGDMLP-1
XX CC protein variants having desired phenotypic improvements, and for
XX CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
XX CC used as immunogens to raise antibodies that specifically recognise hGDMLP
XX CC -1 proteins, as standards in assays used to determine the concentration
XX CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
XX CC capture probes for surface-enhanced laser desorption ionisation, as
XX CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
XX CC production, and in vaccines or for replacement therapy. The
XX CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
XX CC disorder associated with the expression of hGDMLP-1, in particular heart
XX CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
XX CC The present sequence represents an oligomer used in the screening of the
XX CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
XX CC The sequence data for this patent did not form part of the printed
XX CC at ftp.wipo.int/pub/published_pct_sequence

Query Match 9.1%, Score 12; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CCAGAGCTGCT 26
DB 12 CCAGAGCTGCT 1
RESULT 46
ID ABN02193/c
ID ABN02193 standard; DNA; 17 BP.
XX AC ABN02193;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2185.
XX KM Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX OS skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN W0200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US016981.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX DR WPI; 2002-179446/23.
XX PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
XX PT or as specific biomolecule capture probes for surface-enhanced laser
XX PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX PS Disclosure; SEQ ID NO 2185; 214pp; English.
XX PS
XX CC The present invention describes a human genome-derived myosin-like
XX CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
XX CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
XX CC nucleic acids can be used as probes to detect, characterise and quantify
XX CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
XX CC provide initial substrates for the recombinant engineering of hGDMLP-1
XX CC protein variants having desired phenotypic improvements, and for
XX CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
XX CC used as immunogens to raise antibodies that specifically recognise hGDMLP
XX CC -1 proteins, as standards in assays used to determine the concentration
XX CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
XX CC capture probes for surface-enhanced laser desorption ionisation, as
XX CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
XX CC production, and in vaccines or for replacement therapy. The
XX CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a

disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence

Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 CCAGGAGCTGCT 26
13 CCAGGAGCTGCT 2

RESULT 47
ABN02190/C
ID ABN02190 standard; DNA; 17 BP.
AC ABN02190;
XX
XX 29-MAY-2002 (first entry)
DT
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2182.
XX
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KM skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX 30-JAN-2001; 2001WO-US000661.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 05-FEB-2001; 2001US-0266860P.
XX
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
XX
XX or as specific biomolecule capture probes for surface-enhanced laser
XX
XX desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX
XX Disclosure; SEQ ID NO 2182; 214pp; English.

The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify

hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption/ionization, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence

Sequence 17 BP; 3 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 CCAGGAGCTGCT 26
16 CCAGGAGCTGCT 5

RESULT 48
ABN02192/C
ID ABN02192 standard; DNA; 17 BP.
AC ABN02192;
XX
XX 29-MAY-2002 (first entry)
DT
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2184.
XX
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KM skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX 30-JAN-2001; 2001WO-US000661.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 05-FEB-2001; 2001US-0266860P.
XX
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX

```
XX New polypeptide, for raising antibodies that recognize hGDMRP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMRP-1.  
PS Disclosure; SEQ ID NO 2184; 214pp; English.  
XX  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMRP-1). The protein and polynucleotide sequences of hGDMRP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMRP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMRP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMRP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMRP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMRP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMRP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMRP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMRP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMRP-1, in particular heart  
CC and skeletal muscle disorders. hGDMRP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMRP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIFO  
CC at ftp.wifo.int/pub/published_pct_sequence  
XX  
SQ Sequence 17 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 0 Other;  
Query Match 9.1%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.1e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 15 CCAGGACCTGCT 26  
Db 14 CCAGGACCTGCT 3  
RESULT 49  
ABK56932/c  
ID ABK56932 standard; RNA; 17 BP.  
XX  
AC ABK56932;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Human CLCA1 gene enzymatic nucleic acid #1303.  
XX  
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW acetylcysteine.  
XX  
KM  
XX Homo sapiens.  
XX OS  
XX PN WO200211674-A2.  
XX PD 14-FEB-2002.  
XX PF 09-AUG-2001; 2001WO-US024970.  
XX PR 09-AUG-2000; 2000US-0224383P.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PA (SYNT ) SYNTX USA LLC.  
XX PA (THOM/) THOMPSON J.  
XX  
PI Thompson J, Mcswigen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grupe A;
```

```
XX  
DR WPI: 2002-217145/27.  
XX  
PT Enzymatic polynucleotide that down regulates expression of chloride  
PT channel calcium activated gene, useful for treating Chronic obstructive  
PT pulmonary disease (COPD), chronic bronchitis and asthma.  
PS Claim 4; Page 86; 152pp; English.  
XX  
XX  
CC The invention relates to enzymatic nucleic acid molecules that down  
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic  
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of CLCA1 in a cell or  
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of CLCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of CLCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention  
XX  
SQ Sequence 17 BP; 2 A; 9 C; 2 G; 0 T; 4 U; 0 Other;  
Query Match 9.1%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.1e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 89 GGATGAGCGCT 100  
Db 17 GGATGAGCGCT 6  
RESULT 50  
ABK56535/c  
ID ABK56535 standard; RNA; 17 BP.  
XX  
AC ABK56535;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Human CLCA1 gene enzymatic nucleic acid #906.  
XX  
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW acetylcysteine.  
XX  
KM  
XX Homo sapiens.  
XX OS  
XX PN WO200211674-A2.  
XX PD 14-FEB-2002.  
XX PF 09-AUG-2001; 2001WO-US024970.  
XX PR 09-AUG-2000; 2000US-0224383P.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PA (SYNT ) SYNTX USA LLC.  
XX PA (THOM/) THOMPSON J.  
XX  
PI Thompson J, Mcswigen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grupe A;  
XX WPI: 2002-217145/27.
```

PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS Claim 4, Page 73, 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 17 BP, 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;
XX
Query Match 9.1%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86 GCTGGATGAGC 97
DB 12 GCTGGATGAGC 1
XX
RESULT 51
ABT37731/c
ID ABT37731 standard; DNA; 17 BP.
XX
AC ABT37731;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 3368.
XX
XX Cytostatic; virocidic; neuroprotective; nootropic; neuroleptic; gene chip;
XX anti-sense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophtenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-1B004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
PS Disclosure; Page 427, 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,

CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophtenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP, 5 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
XX
Query Match 9.1%; Score 12; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 84 GGGCTGGATGGA 95
DB 14 GGGCTGGATGGA 3
XX
RESULT 52
ABZ65160
ID ABZ65160 standard; RNA; 17 BP.
XX
AC ABZ65160;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HER2 DNAzyme substrate #617.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-02994140P.
XX
PR 06-JUN-2001; 2001US-0296249P.
XX
PR 10-SEP-2001; 2001US-03184771P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI McSwiggen J;
XX
DR WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 4, Page 144, 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates

CC	expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras
CC	human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC	acid molecule of the invention has cytosolic, anti-HIV, and anti-
CC	rheumatic activity. The nucleic acid molecules are useful for reducing
CC	HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC	also useful for treating breast, ovarian, colorectal, lung, prostate,
CC	bladder, or pancreatic cancer, and HIV infection, AIDS. The sequence
CC	shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC	ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX	ribozymes of the invention
SQ	Sequence 17 BP; 4 A; 5 C; 5 G; 0 T; 3 U; 0 Other;
OY	
Query Match	9.1%; Score 12; DB 8; Length 17;
Best Local Similarity	83.3%; Pred. No. 4.1e+04;
Matches 10; Conservative	2; Mismatches 0; Indels 0; Gaps
Db	
16 CAGGACCTGCTG 27	
:: :	
1 CAGGACCTGCTG 12	
RESULT 53	
ACD63405/c	
ID ACD63405 standard; RNA; 17 BP.	
AC ACD63405;	
XX	
DT 30-SEP-2003 (first entry)	
XX	
DE HCV minus strand DNAzyme substrate sequence #1044.	
XX	
Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;	
KW RNA stability; RNA expression; RNA synthesis; antisense;	
KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinozyme;	
KW amberzyme; G-clavier ribozyme; decoy molecule; aptamer;	
KW HBV reverse transcriptase; Enhancer I region; viral replication;	
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;	
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;	
viucide; antiinflammatory; substrate; ss.	
XX	
Hepatitis C virus.	
XX	
WO20281494-A1.	
XX	
17-OCT-2002.	
XX	
PF 26-MAR-2002; 2002MO-US009187.	
XX	
PR 26-MAR-2001; 2001US-00817879.	
PR 08-JUN-2001; 2001US-00877478.	
PR 08-JUN-2001; 2001US-0296876P.	
PR 24-OCT-2001; 2001US-0335059P.	
PR 05-DEC-2001; 2001US-0337055P.	
XX	
(RIBO-) RIBOZYME PHARM INC.	
PA (BLAT/) BLATT L.	
PA (MACE/) MACEJAK D.	
PA (MCSS/) MORRISGEN J.	
PA (MORR/) MORRISSEY D.	
PA (PAVC/) PAVCO P.	
PA (LEBP/) LEE P.	
PA (DRAP/) DRAPER K.	
PA (ROBE/) ROBERTS E.	
XX	
P1 Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P;	
P1 Draper K, Roberts E;	
XX	
DR WPI, 2003-229207/22.	
XX	
PT Novel compound useful for treating cirrhosis, liver failure,	
PT hepatocellular carcinoma, or condition associated with hepatitis C virus	
PT infection.	

XX Claim 1; Page 293; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
XX inozymes, zincymes, amberzymes, and G-cleaver ribozymes. Also disclosed
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX as oligonucleotides that specifically bind the Enhancer I region of HBV
XX DNA. The nucleic acids may be used to modulate the expression of HBV
XX genes and HBV viral replication. Also disclosed is a method for screening
XX compounds and/or potential therapies directed against HBV, and compounds
XX that modulate the expression and/or replication of HCV. The compounds and
XX methods of the invention are useful for the treatment of degenerative and
XX diseases states related to HBV and HCV infection, replication and gene
XX expression such as cirrhosis, liver failure, and hepatocellular
XX carcinoma. The present sequence represents a substrate for one of the HCV
XX DNzyme or minus strand DNzyme sequences disclosed in the present
XX invention

SQ Sequence 17 BP; 3 A; 3 C; 8 G; 0 T; 3 U; 0 Other;

QY Query Match 9.1%; Score 12; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 TCTGCGAGACC 22
|||||||
13 TCTGCGAGACC 2

RESULT 54
ACDS59264
ACDS59264 standard; RNA; 17 BP.

AC ACD59264;
AC ACD59264;
DT 24-SEP-2003 (first entry)

XX HCV DNzyme substrate sequence #1234.

DE HCV DNzyme substrate sequence #1234.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zincyme;
XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virocid; antiinflammatory; substrate; ss.

OS Hepatitis C virus.
XX
XX
XX WO200281494-A1.
XX
XX 17-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009187.
XX
XX 26-MAR-2001; 2001US-00817879.
XX
XX 08-JUN-2001; 2001US-00877478.
XX
XX 08-JUN-2001; 2001US-0296876P.
XX
XX 24-OCT-2001; 2001US-0335059P.
XX
XX 05-DEC-2001; 2001US-0337055P.
XX
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT) BLATT L.
XX (MAGE) MAGEJAK D.
XX (MCSW) MCSWIGEN J.
XX (MORR) MORRISSEY D.
XX (PAVC) PAVCO P.
XX (LEBP) LEE P.

PA (DRAPE/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blact L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Claim 1; Page 256; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinczymes, amberyzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNazyme or minus strand DNazyme sequences disclosed in the present
CC invention
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 0 T; 3 U; 0 Other;
Query Match 9.1%; Score 12; DB 8; Length 17;
Best Local Similarity 83.3%; Pred. No. 4.1e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 11 TCTGCCGAGACC 22
Db 6 UCUGCCAGGACC 17
RESULT 55
ADM11727/c
ID ADM11727 standard; DNA; 17 BP.
XX
AC ADM11727;
XX
DT 20-MAY-2004 (first entry)
XX
DE Amplification method, PCR primer #144.
XX
XX PCR; ss; forensic; paternity testing; disease diagnosis; library; primer.
XX
OS Homo sapiens.
XX
PN US2003207282-A1.
XX
PD 06-NOV-2003.
XX
PF 11-JUN-2002; 2002US-00167634.
XX
PR 24-APR-2002; 2002US-00132067.
XX
PA (LALA-) LOS ALAMOS NAT LAB.
XX
XX Bradbury AM, Zeytun A;
XX
PI WPI; 2003-901051/82.
XX
DR
XX
PT Preparing an amplified product that is free of amplification primer

PT sequences, useful for detecting pathogens, comprises amplifying a target
PT nucleic acid sequence and cleaving the amplified product with restriction
PT enzymes.
XX
PS Example 4; Page 20; 25pp; English.
XX
CC The invention relates to a method of preparing an amplified product that
CC is free of amplification primer sequences comprising amplifying the
CC target nucleic acid sequence in an amplification reaction, and cleaving
CC the amplified product with first and second restriction enzymes to obtain
CC the amplified product that is free of amplification primer sequences.
CC Also included is a method of preparing a library, comprising performing
CC the steps of preparing an amplified product that is free of amplification
CC primer sequences and then linking the amplified product to a library
CC vehicle. In the above methods, at least one restriction enzyme cleaves at
CC 2 sites at a distance from its recognition site. At least one restriction
CC enzyme recognition site is a palindromic sequence or a non-palindromic
CC sequence, or is an interrupted sequence. The target polynucleotide
CC sequence comprises an antibody variable region or an antibody
CC hypervariable region. The first and second primers specifically hybridize
CC to the region encoding an antibody framework region. In preparing a
CC library, the library vehicle comprises a cloning vector, particularly a
CC phage display vector, a bacterial vector or a yeast vector.
CC Alternatively, the library vehicle comprises a nucleic acid that encodes
CC an enzyme, a heterologous protein, a green fluorescent protein (GFP)
CC scaffold or a coat protein. The library vehicle comprises an
CC oligonucleotide joined to puromycin. In addition, the library vehicle
CC comprises a ribosome. The step of linking the amplified product comprises
CC ligating an adaptor oligonucleotide to the amplified product to form a
CC linked amplified product, and amplifying the linked ligated product. The
CC method is useful in amplifying target sequences without including regions
CC flanking the target sequence in the amplified product or imposing primer
CC sequences on the amplified product. The method may be used for detecting
CC human pathogens, detecting human genetic polymorphisms, detecting RNA and
CC DNA sequences, for molecular cloning, sequencing of nucleic acids, in
CC forensics, paternity testing, and disease diagnosis. The present sequence
CC represents a PCR primer used to demonstrate the method of the invention.
XX
SQ Sequence 17 BP; 4 A; 7 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 9.1%; Score 12; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 68 GCGCGGCTTGCT 79
Db 14 GCGCGGCTTGCT 3
RESULT 56
ADK94931/c
ID ADK94931 standard; DNA; 17 BP.
XX
AC ADK94931;
XX
DT 06-MAY-2004 (first entry)
XX
DE Primer of the invention #651.
XX
XX human; single nucleotide polymorphism; SNP; ss; primer.
XX
XX Synthetic.
XX
PN JP2003259875-A.
XX
PD 16-SEP-2003.
XX
PF 08-MAR-2002; 2002JP-00064373.
XX
PR 08-MAR-2002; 2002JP-00064373.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX

DR WPI; 2004-093977/10.
XX
PT Novel polynucleotide useful for PCR amplification along with two DNA
PT fragment from another set of sequences, or for detecting single
PT nucleotide polymorphism in human gene.
XX
PS Claim 2; SEQ ID NO 3960; 2627pp; Japanese.
XX
CC The present invention relates to a polynucleotide isolated from a human
CC gene and is useful for detecting a single nucleotide polymorphism in a
CC human gene or for diagnosing of disease. The invention enables the
CC detection of a single nucleotide polymorphism in a human gene. The
CC present sequence represents a primer of the invention.
XX
SQ Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 9.1%; Score 12; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 GCCAGGACCTGC 25
12 GCCAGGACCTGC 1
Db

RESULT 57
AD186075/c
ID AD186075 standard; RNA; 17 BP.
XX
AC AD186075;
XX
DT 03-JUN-2004 (first entry)
XX
DE HCV DNAzyme substrate sequence #3321.
XX
KM ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KM HCV infection; type I interferon; DNAzyme.
XX
OS Hepatitis C virus.
XX
PN US2003125270-A1.
XX
PD 03-JUL-2003.
XX
PE 18-DEC-2000; 2000US-00740332.
XX
PR 18-DEC-2000; 2000US-00740332.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J.
PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P. A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswigen J, Roberts E, Pavco PA, Macejack D;
XX
DR WPI; 2004-031273/03.
XX
PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX
PS Claim 1; SEQ ID NO 3321; 198pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNAzyme substrate
CC sequence.
XX

SQ Sequence 17 BP; 3 A; 3 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 9.1%; Score 12; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 TCTGCCAGGACC 22
13 TCTGCCAGGACC 2
Db

RESULT 58
AD183988
ID AD183988 standard; RNA; 17 BP.
XX
AC AD183988;
XX
DT 03-JUN-2004 (first entry)
XX
DE HCV DNAzyme substrate sequence #1234.
XX
KM ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KM HCV infection; type I interferon; DNAzyme.
XX
OS Hepatitis C virus.
XX
PN US2003125270-A1.
XX
PD 03-JUL-2003.
XX
PE 18-DEC-2000; 2000US-00740332.
XX
PR 18-DEC-2000; 2000US-00740332.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J.
PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P. A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswigen J, Roberts E, Pavco PA, Macejack D;
XX
DR WPI; 2004-031273/03.
XX
PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX
PS Claim 1; SEQ ID NO 1234; 198pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNAzyme substrate
CC sequence.
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 9.1%; Score 12; DB 12; Length 17;
Best Local Similarity 83.3%; Pred. No. 4.1e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 11 TCTGCCAGGACC 22
6 UUCGCCAGGACC 17
Db

RESULT 59
AA295457/c
ID AA295457 standard; cDNA; 18 BP.

```
XX AC AA295457;
XX DT 01-JUN-2000 (first entry)
XX DE TEIL random binding site selection oligonucleotide #75.
XX KM Tobacco; ethylene insensitive 3; TEIL; transcription factor; plant;
XX KM regulation; ethylene inducible gene; environmental stress; resistance;
XX OS ss.
XX OS Nicotiana tabacum.
XX PN MO200009712-A1.
XX PD 24-FEB-2000.
XX PF 06-MAY-1999; 99WO-JP002347.
XX PR 11-AUG-1998; 98JP-00227448.
XX PA (NORO) NAT INST AGRONOMIC RESOURCES MIN.
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PI Ohashi Y, Kosugi S;
XX DR WPI; 2000-206011/18.
XX PT Transcription factor regulating the expression of ethylene-inducible
XX PT genes and encoding it, useful for imparting resistance to
XX PT environmental stress to plants.
XX PS Example 3; Fig 5; 65pp; Japanese.
XX CC The present invention describes a transcription factor regulating the
XX CC expression of ethylene-inducible genes in plants, having DNA binding
XX CC activity specific to the consensus sequence A(T/C)G(A/T)A(C/T)CT. The
XX CC present invention describes the tobacco ethylene insensitive 3 (EIN3)-
XX CC like protein, designated TEIL, isolated from Nicotiana tabacum cv Samsun
XX CC NM. The transcription factor is used to impart environmental stress
XX CC resistance to plants by transformation with the gene for the
XX CC transcription factor, and screening potential inhibitors of the
XX CC expression of ethylene-inducible genes in plants. AA29533 to AA29546
XX CC represent oligonucleotides used in the exemplification of the present
XX CC invention
XX SQ Sequence 18 BP; 3 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 9.1%; Score 12; DB 3; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+04;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 52 TGCATGCACAG 63
XX Db 14 TGCATGCACAG 3
XX
XX RESULT 60
XX AAF75988/C
XX ID AAF75988 standard; DNA; 18 BP.
XX AC AAF75988;
XX DT 22-MAY-2001 (first entry)
XX DE Human frizzled family gene 584 PCR primer, SEQ ID NO:18.
XX KM Human; frizzled family gene 584; embryo; fetus; cancer; drug discovery;
XX KM cytoskeletal; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200112808-A1.
```

```
XX PD 22-FEB-2001.
XX PF 18-AUG-2000; 2000WO-JP005552.
XX PR 18-AUG-1999; 99JP-00232018.
XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX PI Senoo C, Numata M;
XX DR WPI; 2001-211220/21.
XX PT Novel frizzled family genes 584 strongly expressed in embryo and fetus as
XX PT well as in cancer cells, useful in drug development for diseases with
XX PT abnormal expression including tumor.
XX PS Example 5; Page 47-48; 89pp; Japanese.
XX CC The invention relates to a novel frizzled family gene, 584, from mouse
XX CC and human (CDNAs given in AAF75973 and AAF75974), and to the mouse and
XX CC human 584 proteins (AA75307, AA75308). Gene 584 is strongly expressed
XX CC in the embryo and fetus, and is also strongly expressed in cancer cells.
XX CC The invention also relates to recombinant vectors and host cells
XX CC comprising gene 584 nucleic acids, the recombinant expression of the 584
XX CC protein, methods of screening for modulators of 584 activity or
XX CC expression, and the compounds thus identified. The human and mouse 584
XX CC genes represent a novel gene target for the development of drugs useful
XX CC in the treatment of diseases such as cancer. The present sequence
XX CC represents a PCR primer used in the isolation of human gene 584 cDNA
XX SQ Sequence 18 BP; 4 A; 7 C; 7 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 9.1%; Score 12; DB 4; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+04;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 119 GCCGCTGTCGG 130
XX Db 16 GCCGCTGTCGG 5
XX
XX RESULT 61
XX ADK97335/C
XX ID ADK97335 standard; DNA; 18 BP.
XX AC ADK97335;
XX DT 06-MAY-2004 (first entry)
XX DE Primer of the invention #3055.
XX KM human; single nucleotide polymorphism; SNP; ss; primer.
XX KM Synthetic.
XX OS JP2003259875-A.
XX PN JP2003259875-A.
XX PD 16-SEP-2003.
XX PF 08-MAR-2002; 2002JP-00064373.
XX PR 08-MAR-2002; 2002JP-00064373.
XX PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX DR WPI; 2004-093977/10.
XX PT Novel polynucleotide useful for PCR amplification along with two DNA
XX PT fragment from another set of sequences, or for detecting single
XX PT nucleotide polymorphism in human gene.
XX PS Claim 2; SEQ ID NO 6364; 2627pp; Japanese.
```

XX The present invention relates to a polynucleotide isolated from a human
 CC gene and is useful for detecting a single nucleotide polymorphism in a
 CC human gene or for diagnosing of disease. The invention enables the
 CC detection of a single nucleotide polymorphism in a human gene. The
 CC present sequence represents a primer of the invention.

XX Sequence 18 BP; 5 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 9.1%; Score 12; DB 12; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.1e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 GAGTTTGAGCC 50

Db 18 GAGTTTGAGCC 7

RESULT 62

ADL95352/C

ID ADL95352 standard; DNA; 18 BP.

AC ADL95352;

DT 03-JUN-2004 (first entry)

DE Rat P2X3 antisense oligonucleotide SEQ ID NO:1.

XX neurological disorder; double-stranded RNA; dsRNA;

KW target gene inhibition; P2X3 inhibition; chronic pain; analgesic;

KM gene therapy; cancer pain; osteoarthritis pain; allodynia; hyperalgesia;

KM rat; antisense oligonucleotide; phosphorothioate; ss.

XX Rattus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base

FT 1. .18

FT /*tag= a

FT /mod_base= OTHER

FT /note= "phosphorothioate linkages"

FT 10. .18

FT modified_base

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-O-(2-methoxyethyl) ribonucleotide, where C =

FT 2'-O-(2-methoxyethyl) 5-methyl cytidine and T = 2'-O-(2-

FT methoxyethyl) 5-methyl uridine"

FT modified_base

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-O-(2-methoxyethyl) ribonucleotide, where C =

FT 2'-O-(2-methoxyethyl) 5-methyl cytidine and T = 2'-O-(2-

FT methoxyethyl) 5-methyl uridine"

FT modified_base

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-O-(2-methoxyethyl) ribonucleotide, where C =

FT 2'-O-(2-methoxyethyl) 5-methyl cytidine and T = 2'-O-(2-

FT methoxyethyl) 5-methyl uridine"

FT modified_base

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-O-(2-methoxyethyl) ribonucleotide, where C =

FT 2'-O-(2-methoxyethyl) 5-methyl cytidine and T = 2'-O-(2-

FT methoxyethyl) 5-methyl uridine"

FT modified_base

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-O-(2-methoxyethyl) ribonucleotide, where C =

FT 2'-O-(2-methoxyethyl) 5-methyl cytidine and T = 2'-O-(2-

FT methoxyethyl) 5-methyl uridine"

CC -stranded (ds) RNA that inhibits the expression of a target gene. Also
 CC described is a pharmaceutical composition comprising a dsRNA inhibiting
 CC the expression of P2X3 or P2X2 for treating chronic pain. The dsRNA that
 CC inhibits the expression of a target gene has analgesic activity, and can
 CC be used in gene therapy. The method is useful for treating or
 CC ameliorating chronic pain, e.g., cancer pain, osteoarthritis pain,
 CC allodynia or hyperalgesia. The present sequence represents a rat P2X3
 CC antisense oligonucleotide, which is used in the exemplification of the
 CC present invention.

XX Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 9.1%; Score 12; DB 12; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.1e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GGCTGATGGAG 96

Db 12 GGCTGATGGAG 1

RESULT 63

ADL95356/C

ID ADL95356 standard; DNA; 18 BP.

AC ADL95356;

DT 03-JUN-2004 (first entry)

DE Rat P2X3 antisense oligonucleotide SEQ ID NO:5.

XX neurological disorder; double-stranded RNA; dsRNA;

KW target gene inhibition; P2X3 inhibition; chronic pain; analgesic;

KM gene therapy; cancer pain; osteoarthritis pain; allodynia; hyperalgesia;

KM rat; antisense oligonucleotide; ss.

XX Rattus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base

FT 1. .5

FT /*tag= a

FT /mod_base= OTHER

FT /note= "2'-O-(2-methoxyethyl) ribonucleotide, where C =

FT 2'-O-(2-methoxyethyl) 5-methyl cytidine and T = 2'-O-(2-

FT methoxyethyl) 5-methyl uridine"

FT 14. .18

FT modified_base

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-O-(2-methoxyethyl) ribonucleotide, where C =

FT 2'-O-(2-methoxyethyl) 5-methyl cytidine and T = 2'-O-(2-

FT methoxyethyl) 5-methyl uridine"

FT modified_base

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-O-(2-methoxyethyl) ribonucleotide, where C =

FT 2'-O-(2-methoxyethyl) 5-methyl cytidine and T = 2'-O-(2-

FT methoxyethyl) 5-methyl uridine"

FT modified_base

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-O-(2-methoxyethyl) ribonucleotide, where C =

FT 2'-O-(2-methoxyethyl) 5-methyl cytidine and T = 2'-O-(2-

FT methoxyethyl) 5-methyl uridine"

FT modified_base

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-O-(2-methoxyethyl) ribonucleotide, where C =

FT 2'-O-(2-methoxyethyl) 5-methyl cytidine and T = 2'-O-(2-

FT methoxyethyl) 5-methyl uridine"

FT modified_base

XX Example, SEQ ID NO 5, 42bp, English.
 PS
 XX The present invention describes a method for treating or ameliorating
 CC neurological disorders, which comprises injecting into a subject a double
 CC -stranded (ds) RNA that inhibits the expression of a target gene. Also
 CC described is a pharmaceutical composition comprising a dsRNA inhibiting
 CC the expression of P2X3 or P2X2 for treating chronic pain. The dsRNA that
 CC inhibits the expression of a target gene has analgesic activity, and can
 CC be used in gene therapy. The method is useful for treating or
 CC ameliorating chronic pain, e.g., cancer pain, osteoarthritis pain,
 CC allodynia or hyperalgesia. The present sequence represents a rat P2X3
 CC antisense oligonucleotide, which is used in the exemplification of the
 CC present invention.
 CC
 SQ Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 9.1%; Score 12; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.1e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 85 GGCTGATGGAG 96
 |||||
 12 GGCTGATGGAG 1
 Db
 RESULT 64
 AAQ47546
 ID AAQ47546 standard; cDNA to mRNA, 19 BP.
 XX
 AC AAQ47546;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-JAN-1994 (first entry)
 XX
 DE Rat G8 RATBPCTPD/Go-1397 Go specific probe.
 XX
 KW Probe: quantification; human; GTP binding protein; G protein;
 KW alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
 KW pathophysiology; disease state; hereditary; cancer; infectious;
 KW osteodystrophy; pituitary tumour; acromegaly; melanoma cells; diabetes;
 KW PCR; polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN WO9315221-A1.
 XX
 PD 05-AUG-1993.
 XX
 PF 29-JAN-1993; 93MO-US000977.
 XX
 PR 29-JAN-1992; 92US-00827208.
 PR 24-MAR-1992; 92US-00857059.
 PR 12-NOV-1992; 92US-00974409.
 XX
 PA (HITB) HITACHI CHEM CO LTD.
 PA (HITB) HITACHI CHEM RES CENT INC.
 XX
 PI Akitaya T, Cooper A, Mitsuhashi M;
 XX
 DR WPI, 1993-258695/32.
 XX
 PT Quantitating messenger RNA in sample - using immobilised-polynucleotide
 PT having sequence complementary to sequence unique to the mRNA.
 XX
 XX Example 6; Page 55; 177pp; English.
 CC The sequences given in AAQ47539-50 are probes which were used in the
 CC quantification of human GTP binding protein (G protein)-specific mRNAs.
 CC These probes are based on sequences derived from human and rat G-
 CC proteins. These probes were used in the method of the invention for the
 CC detection and quantification of mRNAs in a sample without the need to
 CC purify the mRNA from cells. The claimed method comprises identifying a

CC polynucleotide sequence unique to the mRNA, and immobilising an oligomer
 CC complementary to this sequence to an insoluble support. The sample is
 CC then incubated with the bound oligomer such that the unique sequence
 CC will hybridise to the bound oligomer and be immobilised. Non-immobilised
 CC components are washed from the support and bound RNA is labelled in such
 CC a way that the label is incorporated onto the support relative to the
 CC amount of mRNA on the support. The amount of bound label is then
 CC determined. This method can be used for the reliable, rapid, simultaneous
 CC quantification of multiple varieties of mRNA. It may be used for
 CC diagnosing and recognition of pathophysiology of various disease states,
 CC eg. hereditary diseases, cancer, and infectious diseases. A genetic
 CC thought to be involved in causing various disease states. A genetic
 CC deficiency of Gs protein is the molecular basis of hereditary
 CC osteodystrophy. Pituitary tumours in acromegaly patients have been shown
 CC to contain mutant Gs proteins. G proteins are also involved in invasive
 CC and metastatic melanoma cells, and diabetes. See also AAQ47361-666.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 9.1%; Score 12; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.1e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 CCAGGACCTGCT 26
 |||||
 6 CCAGGACCTGCT 17
 Db
 RESULT 65
 AA17327
 ID AA17327 standard; DNA, 19 BP.
 XX
 AC AA17327;
 XX
 DT 02-JUN-1998 (first entry)
 XX
 DE Primer used in construction of antibody of the invention.
 XX
 KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
 KW cancer diagnosis; complementarity determining region; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9742329-A1.
 XX
 PD 13-NOV-1997.
 XX
 PF 29-APR-1997; 97WO-GB001165.
 XX
 PR 04-MAY-1996; 96GB-00009405.
 PR 14-FEB-1997; 97GB-00003103.
 XX
 PA (ZENB) ZENBICA LTD.
 XX
 PI Copley CG, Edge MD, Emery SC;
 XX
 DR WPI, 1997-558987/51.
 XX
 PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis
 PT and therapy of cancer.
 XX
 XX Example 48; Page 170; 208pp; English.
 CC This sequence is a primer that was used to construct the antibody of the
 CC invention. The antibody is an anti-CEA (carcinoembryonic antigen)
 CC antibody (806.077 Ab). Host cells or transgenic organisms transformed
 CC with DNA encoding the antibody, are used to make the antibody or
 CC conjugate. The conjugate is used in a medicament suitable for intravenous
 CC administration. The conjugate can be used for cancer therapy, selectively
 CC killing tumour cells. The antibody can be used for in vivo or in vitro
 CC diagnosis of cancer

SO Sequence 19 BP; 3 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 9.1%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GGACCTGCTGCA 29
DB 1 GGACCTGCTGCA 12

RESULT 66
AAV41791
ID AAV41791 standard; DNA; 19 BP.
AC AAV41791;
XX
XX 20-NOV-1998 (first entry)
XX
XX Human pancreatic carboxypeptidase B primer 677.
XX
XX ss; primer; PCR; amplification; human; pancreatic carboxypeptidase B;
XX insulin; protein sequencing; prodrug therapy.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9835988-A1.
XX
XX 20-AUG-1998.
XX
XX 10-FEB-1998; 98WO-GB000415.
XX
XX 14-FEB-1997; 97GB-00003104.
XX 18-OCT-1997; 97GB-00022003.
XX 29-OCT-1997; 97GB-00022727.
XX
XX (GENE) ZENECA LTD.
XX
XX Edge MD;
XX
XX WPI; 1998-467168/40.
XX
XX New modified pro-domain of carboxypeptidase B - enhances expression of
XX co-expressed proteins for production of recombinant carboxypeptidase or
XX its fusions with antibodies, used, e.g. in enzyme prodrug therapy.
XX
XX Example 1; Page 51; 83pp; English.
XX
XX The primers AAV41785-V41794 were used in the cloning of human pancreatic
XX carboxypeptidase B (CPB). The co-expression of a modified pro-domain of
XX CPB from a separate gene enhances recombinant expression. This process
XX can be used to produce recombinant CPB in eukaryotic cells, or fusions of
XX CPB with antibody chains. CPB is used in insulin production and protein
XX sequencing, while its fusions with antibody are useful in antibody-
XX directed enzyme prodrug therapy. The modified pro-domain provide
XX increased yields of recombinant CPB, possibly by protecting the C-
XX terminus against enzymatic degradation or by increasing intracellular
XX trafficking
XX
XX Sequence 19 BP; 3 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 9.1%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GGACCTGCTGCA 29
DB 1 GGACCTGCTGCA 12

RESULT 67
ADP84430

ID ADF84430 standard; RNA; 19 BP.
XX
XX ADF84430;
AC
XX 26-FEB-2004 (first entry)
XX
XX Human ABL1-targeted siRNA - SEQ ID 724.
XX
XX short interfering nucleic acid; siRNA; breakpoint cluster region;
XX v-abl Abelson murine leukaemia viral oncogene homologue 1; BCR-ABL;
XX cytosolic; leukaemia; lymphoma; human; ss; siRNA; ABL1.
XX
XX Homo sapiens.
XX
XX WO2003070972-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005234.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 06-JUN-2002; 2002US-0386782P.
XX 15-AUG-2002; 2002US-0404039P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409253P.
XX 14-JAN-2003; 2003US-0439222P.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Beigelman L, Chowrira B;
XX
XX WPI; 2003-679889/64.
XX
XX New double-stranded interfering nucleic acid, useful e.g. for treatment
XX and diagnosis of leukemia and lymphoma, downregulates the breakpoint
XX cluster region-Abelson (BCR-ABL) gene.
XX
XX Example 7; SEQ ID NO 724; 197pp; English.
XX
XX The invention relates to a novel double-stranded short interfering
XX nucleic acid (siNA) that downregulates expression of the breakpoint
XX cluster region-v-abl Abelson murine leukaemia viral oncogene homologue 1
XX (BCR-ABL) gene. The siRNA of the invention demonstrates cytostatic
XX activity and may be useful for modulating expression of the BCR-ABL gene,
XX as well as for treating leukemia or lymphoma and in diagnosis, drug
XX screening, target identification and validation, genetic engineering,
XX gene function studies and gene mapping. The current sequence is that of
XX the human ABL1-targeted siRNA of the invention.
XX
XX Sequence 19 BP; 3 A; 7 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 9.1%; Score 12; DB 10; Length 19;
Best Local Similarity 75.0%; Pred. No. 4.1e+04;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 59 ACACGTCCTGCG 70
DB 7 ACACGTCCTGCG 18

RESULT 68
ADP84749/C
ID ADF84749 standard; RNA; 19 BP.
XX
XX ADF84749;
AC
XX 26-FEB-2004 (first entry)
XX
XX Human ABL1-targeted siRNA - SEQ ID 1043.
XX

KM short interfering nucleic acid; siNA; breakpoint cluster region;
 KM v-abl Abelson murine leukaemia viral oncogene homologue 1; BCR-ABL;
 KM cytosolic; leukaemia; lymphoma; human; ss; siRNA; ABL1.
 XX
 OS Homo sapiens.
 XX
 PN MO2003070972-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 20-FEB-2003; 2003WO-US005234.
 XX
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 15-AUG-2002; 2002US-0404039P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 14-JAN-2003; 2003US-0439922P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcawiggen J, Belgelman L, Chowrira B;
 DR WPI; 2003-679889/64.
 XX
 PT New double-stranded interfering nucleic acid, useful e.g. for treatment
 PT and diagnosis of leukemia and lymphoma, downregulates the breakpoint
 PT cluster region-Abelson (BCR-ABL) gene.
 XX
 PS Example 7; SEQ ID NO 1043; 197pp; English.
 XX
 CC The invention relates to a novel double-stranded short interfering
 CC nucleic acid (siNA) that downregulates expression of the breakpoint
 CC cluster region-v-abl Abelson murine leukaemia viral oncogene homologue 1
 CC (BCR-ABL) gene. The siRNA of the invention demonstrates cytostatic
 CC activity and may be useful for modulating expression of the BCR-ABL gene,
 CC as well as for treating leukemia or lymphoma and in diagnosis, drug
 CC screening, target identification and validation, genetic engineering,
 CC gene function studies and gene mapping. The current sequence is that of
 CC the human ABL1-targeted siRNA of the invention.
 XX
 SQ Sequence 19 BP; 6 A; 3 C; 7 G; 0 T; 3 U; 0 Other;
 Query Match 9.1%; Score 12; DB 10; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.1e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 59 ACACGTTCTGCG 70
 DB 13 ACACGTTCTGCG 2
 XX
 RESULT 69
 AA205043/c
 ID AA205043 standard; DNA; 20 BP.
 XX
 AC AA205043;
 XX
 DT 07-OCT-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX
 KM Vaccine, eye disease; conventional trachoma; nongonococcal urethritis;
 KM paratrachoma; inclusion conjunctivitis; genital disease; perithenitis;
 KM nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KM Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
 XX
 OS Synthetic.
 OS Chlamydia trachomatis.
 XX

PN MO928475-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 27-NOV-1998; 98WO-IB001939.
 XX
 PR 28-NOV-1997; 97FR-00015041.
 PR 17-DEC-1997; 97FR-00016034.
 PR 04-NOV-1998; 98US-0107077P.
 XX
 PA (BEST) GENSET.
 XX
 PI Grifffais R;
 DR WPI; 1999-371125/31.
 XX
 PT Genome sequence of Chlamydia trachomatis.
 PS Disclosure; Page 1738; 1755pp; English.
 XX
 CC PCR primers AA201426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
 CC encode polypeptides (see AA36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
 CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conjunctivitis; genital diseases such as nongonococcal urethritis;
 CC epididymitis; cervicitis; salpingitis; perithenitis; Bartholinitis;
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
 CC The polypeptides of the invention may be of use in treating these
 CC diseases
 XX
 SQ Sequence 20 BP; 9 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 9.1%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.1e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 101 CGTCCCTGTGTC 112
 DB 20 CGTCCCTGTGTC 9
 XX
 RESULT 70
 AA95935/c
 ID AA95935 standard; DNA; 20 BP.
 XX
 AC AA95935;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX
 KM Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KM sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KM neutralising epitope; PCR primer; ss.
 XX
 OS Synthetic.
 OS Chlamydia pneumoniae.
 XX
 PN MO9927105-A2.
 XX
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-IB001890.
 PR 21-NOV-1997; 97FR-00014673.
 PR 04-NOV-1998; 98US-0107078P.
 XX
 PA (BEST) GENSET.
 XX
 PI Grifffais R;
 XX

```

XX  WPI; 1999-357842/30.
XX
XX  Genome sequence of Chlamydia pneumoniae.
XX
XX  Page 1787; Disclosure; 1912pp; English.
XX
CC  AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC  and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC  (see AAX91990). C. pneumoniae causes respiratory disease such as
CC  pneumonia and bronchitis and is thought to be a contributing factor in
CC  heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC  nodosum or pharyngitis. The polypeptides encoded by the open reading
CC  frames of the C. pneumoniae genome (see AAY34584 - AAY35879) can be used
CC  in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC  nucleic acid sequences can also be used as immunogenic compositions,
CC  especially where the vector directs the expression of a neutralising
CC  epitope of C. pneumoniae
XX
SQ  Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match          9.1%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5 GCATCATCTGCC 16
    |||||
Db  18 GCATCATCTGCC 7

RESULT 71
AAX95827
ID  AAX95827 standard; DNA; 20 BP.
XX
XX  AAX95827;
XX
XX  13-SEP-1999 (first entry)
XX
XX  PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
XX  Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX  sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
XX  neutralising epitope; PCR primer; ss.
XX
XX  Synthetic.
XX  Chlamydia pneumoniae.
XX
XX  WO9927105-A2.
XX
XX  03-JUN-1999.
XX
XX  20-NOV-1998; 98WO-IB001890.
XX
XX  21-NOV-1997; 97FR-00014673.
XX  04-NOV-1998; 98US-0107078P.
XX
XX  (GEST ) GENSET.
XX
XX  Griffiths R;
XX
XX  WPI; 1999-357842/30.
XX
XX  Genome sequence of Chlamydia pneumoniae.
XX
XX  Page 1778; Disclosure; 1912pp; English.
XX
XX  AAX91991-X97517 represent PCR primers used to amplify open reading frames
XX  and other nucleic acid sequences from the genome of Chlamydia pneumoniae
XX  (see AAX91990). C. pneumoniae causes respiratory disease such as
XX  pneumonia and bronchitis and is thought to be a contributing factor in
XX  heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
XX  nodosum or pharyngitis. The polypeptides encoded by the open reading
XX  frames of the C. pneumoniae genome (see AAY34584 - AAY35879) can be used
XX  in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
XX  nucleic acid sequences can also be used as immunogenic compositions,
XX  especially where the vector directs the expression of a neutralising
XX  epitope of C. pneumoniae

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CC  in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC  nucleic acid sequences can also be used as immunogenic compositions,
CC  especially where the vector directs the expression of a neutralising
CC  epitope of C. pneumoniae
XX
SQ  Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match          9.1%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  13 TGCCAGACCTG 24
    |||||
Db  5 TGCCAGACCTG 16

RESULT 72
AAC79573
ID  AAC79573 standard; DNA; 20 BP.
XX
XX  AAC79573;
XX
XX  07-FEB-2001 (first entry)
XX
XX  Human p38beta antisense oligonucleotide SEQ ID 98.
XX
XX  Antisense oligonucleotide; p38 mitogen activated protein kinase; MAPK;
XX  antirheumatic; antiarthritic; immunosuppressive; cardiac; heart disease;
XX  antiinflammatory; autoimmune disease; rheumatoid arthritis; apoptosis;
XX  phosphorothioate; ss.
XX
XX  Homo sapiens.
XX
XX  WO200059919-A1.
XX
XX  12-OCT-2000.
XX
XX  04-APR-2000; 2000WO-US008794.
XX
XX  06-APR-1999; 99US-00286904.
XX
XX  (ISIS-) ISIS PHARM INC.
XX
XX  Monia BP, Gaarde WA, Nero PS, McKay R, Popoff I;
XX
XX  WPI; 2000-664982/64.
XX
XX  Claim 19; Page 63; 90pp; English.
XX
XX  This invention relates to antisense compounds 8-30 nucleobases in length
XX  targeted to the 5'-untranslated region, translational start site,
XX  translational termination region or 3'-untranslated region of a nucleic
XX  acid encoding a p38 mitogen activated protein kinase (MAPK), where the
XX  antisense oligonucleotides inhibit the expression of MAPK. Sequences
XX  AAC79480 and AAC79501 represent human p38alpha MAPK and p38beta MAPK cDNA
XX  sequences. AAC79481 - AAC79500 and AAC79553 - AAC79570 represent human
XX  p38alpha antisense oligonucleotides, while AAC79502 - AAC79521 and
XX  AAC79571 - AAC79580 represent human p38beta antisense oligonucleotides.
XX  Also included in the invention are a p38alpha cDNA sequence AAC79523 and
XX  antisense oligonucleotides AAC79523 - AAC79536 isolated from rat tissue.
XX  Murine p38beta MAPK cDNA is represented in AAC79537 and antisense
XX  oligonucleotides targeting the sequence are given in AAC79538 - AAC79552.
XX  The antisense oligonucleotides have antirheumatic, antiarthritic,
XX  immunosuppressive, cardiac and antiinflammatory activity. The antisense
XX  oligonucleotides are useful for inhibiting the expression of p38 MAPK in
XX  cells or tissues. The oligonucleotides are used for treating an animal
XX  with diseases such as inflammatory or autoimmune diseases e.g. rheumatoid
XX  arthritis, or heart disease. The oligonucleotides are also useful for
XX  inhibiting inflammation or apoptosis

```


Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 CCAGGACCTGCT 26
|||||
Db 2 CCAGGACCTGCT 13

RESULT 75

ABK87895
ID ABK87895 standard; DNA, 20 BP.

XX
AC ABK87895;

XX
DT 07-OCT-2002 (first entry)

XX
DE Synthetic p38 beta antisense (AS) oligonucleotide.

XX G2/M checkpoint; genotoxic; p53-mediated apoptosis; cell division; MAPK;

KW p38 mitogen-activated protein kinase; tumour; cardiac; cytosolic;
KW modulator of p38-MAPK activity; inhibitor of apoptosis; beta antisense;

KW AS; ss.

XX
OS Synthetic.

XX
FN WO200238143-A2.

XX
PD 16-MAY-2002.

XX
PF 06-NOV-2001; 2001WO-US047669.

XX
PR 07-NOV-2000; 2000US-0246912P.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PI Bulavin DV, Fornace AJ;

XX
DR WPI; 2002-557439/59.

PT Interfering with G2/M checkpoint function in cells exposed to genotoxic
PT stress for treating tumors, by inhibiting p38 mitogen-activated protein
PT kinase activity in cell, thus interfering with G2/M checkpoint function.

XX
PS Example 13; Page 43; 80pp; English.

CC The present invention relates to a new method of interfering with G2/M

CC checkpoint function in cells exposed to a genotoxic stress thus

CC inhibiting p53-mediated apoptosis in a cell exposed to genotoxic stress.

CC The method of the invention involves inhibiting p38 mitogen-activated

CC protein kinase (MAPK) activity in the cell and thus interfering with G2/M

CC checkpoint (cell division) function. The invention can be used for

CC interfering with G2/M checkpoint function in cells (e.g. tumour, non

CC tumour or cardiac cells) exposed to a genotoxic stress, and thus

CC inhibiting p53-mediated apoptosis in a cell exposed to genotoxic stress.

CC The method of the invention can also be used for treating a tumour in a

CC subject and inhibiting p53-mediated apoptosis in a cell exposed to

CC genotoxic stress. The methods of the invention are suitable for enhancing

CC the efficacy and safety of genotoxic therapy. The present nucleic acid

CC sequence represents synthetic p38 beta antisense (AS) oligonucleotide

CC that was used in the methods of the invention for antisense suppression

CC of p38 MAPK expression in human cancer cells

CC
XX

SQ Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 9.1%; Score 12; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.1e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 ACGTTCTGCGCG 72
|||||
Db 3 ACGTTCTGCGCG 14

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SUMMARIES

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1	15	11.4	17	10	US-09-927-046-304 Sequence 304, App
2	15	11.4	17	10	US-09-927-046-304 Sequence 904, App
3	15	11.4	17	10	US-09-927-046-305 Sequence 905, App
4	14	10.6	17	10	US-09-927-046-303 Sequence 903, App
5	13	9.8	17	10	US-09-927-046-305 Sequence 305, App
6	13	9.8	17	15	US-10-163-552-616 Sequence 167, App
7	13	9.8	19	15	US-10-251-117-147 Sequence 147, App
8	13	9.8	19	15	US-10-251-117-396 Sequence 396, App
9	13	9.8	20	16	US-10-435-696-217 Sequence 217, App
10	13	9.8	20	16	US-10-092-900A-475 Sequence 475, App
11	13	9.8	20	16	US-10-092-900A-481 Sequence 481, App
12	13	9.8	20	16	US-10-333-108-26 Sequence 26, App

13	13	9.8	21	18	US-10-751-736-10681 Sequence 10681, A
14	13	9.8	21	18	US-10-751-736-10682 Sequence 10682, A
15	13	9.8	25	15	US-10-098-263B-42570 Sequence 42570, A
16	13	9.8	29	13	US-10-114-893-302 Sequence 302, App
17	12	9.1	15	9	US-09-263-959-62 Sequence 62, App
18	12	9.1	17	9	US-09-866-108-2181 Sequence 2181, App
19	12	9.1	17	9	US-09-866-108-2182 Sequence 2182, App
20	12	9.1	17	9	US-09-866-108-2183 Sequence 2183, App
21	12	9.1	17	9	US-09-866-108-2184 Sequence 2184, App
22	12	9.1	17	9	US-09-866-108-2185 Sequence 2185, App
23	12	9.1	17	10	US-09-866-108-2186 Sequence 2186, App
24	12	9.1	17	10	US-09-825-805-442 Sequence 442, App
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36	12	9.1	17	17	US-10-723-361-2183 Sequence 2183, App
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76	12	9.1	23	14	US-10-081-756-43 Sequence 43, App
77	12	9.1	23	14	US-10-092-771-56 Sequence 56, App
78	12	9.1	23	14	US-10-067-443-48 Sequence 48, App
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C 113 12 9.1 23 16 US-10-351-891-26
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C 137 12 9.1 25 9 US-09-866-108-5122
C 138 12 9.1 25 9 US-09-866-108-5123
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ALIGNMENTS

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Sequence 38, App
Sequence 62, App
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Publication No. US20030064946A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Thompson, Jim
APPLICANT: McKenzie, Tim
APPLICANT: Ayers, Dave
APPLICANT: Grupe, Andrew
APPLICANT: Szymkowski, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlor
FILE REFERENCE: 249/021
CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT FILING DATE: 2001-08-09
SOFTWARE: PatentIn version 3.0
SEQ ID NO 304
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-927-046-304
Query Match 11.4% Score 15; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 86 GCTGATGAGCGCT 100
Db 17 GCTGATGAGCGCT 3
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RESULT 2

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US-09-927-046-904/c
Sequence 904, Application US/09927046
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Publication No. US20030064946A1
GENERAL INFORMATION:
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```
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Thompson, Jim
APPLICANT: McKenzie, Tim
APPLICANT: Ayers, Dave
APPLICANT: Grupe, Andrew
APPLICANT: Szymkowski, Edmund
```

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TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlor
```

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TITLE OF INVENTION: Channel-1
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```
FILE REFERENCE: 249/021
```

```
CURRENT APPLICATION NUMBER: US/09/927,046
```

```
CURRENT FILING DATE: 2001-08-09
```

```
NUMBER OF SEQ. ID NOS: 5450
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SOFTWARE: PatentIn version 3.0
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```
SEQ ID NO 904
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```
LENGTH: 17
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TYPE: RNA
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ORGANISM: Homo sapiens
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US-09-927-046-904
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Query Match 11.4% Score 15; DB 10; Length 17;
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Best Local Similarity 100.0%; Pred. No. 4.7e+02;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 86 GCTGATGAGCGCT 100
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Db 16 GCTGATGAGCGCT 2
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RESULT 3
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US-09-927-046-905/c
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Sequence 905, Application US/09927046
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```
Publication No. US20030064946A1
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GENERAL INFORMATION:
```

```
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Thompson, Jim
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APPLICANT: Thompson, Jim
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APPLICANT: Thompson, Jim
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APPLICANT: Thompson, Jim
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APPLICANT: Thompson, Jim
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APPLICANT: Thompson, Jim
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APPLICANT: Thompson, Jim
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; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 905
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-905

Query Match      11.4%; Score 15; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      86 GCTGATGAGCGCT 100
DB      15 GCTGATGAGCGCT 1

RESULT 4
US-09-927-046-903/c
; Sequence 903, Application US/09927046
; Publication No. US20030064946a1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwigen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 903
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-903

Query Match      10.6%; Score 14; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      87 CTGATGAGCGCT 100
DB      17 CTGATGAGCGCT 4

RESULT 5
US-09-927-046-305/c
; Sequence 305, Application US/09927046
; Publication No. US20030064946a1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwigen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride
```

```

; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 305
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-305

Query Match      9.8%; Score 13; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      86 GCTGATGAGCG 98
DB      13 GCTGATGAGCG 1

RESULT 6
US-10-163-552-616
; Sequence 616, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
; FILE REFERENCE: MHB01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 616
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-163-552-616

Query Match      9.8%; Score 13; DB 15; Length 17;
Best Local Similarity 84.6%; Pred. No. 6e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      15 CCAGACCTGCTG 27
DB      4 CCAGACCTGCTG 16

RESULT 7
US-10-251-117-147
; Sequence 147, Application US/10251117
; Publication No. US20030170891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA interference mediated inhibition of Epidermal Growth Factor
; FILE REFERENCE: 900/042 (MHB02-468-A)
; CURRENT APPLICATION NUMBER: US/10/251,117
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 1213
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 147
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-251-117-147

Query Match
Best Local Similarity 9.8%; Score 13; DB 15; Length 19;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGAGCTGCTG 27
Db 3 CCAGAGCTGCTG 15

RESULT 8
US-10-251-117-396/C
; Sequence 396, Application US/10251117
; Publication No. US20030170891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
; FILE REFERENCE: 900/042 (MEB02-468-A)
; CURRENT APPLICATION NUMBER: US/10/251,117
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 1213
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 396
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-251-117-396

Query Match
Best Local Similarity 9.8%; Score 13; DB 15; Length 19;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGAGCTGCTG 27
Db 17 CCAGAGCTGCTG 5

RESULT 9
US-10-435-696-217
; Sequence 217, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
; APPLICANT: Wirtz, Ralph
; APPLICANT: Munnes, Marc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
; FILE REFERENCE: Ica 36 108
; CURRENT APPLICATION NUMBER: US/10/435,696
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: EP03003112.4
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; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: LOC51242 for
US-10-435-696-217

Query Match
Best Local Similarity 9.8%; Score 13; DB 16; Length 20;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GTCCCTGTGCTCT 114
Db 4 GTCCCTGTGCTCT 16

RESULT 10
US-10-092-900A-475
; Sequence 475, Application US/10092900A
; Publication No. US2004004382A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Maralichara
; APPLICANT: Splek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patlurajan, Meera
; APPLICANT: Gangolli, Bsha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Lette, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US2004004382A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/325,681
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; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 475
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-092-900A-475

Query Match          9.8%; Score 13; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      102 GTCCCTGTGTCCT 114
Db      5 GTCCCTGTGTCCT 17

RESULT 11
US-10-092-900A-481
; Sequence 481, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zernhusen, Bryan D.
; APPLICANT: Gusev, Vladimyr Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Paturajan, Meera
; APPLICANT: Gangoli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Saaba
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Caeman, Stacie J.
; APPLICANT: Malyanekar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Hailong
; APPLICANT: Algebrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
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; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 481
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-092-900A-481

Query Match          9.8%; Score 13; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      102 GTCCCTGTGTCCT 114
Db      5 GTCCCTGTGTCCT 17

RESULT 12
US-10-333-108-26/c
; Sequence 26, Application US/10333108
; Publication No. US20040076968A1
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; APPLICANT: Acuna, Gonzalo
; APPLICANT: Foerzler, Dorothee
; APPLICANT: Leong, Diane U.
; TITLE OF INVENTION: Method for Detecting Pre-Disposition to
; FILE REFERENCE: 22140-1026
; CURRENT APPLICATION NUMBER: US/10/333,108
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/07524
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: EP 00115353.5
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-333-108-26

Query Match          9.8%; Score 13; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      104 CCCTGTGTCCTAC 116
Db      17 CCCTGTGTCCTAC 5

RESULT 13
US-10-751-736-10681/c
; Sequence 10681, Application US/10751736
; Publication No. US20040265230A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Martinez, Robert
/ APPLICANT: Brown, Eugene
/ APPLICANT: Liu, Wei
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
/ FILE REFERENCE: AM100927 (031896-002000)
/ CURRENT APPLICATION NUMBER: US/10/751,736
/ PRIOR FILING DATE: 2003-01-06
/ PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
/ PRIOR FILING DATE: 2003-01-06
/ NUMBER OF SEQ ID NOS: 54873
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 10681
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: homo sapiens
US-10-751-736-10681
```

```
Query Match          9.8%; Score 13; DB 18; Length 21;
Best Local Similarity 100.0%; Pred.No. 5.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      13 TGCCAGGACCTGC 25
Db      16 TGCCAGGACCTGC 4
```

```
RESULT 14
US-10-751-736-10682/c
/ Sequence 10682, Application US/10751736
/ Publication No. US20040255230A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Martinez, Robert
/ APPLICANT: Brown, Eugene
/ APPLICANT: Liu, Wei
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
/ FILE REFERENCE: AM100927 (031896-002000)
/ CURRENT APPLICATION NUMBER: US/10/751,736
/ PRIOR FILING DATE: 2003-01-06
/ PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
/ PRIOR FILING DATE: 2003-01-06
/ NUMBER OF SEQ ID NOS: 54873
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 10682
/ LENGTH: 21
/ TYPE: RNA
/ ORGANISM: RNAi
US-10-751-736-10682
```

```
Query Match          9.8%; Score 13; DB 18; Length 21;
Best Local Similarity 100.0%; Pred.No. 5.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 TGCCAGGACCTGC 25
Db      14 TGCCAGGACCTGC 2
```

```
RESULT 15
US-10-098-263B-42570
/ Sequence 42570, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
```

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/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 42570
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-42570
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Query Match          9.8%; Score 13; DB 15; Length 25;
Best Local Similarity 100.0%; Pred.No. 5.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      106 CTGTGCTCCTACT 118
Db      9  CTGTGCTCCTACT 21
```

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RESULT 16
US-10-114-893-302/c
/ Sequence 302, Application US/10114893
/ Publication No. US20020193567A1
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: McCoy, John M.
/ APPLICANT: Lavallee, Edward R.
/ APPLICANT: Collins-Racie, Lisa A.
/ APPLICANT: Evans, Cheryl
/ APPLICANT: Werberg, David
/ APPLICANT: Treacy, Maurice
/ APPLICANT: Bowman, Michael R.
/ APPLICANT: Spaulding, Vikki
/ APPLICANT: Carlin-Duckett, McKeough
/ APPLICANT: Kelleher, Kerry S.
/ TITLE OF INVENTION: SECRETED PROTEINS AND POLYPEPTIDES ENCODING THEM
/ FILE REFERENCE: GI 6000-10A
/ CURRENT APPLICATION NUMBER: US/10/114,893
/ EARLIER APPLICATION NUMBER: 09/413,232
/ PRIOR FILING DATE: 1999-10-06
/ NUMBER OF SEQ ID NOS: 321
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 302
/ LENGTH: 29
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: oligonucleotide
/ NAME/KEY: misc_feature
/ LOCATION: (2)
/ OTHER INFORMATION: biotinylated phosphoramidite residue
US-10-114-893-302
```

```
Query Match          9.8%; Score 13; DB 13; Length 29;
Best Local Similarity 100.0%; Pred.No. 5.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      46 CAGCCCTGCATGC 58
Db      25 CAGCCCTGCATGC 13
```

```
RESULT 17
US-09-263-959-62/c
/ Sequence 62, Application US/09263959
/ Patent No. US20020150891A1
/ GENERAL INFORMATION:
/ APPLICANT: Hood, Leroy E.
/ APPLICANT: Rowen, Lee
/ APPLICANT: Koop, Ben F.
/ TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
```


NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaesters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-62

Query Match 9.1%; Score 12; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 TCCTGTGTCT 114
Db 14 TCCTGTGTCT 3

RESULT 18
US-09-866-108-2181/c
Sequence 2181, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2181
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-2181

Query Match 9.1%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 CCAGGACCTGCT 26
Db 17 CCAGGACCTGCT 6

RESULT 19
US-09-866-108-2182/c
Sequence 2182, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2182
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-2182

Query Match 9.1%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACTGCT 26
DB 16 CCAGGACTGCT 5

RESULT 20
US-09-866-108-2183/c
Sequence 2183, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2183
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens

US-09-866-108-2183

Query Match 9.1%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACTGCT 26
DB 15 CCAGGACTGCT 4

RESULT 21
US-09-866-108-2184/c
Sequence 2184, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2184
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-2184

Query Match 9.1%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACTGCT 26
DB 14 CCAGGACTGCT 3

RESULT 22

```
US-09-866-108-2185/c
; Sequence 2185, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2185
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2185
```

```
Query Match          9.1%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      15 CCAGAGCTGCT 26
Db      13 CCAGAGCTGCT 2
```

RESULT 23

```
US-09-866-108-2186/c
; Sequence 2186, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
```

```
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
```

```
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2186
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2186
```

```
Query Match          9.1%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      15 CCAGAGCTGCT 26
Db      12 CCAGAGCTGCT 1
```

RESULT 24

```
US-09-825-805-442
; Sequence 442, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpelsky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Swedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MBH00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
```

```

1 Prior Filing Date: 1999-12-30
2 Prior Application Number: 09/474,432
3 Prior Filing Date: 1999-12-29
4 Prior Application Number: 09/301,511
5 Prior Filing Date: 1999-04-28
6 Prior Application Number: 09/186,675
7 Prior Filing Date: 1998-11-04
8 Prior Application Number: 60/083,727
9 Prior Filing Date: 1998-04-29
10 Prior Application Number: 60/064,866
11 Prior Filing Date: 1997-11-05
12 Number of SEQ ID NOS: 1558
13 SOFTWARE: PatentIn version 3.0
14 SEQ ID NO: 442
15
16 LENGTH: 17
17
18 TYPE: RNA
19
20 ORGANISM: Homo sapiens
21
22 US-09-825-805-442

```

Query Match	9.1%	Score 12;	DB 10;	Length 17;
Best Local Similarity	83.3%	Pred No. 2.1e+04;		
Matches 10;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0

QY	16	CAGGACCTGCTG	27
		: :	
Db	1	CAGGACCTGCTG	12

```

RESULT 25
US-09-927-046-906/C
; Sequence 906, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 906
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-906

```

```

Query Match 9.1%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Gaps 0;

```

Qy	86	GCTGGATGGAGC	97
Db	12	GCTGGATGGAGC	1

```

RESULT 26
US-09-927-046-1303/c
: Sequence 1303, AP/099227046
: Publication No. US20030066946A1
GENERAL INFORMATION:
: APPLICANT: Ribozyne Pharmaceuticals, Inc
: APPLICANT: MCSwiggan, Jim
: APPLICANT: Thompson, Jim
: APPLICANT: McKenzie, Tim
: APPLICANT: Ayers, Dave
: APPLICANT: Grupe, Andrew

```

```

APPLICANT: Szymkowski, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channels
TITLE OF INVENTION: Channel-1
FILE REFERENCE: 249/021
CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: Patentin version 3.0
SEQ ID NO 1303
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-927-046-1303

```

```
Query Match      9.1%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

QY	89	GGATGGAGCGCT	100
Db	17	GGATGGAGCGCT	6

```

RESULT 27
US-09-740-332-1234
; Sequence 1234, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1234
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-1234

```

```
Query Match      9.1%; Score 12; DB 10; length 17;
Best Local Similarity 83.3%; Pred. No. 2.1e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0
```

Qy	11	TCTGCCAGGACC	22
		: :	
Db	6	UCUGCCAGGACC	17

```

RESULT 28
US-09-740-332-3321/c
; Sequence 3321, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740.332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3321
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:

```

```
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-3321
```

```
Query Match          9.1%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      11 TCTGCCAGGACC 22
         |||
Db       13 TCTGCCAGGACC 2
```

```
RESULT 29
US-09-817-879-1234
Sequence 1234, Application US/09817879
Publication No. US2003017311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
FILE REFERENCE: MHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1234
LENGTH: 17
TYPE: RNA
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-1234
```

```
Query Match          9.1%; Score 12; DB 10; Length 17;
Best Local Similarity 83.3%; Pred. No. 2.1e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      11 TCTGCCAGGACC 22
         |||
Db       6  UTCGCCAGGACC 17
```

```
RESULT 30
US-09-817-879-3321/c
Sequence 3321, Application US/09817879
Publication No. US2003017311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
FILE REFERENCE: MHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3321
LENGTH: 17
TYPE: RNA
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-3321
```

```
Query Match          9.1%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      11 TCTGCCAGGACC 22
         |||
Db       13 TCTGCCAGGACC 2
```

```
RESULT 31
US-10-163-552-617
Sequence 617, Application US/10163552
Publication No. US20030105051A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to leve
FILE REFERENCE: MHB01-1653-A (400/014)
CURRENT APPLICATION NUMBER: US/10/163,552
CURRENT FILING DATE: 2002-06-06
NUMBER OF SEQ ID NOS: 1997
SOFTWARE: PatentIn version 3.0
SEQ ID NO 617
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-163-552-617
```

```
Query Match          9.1%; Score 12; DB 15; Length 17;
Best Local Similarity 83.3%; Pred. No. 2.1e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      16 CAGGACCTGCTG 27
         |||
Db       1  CAGGACCTGCTG 12
```

```
RESULT 32
US-10-669-841-3827
Sequence 3827, Application US/10669841
Publication No. US20040127446A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
TITLE OF INVENTION: VIRUS REPLICATION
FILE REFERENCE: 400/042US (MHB02-245-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/236,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 60/337,055
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 09/817,879
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/740,332
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR FILING DATE: 2000-02-15
```

```

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: Patent version 3.0
; SEQ ID NO 3827
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-3827

Query Match          9.1%; Score 12; DB 17; Length 17;
Best Local Similarity 83.3%; Pred. No. 2.1e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      11 TCTGCCAGGACC 22
Db      6 UCUGCCAGGACC 17

RESULT 33
US-10-669-841-5914/c
; Sequence 5914, Application US/10668841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blact
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/04205 (MBH02-249-E)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: Patent version 3.0
; SEQ ID NO 5914
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
```

```

; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-5914

Query Match          9.1%; Score 12; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TCTGCCAGGACC 22
Db      13 TCTGCCAGGACC 2

RESULT 34
US-10-723-361-2181/c
; Sequence 2181, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wenheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART A
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2181
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2181

Query Match          9.1%; Score 12; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CCAGGACCTGCT 26
Db      17 CCAGGACCTGCT 6

RESULT 35
US-10-723-361-2182/c
; Sequence 2182, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
```

```

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2182
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2182

Query Match
Best Local Similarity 100.0%; Score 12; DB 17; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACTGCT 26
Db 16 CCAGGACTGCT 5

RESULT 36
US-10-723-361-2183/c
; Sequence 2183, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
```

```

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2183
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2183

Query Match
Best Local Similarity 100.0%; Score 12; DB 17; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACTGCT 26
Db 15 CCAGGACTGCT 4

RESULT 37
US-10-723-361-2184/c
; Sequence 2184, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART A
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2184
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-10-723-361-2184

Query Match 9.1%; Score 12; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGAGCTGCT 26
DB 14 CCAGAGCTGCT 3

RESULT 38

US-10-723-361-2185/c

; Sequence 2185, Application US/10723361

; Publication No. US20040137589A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharon G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

; FILE REFERENCE: PB0105

; CURRENT APPLICATION NUMBER: US/10/723.361

; PRIOR FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 09/866,108

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeomica Sequence Listing Engine

; SEQ ID NO 2185

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-723-361-2185

Query Match 9.1%; Score 12; DB 17; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGAGCTGCT 26
DB 13 CCAGAGCTGCT 2

RESULT 39

US-10-723-361-2186/c

; Sequence 2186, Application US/10723361

; Publication No. US20040137589A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharon G.

Query Match 9.1%; Score 12; DB 17; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGAGCTGCT 26
DB 13 CCAGAGCTGCT 2

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

; FILE REFERENCE: PB0105

; CURRENT APPLICATION NUMBER: US/10/723.361

; PRIOR FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 09/866,108

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeomica Sequence Listing Engine

; SEQ ID NO 2186

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-723-361-2186

Query Match 9.1%; Score 12; DB 17; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGAGCTGCT 26
DB 12 CCAGAGCTGCT 1

RESULT 40

US-09-969-373-3339

; Sequence 3339, Application US/09969373

; Patent No. US20020133852A1

; GENERAL INFORMATION:

; APPLICANT: Eifert, Roger J.

; APPLICANT: Hauge, Brian M.

; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping

; FILE REFERENCE: 38-10(52679) A

; CURRENT APPLICATION NUMBER: US/09/969,373

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 09/754,853

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: US 09/760,427

; PRIOR FILING DATE: 2001-01-13

; PRIOR APPLICATION NUMBER: US 09/855,768

; PRIOR FILING DATE: 2001-05-15

; NUMBER OF SEQ ID NOS: 4593

; SEQ ID NO 3339

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Glycine max

US-09-969-373-3339

Query Match 9.1%; Score 12; DB 9; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.1e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGAGCTGCT 26
DB 12 CCAGAGCTGCT 1

OY 73 GCTGCTACTCG 84
|||||
Db 8 GCTGCTACTCG 19

RESULT 41
US-09-910-059-110
; Sequence 110, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic Use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GS97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer for preprohCBP
US-09-910-059-110

Query Match 9.1%; Score 12; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GGACCTGCTGCA 29
|||||
Db 1 GGACCTGCTGCA 12

RESULT 42
US-09-767-421-22
; Sequence 22, Application US/09767421
; Publication No. US20030175954A1
; GENERAL INFORMATION:
; APPLICANT: Shamblott, Michael
; APPLICANT: Gearhart, John
; TITLE OF INVENTION: Human Embryoid Body-Derived Cells
; FILE REFERENCE: Unassigned
; CURRENT APPLICATION NUMBER: US/09/767,421
; CURRENT FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-767-421-22

Query Match 9.1%; Score 12; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 CCAGGACCTGCT 26
|||||
Db 2 CCAGGACCTGCT 13

RESULT 43
US-10-238-442-99
; Sequence 99, Application US/10238442
; Publication No. US20030176383A1
; GENERAL INFORMATION:
; APPLICANT: Monla, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; APPLICANT: McKay, Robert
; TITLE OF INVENTION: Antisense Modulation of p38 Mitogen
; TITLE OF INVENTION: Activated Protein Kinase Expression
; FILE REFERENCE: ISPH-0488
; CURRENT APPLICATION NUMBER: US/10/238,442
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 09/640,101
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 09/286,904
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-238-442-99

Query Match 9.1%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 ACCTTCTGCGCG 72
|||||
Db 3 ACCTTCTGCGCG 14

RESULT 44
US-10-161-996-81/c
; Sequence 81, Application US/10161996
; Publication No. US20030224515A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freiler
; APPLICANT: Brenda F. Baker
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEROL REGULATORY ELEMENT-BINDING PROTEI
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0395
; CURRENT APPLICATION NUMBER: US/10/161,996
; CURRENT FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 273
; SEQ ID NO 81
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-161-996-81

Query Match 9.1%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 GCTGACGACTG 35
|||||
Db 20 GCTGACGACTG 9

RESULT 45
US-10-175-239-15/c
; Sequence 15, Application US/10175239
; Publication No. US20030232774A1

```

; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROFILIN 1 EXPRESSION
; FILE REFERENCE: HTS-0017
; CURRENT APPLICATION NUMBER: US/10/175,239
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-175-239-15
```

```

Query Match
Best Local Similarity 9.1%; Score 12; DB 15; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 84 GGGCTGGATGGA 95
Db 20 GGGCTGGATGGA 9
```

```

RESULT 46
US-10-175-239-52
; Sequence 52, Application US/10175239
; Publication No. US2003023774A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROFILIN 1 EXPRESSION
; FILE REFERENCE: HTS-0017
; CURRENT APPLICATION NUMBER: US/10/175,239
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-175-239-52
```

```

Query Match
Best Local Similarity 9.1%; Score 12; DB 15; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 84 GGGCTGGATGGA 95
Db 1 GGGCTGGATGGA 12
```

```

RESULT 47
US-10-289-762-5153
; Sequence 5153, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5153
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5153
```

```

Query Match
9.1%; Score 12; DB 16; Length 20;
```

```

Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 13 TGCCAGACCTG 24
Db 5 TGCCAGACCTG 16
```

```

RESULT 48
US-10-289-762-5261/c
; Sequence 5261, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5261
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5261
```

```

Query Match
Best Local Similarity 9.1%; Score 12; DB 16; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 5 GCATCATCTGCC 16
Db 18 GCATCATCTGCC 7
```

```

RESULT 49
US-10-304-105-30/c
; Sequence 30, Application US/10304105
; Publication No. US20040101854A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: MODULATION OF BCL2-ASSOCIATED ATRANOGENE EXPRESSION
; FILE REFERENCE: HTS-0003
; CURRENT APPLICATION NUMBER: US/10/304,105
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-105-30
```

```

Query Match
Best Local Similarity 9.1%; Score 12; DB 17; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 9 CATCTGCCAGGA 20
Db 14 CATCTGCCAGGA 3
```

```

RESULT 50
US-10-304-105-36/c
; Sequence 36, Application US/10304105
; Publication No. US20040101854A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
```

```

; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF BCL2-ASSOCIATED APHANOGENE EXPRESSION
; FILE REFERENCE: HTS-0003
; CURRENT APPLICATION NUMBER: US/10/304,105
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-105-36
```

```

Query Match      9.1%; Score 12; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 CATCTGCCAGCA 20
DB      12 CATCTGCCAGCA 1
```

```

RESULT 51
US-10-346-268-144/c
; Sequence 144, Application US/10346268
; Publication No. US20040137441A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Doble
; APPLICANT: Ravi Jain
; TITLE OF INVENTION: MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 3 EXPRESSION
; FILE REFERENCE: PIS-0076
; CURRENT APPLICATION NUMBER: US/10/346,268
; CURRENT FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 200
; SEQ ID NO 144
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-346-268-144
```

```

Query Match      9.1%; Score 12; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      53 GCATGCACACGT 64
DB      16 GCATGCACACGT 5
```

```

RESULT 52
US-10-641-455A-99
; Sequence 99, Application US/10641455A
; Publication No. US20040171566A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; APPLICANT: McKay, Robert
; APPLICANT: Popoff, Ian
; APPLICANT: Wong, Wai Shin Fred
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of p38 Mitogen
; FILE REFERENCE: ISPH-0762
; CURRENT APPLICATION NUMBER: US/10/641,455A
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/238,442
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/640,101
```

```

; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 09/286,904
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-641-455A-99
```

```

Query Match      9.1%; Score 12; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      61 ACGTTCTGCGCG 72
DB      3 ACGTTCTGCGCG 14
```

```

RESULT 53
US-10-484-669-53/c
; Sequence 53, Application US/10484669
; Publication No. US20040209358A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF SAP-1 EXPRESSION
; FILE REFERENCE: RTS-0267
; CURRENT APPLICATION NUMBER: US/10/484,669
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/09/920,759
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-669-53
```

```

Query Match      9.1%; Score 12; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      84 GGGCTGGATGGA 95
DB      15 GGGCTGGATGGA 4
```

```

RESULT 54
US-10-010-066-59
; Sequence 59, Application US/10010066
; Publication No. US20020173001A1
; GENERAL INFORMATION:
; APPLICANT: University of Iowa Research Foundation
; APPLICANT: Schwartz, David A.
; APPLICANT: Schutte, Brian C.
; TITLE OF INVENTION: Variant TLR4 nucleic acid and uses thereof
; FILE REFERENCE: 875.010W01
; CURRENT APPLICATION NUMBER: US/10/010,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 09/329,515
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-10-010-066-59

Query Match 9.1%; Score 12; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GCAGCCCTGCAT 56
|||||
DB 6 GCAGCCCTGCAT 17

RESULT 55

US-10-381-779-183/C
; Sequence 183, Application US/10381779
; Publication No. US20030219798A1
; GENERAL INFORMATION:
; APPLICANT: Gokarn, Ravi R
; APPLICANT: Jeessen, Holly
; APPLICANT: Zidwick, Mary Jo
; TITLE OF INVENTION: Isoprenoid Production
; FILE REFERENCE: 12904/002051
; CURRENT APPLICATION NUMBER: US/10/381,779
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/30328
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/236,580
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-381-779-183

Query Match 9.1%; Score 12; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 GTGTCTACTCTG 119
|||||
DB 17 GTGTCTACTCTG 6

RESULT 56
US-10-758-672A-29
; Sequence 29, Application US/10758672A
; Publication No. US20040185037A1
; GENERAL INFORMATION:
; APPLICANT: Han, et al.
; TITLE OF INVENTION: HUMAN E3 ALPHA UBQUITIN LIGASE FAMILY
; FILE REFERENCE: 01017/35966B
; CURRENT APPLICATION NUMBER: US/10/758,672A
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: US 09/724,126
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,911
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 29
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-10-758-672A-29

Query Match 9.1%; Score 12; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 CCCTGATGCAC 60
|||||
DB 5 CCCTGATGCAC 16

RESULT 57

US-10-751-736-10507/C
; Sequence 10507, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10507
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-10507

Query Match 9.1%; Score 12; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGCCAGGACCTG 24
|||||
DB 12 TGCCAGGACCTG 1

RESULT 58
US-10-090-011-5
; Sequence 5, Application US/10090011
; Publication No. US20030082810A1
; GENERAL INFORMATION:
; APPLICANT: Serup, Palle
; APPLICANT: Heindberg, Harry
; APPLICANT: Gradwohl, Gerard
; TITLE OF INVENTION: Methods For Generating Insulin-Secreting
; FILE REFERENCE: 6246-200-US
; CURRENT APPLICATION NUMBER: US/10/090,011
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US 60/271,474
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-090-011-5

Query Match 9.1%; Score 12; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CATCATCTGCCA 17
|||||
DB 6 CATCATCTGCCA 17

RESULT 59
US-10-697-036-83

: Sequence 83 Application US/10697036
 : Publication No. US20040137594A1
 : GENERAL INFORMATION:
 : APPLICANT: Sumitomo Chemical Co., Ltd.
 : TITLE OF INVENTION: TRANSFORMED CELL WITH ENHANCED SENSITIVITY TO ANTIFUNGAL COMPOUNTS
 : FILE REFERENCE: 078242
 : CURRENT APPLICATION NUMBER: US/10/697,036
 : CURRENT FILING DATE: 2003-10-31
 : PRIOR APPLICATION NUMBER: JP 2002/317736
 : PRIOR FILING DATE: 2002-10-31
 : NUMBER OF SEQ ID NOS: 90
 : SOFTWARE: PatentIn version 3.2
 : SEQ ID NO 83
 : LENGTH: 22
 : TYPE: DNA
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: Description of Artificial Sequence:Designed
 : oligonucleotide primer for PCR
 : US-10-697-036-83

```

Query Match      9.1%; Score 12; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

Oy	16	CAGGACCTGCTG	27
db	8	CAGGACCTGCTG	19

RESULT 60
US-09-779-879A-38/C

```

Sequence 38, Application US/09779879A
Patent No. US20020048786A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Roschke, Viktor
APPLICANT: Li, Yi
APPLICANT: Ribben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10.0
FILE REFERENCE: 1486.115000A
CURRENT APPLICATION NUMBER: US/09/779,879A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/234,336
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.0
SEQ ID NO 38
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 5' Oligonucleotide primer for VL Domain
US-09-779-879A-38

```

Query Match 9.1%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Gaps 0;

QY	31	GACTGCGTGAGT	42
Db	20	GACTGCGTGAGT	9

RESULT 61
US-09-779-880A-38/C
; Sequence 38, Application US/09779880A
; Patent No. US20020061834A1

```

: GENERAL INFORMATION:
: APPLICANT: Rosen, Craig A.
: APPLICANT: Roschke, Viktor
: APPLICANT: Li, Yi
: APPLICANT: Ribben, Steven, M.
: TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
: FILE REFERENCE: 1488.115000C
: CURRENT APPLICATION NUMBER: US/09/779,880A
: CURRENT FILING DATE: 2001-02-09
: PRIOR APPLICATION NUMBER: US 60/181,258
: PRIOR FILING DATE: 2000-02-09
: PRIOR APPLICATION NUMBER: US 60/187,999
: PRIOR FILING DATE: 2000-03-09
: PRIOR APPLICATION NUMBER: US 60/234,336
: PRIOR FILING DATE: 2000-09-22
: NUMBER OF SEQ. ID NOS: 58
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 38
: LENGTH: 23
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: 5' Oligonucleotide primer for VL Domain
US-03-779-880A-38

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Query Match	9.1%	Score 12:	DB 9;	length 23;
Best Local Similarity	100.0%	Pred. No.	2.1e+04;	
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	31	GACTGCCGTGAGT	42
Db	20	GACTGCCGTGAGT	9

```

RESULT 62
US-09-988-899-26/c
: Sequence 26, Application US/09988899
: Patent No. US20020102613A1
: GENERAL INFORMATION:
: APPLICANT: HOOSENDOOM, HENDRICUS R.J.M.
: TITLE OF INVENTION: NOVEL F&B FRAGMENT LIBRARIES AND METHOD FOR THEIR USE
: FILE REFERENCE: DX/003 CON
: CURRENT APPLICATION NUMBER: US/09/988, 899
: PRIORITY FILING DATE: 2001-11-19
: PRIOR APPLICATION NUMBER: PCT/US00/13682
: PRIOR FILING DATE: 2000-05-18
: PRIOR APPLICATION NUMBER: 99201558.6
: PRIOR FILING DATE: 1999-05-18
: NUMBER OF SEQ ID NOS: 71
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 26
: LENGTH: 23
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURES:
: OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-988-899-26

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Query Match	9.1%	Score 12	DB 9	length 23
Best Local Similarity	100.0%	Pred. No.	2.1e+04	
Matches 12	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	31	GACTGCCGTGAGT	42
Db	20	GACTGCCGTGAGT	9

RESULT 63
US-09-910-120-26/c
; Sequence 26, Application US/09910120
; Patent No. US2002013705A1
; GENERAL INFORMATION:
; APPLICANT: DANA AULT-RICHE

```

; APPLICANT: PAUL D. KASSNER
; TITLE OF INVENTION: COLLECTIONS OF BINDING PROTEINS AND TAGS
; TITLE OF INVENTION: AND USUS THEREOF FOR NESTED SORTING AND HIGH THROUGHPUT
; TITLE OF INVENTION: SCREENING
; FILE REFERENCE: 25885-1751
; CURRENT APPLICATION NUMBER: US/09/910,120
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,183
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer: HuvKappa5ABACK
US-09-910-120-26

Query Match          9.1%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGAGT 42
Db 20 GACTGCGTGAGT 9

RESULT 64
US-09-939-769-45/c
; Sequence 45, Application US/09939769
; Publication No. US20030017149A1
; GENERAL INFORMATION:
; APPLICANT: ROSEFIELD, JAMES P.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY FUSION REAGENTS THAT REGULATE
; TITLE OF INVENTION: TRANSCRIPTION IN VIVO
; FILE REFERENCE: 039322/0226
; CURRENT APPLICATION NUMBER: US/09/939,769
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 08/728,890
; PRIOR FILING DATE: 1996-10-10
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-939-769-45

Query Match          9.1%; Score 12; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGAGT 42
Db 20 GACTGCGTGAGT 9

RESULT 65
US-09-833-041-51/c
; Sequence 51, Application US/09833041
; Publication No. US20030125247A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF545
; CURRENT APPLICATION NUMBER: US/09/833,041
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
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; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer bind
; OTHER INFORMATION: Degenerate V kappa forward primer useful for
; OTHER INFORMATION: amplifying human VL domains
US-09-833-041-51

Query Match          9.1%; Score 12; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGAGT 42
Db 20 GACTGCGTGAGT 9

RESULT 66
US-09-833-245-51/c
; Sequence 51, Application US/09833245
; Publication No. US2004001034A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer bind
; OTHER INFORMATION: Degenerate V kappa forward primer useful for
; OTHER INFORMATION: amplifying human VL domains
US-09-833-245-51

Query Match          9.1%; Score 12; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGAGT 42
Db 20 GACTGCGTGAGT 9

RESULT 67
US-09-832-929-51/c
; Sequence 51, Application US/09832929
; Publication No. US20040171123A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF547
; CURRENT APPLICATION NUMBER: US/09/832,929
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; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; NAME/KEY: primer bind
; OTHER INFORMATION: Degenerate Vkapra forward primer useful for
; OTHER INFORMATION: amplifying human VL domains
US-09-832-929-51
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```

Query Match          9.1%; Score 12; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy          31 GACTGCGTGAGT 42
            |||||
Db          20 GACTGCGTGAGT 9
```

```

RESULT 68
US-10-039-785-21/c
; Sequence 21, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: PCR primer useful for amplifying VH and VL domains
US-10-039-785-21
```

```

Query Match          9.1%; Score 12; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy          31 GACTGCGTGAGT 42
            |||||
Db          20 GACTGCGTGAGT 9
```

```

Db          20 GACTGCGTGAGT 9

RESULT 69
US-10-153-064-48/c
; Sequence 48, Application US/10153064
; Publication No. US20020142814A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Degenerate Vkapra forward primer useful for
; OTHER INFORMATION: amplifying human VL domains
US-10-153-064-48
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```

Query Match          9.1%; Score 12; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy          31 GACTGCGTGAGT 42
            |||||
Db          20 GACTGCGTGAGT 9
```

```

RESULT 70
US-10-077-023-100/c
; Sequence 100, Application US/10077023
; Publication No. US20030031675A1
; GENERAL INFORMATION:
; APPLICANT: MIKESSELL, GLEN E.
; APPLICANT: CHANG, HAN
; APPLICANT: FINGER, JOSHUA N.
; APPLICANT: YANG, GUCHEN
; APPLICANT: LU, PIN
; APPLICANT: ZHOU, XIA-DI
; APPLICANT: PEACH, ROBERT
; TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
; FILE REFERENCE: 3053-4071US3
; CURRENT APPLICATION NUMBER: US/10/077,023
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/272,107
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/209,811
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-077-023-100
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```

Query Match          9.1%; Score 12; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy          31 GACTGCGTGAGT 42
            |||||
Db          20 GACTGCGTGAGT 9
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```
RESULT 71
US-10-075-846-53/c
; Sequence 53, Application US/10075846
; Publication No. US20030032608A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT E
; TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF
; FILE REFERENCE: D0079 NP
; CURRENT APPLICATION NUMBER: US/10/075,846
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: US 60/269,535
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-075-846-53

Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+04; Length 23;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9

RESULT 72
US-10-056-884-46/c
; Sequence 46, Application US/10056884
; Publication No. US20030032786A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBU
; TITLE OF INVENTION: K-beta24
; FILE REFERENCE: D0076 NP
; CURRENT APPLICATION NUMBER: US/10/056,884
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,872
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/269,794
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-056-884-46

Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+04; Length 23;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9

RESULT 73
US-10-080-980-43/c
; Sequence 43, Application US/10080980
; Publication No. US20030036115A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBU
; TITLE OF INVENTION: K-beta46, EXPRESSED HIGHLY IN THE SMALL INTESTINE
; FILE REFERENCE: D0121 NP
```

```
; CURRENT APPLICATION NUMBER: US/10/080,980
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,132
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/278,953
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-080-980-43

Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+04; Length 23;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9

RESULT 74
US-10-092-135-53/c
; Sequence 53, Application US/10092135
; Publication No. US20030054374A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; TITLE OF INVENTION: HGRBMY27
; FILE REFERENCE: D0134.NP
; CURRENT APPLICATION NUMBER: US/10/092,135
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/273,808
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/278,983
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-135-53

Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+04; Length 23;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9

RESULT 75
US-10-086-156-73/c
; Sequence 73, Application US/10086156
; Publication No. US20030054989A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-S
; TITLE OF INVENTION: K-beta4 and K-beta5
; FILE REFERENCE: D0115NP
; CURRENT APPLICATION NUMBER: US/10/086,156
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/272,190
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/274,258
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
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; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-086-156-73

Query Match 9.1%; Score 12; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9

Search completed: February 3, 2005, 00:11:24
Job time : 75.8037 secs

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OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:25:00 ; Search time 12.6615 Seconds
(without alignments)
7410.178 Million cell updates/sec

Title: US-10-048-046-1_COPY_997_1128

Perfect score: 132
Sequence: 1 acctgcctctctgcgcagga.....ctaccgcgcgtcccgctg 132

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

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Total number of hits satisfying chosen parameters: 682300

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

Database :

Issued Patents NA: *
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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
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6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	13	9.8	20	2	US-08-418-848A-49
2	13	9.8	25	1	US-08-435-350-67
3	13	9.8	29	1	US-08-702-344-33
4	12	9.1	17	4	US-09-474-432B-443
5	12	9.1	17	4	US-09-476-387-442
6	12	9.1	17	4	US-09-866-108A-2181
7	12	9.1	17	4	US-09-866-108A-2182
8	12	9.1	17	4	US-09-866-108A-2183
9	12	9.1	17	4	US-09-866-108A-2184
10	12	9.1	17	4	US-09-866-108A-2185
11	12	9.1	17	4	US-09-866-108A-2186
12	12	9.1	19	1	US-08-379-078-717
13	12	9.1	19	2	US-08-860-882A-52
14	12	9.1	19	3	US-09-171-945-110
15	12	9.1	19	3	US-07-974-409C-289
16	12	9.1	19	4	US-09-011-769A-34
17	12	9.1	19	5	PCT-US93-00977-289
18	12	9.1	20	3	US-08-930-001-6
19	12	9.1	20	4	US-09-640-101-99
20	12	9.1	20	4	US-09-920-759-53
21	12	9.1	20	4	US-09-198-452A-5153
22	12	9.1	20	4	US-09-198-452A-5261
23	12	9.1	20	4	US-09-091-885-6
24	12	9.1	21	4	US-09-724-126A-29
25	12	9.1	21	4	US-09-329-515A-59
26	12	9.1	22	3	US-09-339-775-4
27	12	9.1	23	1	US-08-211-202-76

C 28	12	9.1	23	2	US-08-350-260A-554	Sequence 554, App
C 29	12	9.1	23	2	US-08-860-882A-39	Sequence 39, Appl
C 30	12	9.1	23	2	US-08-860-882A-51	Sequence 51, Appl
C 31	12	9.1	23	4	US-09-011-769A-6	Sequence 6, Appl1
C 32	12	9.1	23	4	US-09-011-769A-33	Sequence 33, Appl
C 33	12	9.1	23	4	US-09-104-337A-554	Sequence 554, App
C 34	12	9.1	23	4	US-10-067-443-48	Sequence 48, Appl
C 35	12	9.1	23	4	US-10-153-064-48	Sequence 48, Appl
C 36	12	9.1	23	4	US-09-724-126A-28	Sequence 28, Appl
C 37	12	9.1	24	3	US-09-123-030-33	Sequence 33, Appl
C 38	12	9.1	25	4	US-09-866-108A-5110	Sequence 5110, App
C 39	12	9.1	25	4	US-09-866-108A-5111	Sequence 5111, App
C 40	12	9.1	25	4	US-09-866-108A-5112	Sequence 5112, App
C 41	12	9.1	25	4	US-09-866-108A-5113	Sequence 5113, App
C 42	12	9.1	25	4	US-09-866-108A-5114	Sequence 5114, App
C 43	12	9.1	25	4	US-09-866-108A-5115	Sequence 5115, App
C 44	12	9.1	25	4	US-09-866-108A-5116	Sequence 5116, App
C 45	12	9.1	25	4	US-09-866-108A-5117	Sequence 5117, App
C 46	12	9.1	25	4	US-09-866-108A-5118	Sequence 5118, App
C 47	12	9.1	25	4	US-09-866-108A-5119	Sequence 5119, App
C 48	12	9.1	25	4	US-09-866-108A-5120	Sequence 5120, App
C 49	12	9.1	25	4	US-09-866-108A-5121	Sequence 5121, App
C 50	12	9.1	25	4	US-09-866-108A-5122	Sequence 5122, App
C 51	12	9.1	25	4	US-09-866-108A-5123	Sequence 5123, App
C 52	12	9.1	26	2	US-08-859-998-358	Sequence 358, App
C 53	12	9.1	26	3	US-08-486-857-3	Sequence 3, Appl1
C 54	12	9.1	26	3	US-08-724-752-19	Sequence 19, Appl
C 55	12	9.1	26	3	US-09-225-201B-358	Sequence 358, App
C 56	12	9.1	26	4	US-09-923-138-3	Sequence 3, Appl1
C 57	12	9.1	26	4	US-09-614-092A-19	Sequence 19, Appl
C 58	12	9.1	27	3	US-08-911-894-25	Sequence 25, Appl
C 59	12	9.1	27	3	US-08-180-109A-47	Sequence 47, Appl
C 60	12	9.1	28	4	US-09-304-232-669	Sequence 669, App
C 61	12	9.1	29	4	US-07-931-473B-27	Sequence 27, Appl
C 62	12	9.1	30	1	US-07-714-131C-27	Sequence 27, Appl
C 63	12	9.1	30	1	US-08-412-110-27	Sequence 27, Appl
C 64	12	9.1	30	1	US-08-409-442A-27	Sequence 27, Appl
C 65	12	9.1	30	2	US-08-469-609A-27	Sequence 27, Appl
C 66	12	9.1	30	3	US-09-143-190-27	Sequence 27, Appl
C 67	12	9.1	30	3	US-09-502-444-27	Sequence 27, Appl
C 68	12	9.1	30	3	US-09-937-832-16	Sequence 16, Appl
C 69	12	9.1	30	3	US-09-419-212-6	Sequence 4, Appl1
C 70	11	8.3	15	3	US-09-419-212-6	Sequence 4, Appl1
C 71	11	8.3	16	4	US-09-060-299-454	Sequence 454, App
C 72	11	8.3	17	1	US-07-990-297-13	Sequence 13, Appl
C 73	11	8.3	17	1	US-08-373-124A-1749	Sequence 1749, App
C 74	11	8.3	17	1	US-08-435-628-1749	Sequence 1749, App
C 75	11	8.3	17	3	US-08-985-162-452	Sequence 452, App
C 76	11	8.3	17	3	US-08-985-162-452	Sequence 452, App
C 77	11	8.3	17	3	US-08-246-489-17	Sequence 17, Appl
C 78	11	8.3	17	4	US-09-401-063-452	Sequence 452, App
C 79	11	8.3	17	4	US-09-866-108A-2180	Sequence 2180, App
C 80	11	8.3	17	4	US-09-866-108A-2181	Sequence 2181, App
C 81	11	8.3	17	4	US-09-866-108A-2182	Sequence 2182, App
C 82	11	8.3	17	4	US-09-866-108A-2183	Sequence 2183, App
C 83	11	8.3	17	4	US-09-866-108A-2184	Sequence 2184, App
C 84	11	8.3	17	4	US-09-866-108A-2185	Sequence 2185, App
C 85	11	8.3	17	4	US-09-866-108A-2186	Sequence 2186, App
C 86	11	8.3	17	4	US-09-866-108A-2645	Sequence 2645, App
C 87	11	8.3	17	4	US-09-866-108A-2646	Sequence 2646, App
C 88	11	8.3	17	4	US-09-866-108A-2647	Sequence 2647, App
C 89	11	8.3	17	4	US-09-866-108A-2648	Sequence 2648, App
C 90	11	8.3	17	5	PCT-US93-11702-13	Sequence 13, Appl
C 91	11	8.3	18	4	US-08-556-627A-8	Sequence 8, Appl1
C 92	11	8.3	18	4	US-09-422-978-4638	Sequence 4638, App
C 93	11	8.3	18	4	US-09-163-099-8	Sequence 8, Appl1
C 94	11	8.3	19	3	US-10-337-060-8	Sequence 8, Appl1
C 95	11	8.3	19	3	US-09-338-907-562	Sequence 562, App
C 96	11	8.3	19	3	US-09-338-907-563	Sequence 563, App
C 97	11	8.3	19	3	US-09-218-207-562	Sequence 562, App
C 98	11	8.3	20	1	US-09-218-207-563	Sequence 563, App
C 99	11	8.3	20	1	US-08-741-106-10	Sequence 10, Appl
C 100	11	8.3	20	1	US-08-450-945-19	Sequence 19, Appl
C 100	11	8.3	20	2	US-08-655-821-12	Sequence 12, Appl

101 11 8.3 20 2 US-08-117-952-399 Sequence 399, App
102 11 8.3 20 3 US-08-589-939-42 Sequence 42, App1
103 11 8.3 20 3 US-07-998-2898-18 Sequence 18, App1
104 11 8.3 20 3 US-09-358-685-16 Sequence 16, App1
105 11 8.3 20 3 US-09-358-685-17 Sequence 17, App1
106 11 8.3 20 3 US-09-358-685-18 Sequence 18, App1
107 11 8.3 20 3 US-09-358-685-19 Sequence 19, App1
108 11 8.3 20 3 US-09-358-685-20 Sequence 20, App1
109 11 8.3 20 3 US-09-358-685-21 Sequence 21, App1
110 11 8.3 20 3 US-08-927-219-58 Sequence 58, App1
111 11 8.3 20 3 US-08-976-161-19 Sequence 18, App1
112 11 8.3 20 3 US-09-659-791A-18 Sequence 9, App1
113 11 8.3 20 4 US-09-199-865-9 Sequence 297, App
114 11 8.3 20 4 US-09-517-467B-297 Sequence 209, App
115 11 8.3 20 4 US-09-668-113A-209 Sequence 5093, App
116 11 8.3 20 4 US-09-422-978-5093 Sequence 2711, App
117 11 8.3 20 4 US-09-198-452A-2711 Sequence 4232, App
118 11 8.3 20 4 US-09-198-452A-4232 Sequence 196, App
119 11 8.3 20 4 US-09-980-052-196 Sequence 28, App1
120 11 8.3 20 4 US-09-765-400-28 Sequence 63, App1
121 11 8.3 20 4 US-09-765-400-28 Sequence 28, App1
122 11 8.3 20 4 US-09-705-400-28 Sequence 63, App1
123 11 8.3 20 4 US-09-705-400-28 Sequence 63, App1
124 11 8.3 20 4 US-09-579-536C-9 Sequence 9, App1
125 11 8.3 21 1 US-08-240-547-42 Sequence 42, App1
126 11 8.3 21 1 US-08-229-145-3 Sequence 3, App1
127 11 8.3 21 1 US-08-229-145-8 Sequence 8, App1
128 11 8.3 21 1 US-08-602-713-1 Sequence 1, App1
129 11 8.3 21 1 US-08-602-713-3 Sequence 3, App1
130 11 8.3 21 3 US-08-989-493-1 Sequence 3, App1
131 11 8.3 21 3 US-08-989-493-3 Sequence 35, App1
132 11 8.3 21 4 US-08-803-346-35 Sequence 1, App1
133 11 8.3 21 4 US-09-610-271-1 Sequence 3, App1
134 11 8.3 21 4 US-09-610-271-3 Sequence 49, App1
135 11 8.3 21 4 US-09-380-836-49 Sequence 244, App
136 11 8.3 21 5 PCT-US91-05802-3 Sequence 8, App1
137 11 8.3 21 5 PCT-US91-05802-8 Sequence 7, App1
138 11 8.3 22 1 US-08-358-810A-7 Sequence 14, App1
139 11 8.3 22 1 US-08-484-712A-7 Sequence 14, App1
140 11 8.3 22 2 US-08-359-295C-14 Sequence 14, App1
141 11 8.3 22 2 US-08-485-105A-14 Sequence 14, App1
142 11 8.3 22 3 US-09-183-650-14 Sequence 10, App1
143 11 8.3 22 3 US-09-315-794-10 Sequence 10, App1
144 11 8.3 22 3 US-09-389-341-10 Sequence 10, App1
145 11 8.3 22 3 US-09-315-793-10 Sequence 10, App1
146 11 8.3 22 4 US-09-142-593-63 Sequence 15, App1
147 11 8.3 22 4 US-09-478-189-145 Sequence 26, App1
148 11 8.3 22 4 US-09-250-124A-26 Sequence 66, App1
149 11 8.3 22 4 US-09-771-357-66 Sequence 66, App1
150 11 8.3 22 4 US-09-771-357-66 Sequence 66, App1

ALIGNMENTS

RESULT 1
US-08-418-848A-49
Sequence 49, Application US/08418848A
Patent No. 5847096
GENERAL INFORMATION:
APPLICANT: SCHUBERT, MANFRED, HARMISON II,
APPLICANT: GEORGE G., CHANG-JIE, CHEN, BANMERJEA, AKHIL
TITLE OF INVENTION: DEFECTIVE, INTERFERING
TITLE OF INVENTION: HIV PARTICLES
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,848A
FILING DATE: 07-APR-1995
CLASSIFICATION: 526
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936,849
FILING DATE: 28-AUG-1992
CLASSIFICATION: 526
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4091US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-418-848A-49

Query Match 9.8%; Score 13; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 GCCCTGCATGCAC 60
DB 2 GCCCTGCATGCAC 14

RESULT 2
US-08-435-350-67
Sequence 67, Application US/08435350
Patent No. 559704
GENERAL INFORMATION:
APPLICANT: James D. Thompson
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: TREATMENT OF BREAST CANCER
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,350
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936,531
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/245
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-350-67

Query Match 9.8%; Score 13; DB 1; Length 25;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CCAGACCTGCTG 27
Db 2 CCAGACCTGCTG 14

RESULT 3
US-08-702-344-33/C
Sequence 33, Application US/08702344
Patent No. 572315
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Lavallee, Edward
APPLICANT: Racle, Lisa
APPLICANT: Werberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702.344
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A. 32,724
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
US-08-702-344-33

Query Match 9.8%; Score 13; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 CAGCCCTGCATGC 58
Db 25 CAGCCCTGCATGC 13

RESULT 4
US-09-474-432B-443
Sequence 443, Application US/09474432B
Patent No. 6528640
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn

TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
FILE REFERENCE: MBH00-831-B (247/276)
CURRENT APPLICATION NUMBER: US/09/474.432B
PRIOR FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: Patentn version 3.0
SEQ ID NO 443
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-474-432B-443

Query Match 9.1%; Score 12; DB 4; Length 17;
Best Local Similarity 83.3%; Pred. No. 4.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CAGACCTGCTG 27
Db 1 CAGACCTGCTG 12

RESULT 5
US-09-476-387-442
Sequence 442, Application US/09476387
Patent No. 6617438
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka Matulic
APPLICANT: Sweedler, Dave
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
FILE REFERENCE: MBH00-831-C (249/073)
CURRENT APPLICATION NUMBER: US/09/476.387
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 09/474,432
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/301,511
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: 60/083,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/064,866
PRIOR FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: Patentn version 3.0
SEQ ID NO 442
LENGTH: 17
TYPE: RNA

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; ORGANISM: Homo sapiens
; US-09-476-387-442

Query Match          9.1%; Score 12; DB 4; Length 17;
Best Local Similarity 83.3%; Pred. No. 4.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      16 CAGGACCTGCTG 27
      |||||:||||:|
Db      1 CAGGACCTGCTG 12

RESULT 6
US-09-866-108A-2181/c
; Sequence 2181, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: UT, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2181
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2181

Query Match          9.1%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CCAGGACCTGCT 26
      |||||:|||||
Db      17 CCAGGACCTGCT 6

RESULT 7
US-09-866-108A-2182/c
; Sequence 2182, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: UT, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
```

```

; APPLICANT: UT, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2182
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2182

Query Match          9.1%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CCAGGACCTGCT 26
      |||||:|||||
Db      16 CCAGGACCTGCT 5

RESULT 8
US-09-866-108A-2183/c
; Sequence 2183, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: UT, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2183
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2183

Query Match
Best Local Similarity 100.0%; Score 12; DB 4; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGAGCTGCT 26
DB 15 CCAGAGCTGCT 4

RESULT 9
US-09-866-108A-2184/C
; Sequence 2184, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2184
; LENGTH: 17
```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2184

Query Match
Best Local Similarity 100.0%; Score 12; DB 4; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGAGCTGCT 26
DB 14 CCAGAGCTGCT 3

RESULT 10
US-09-866-108A-2185/C
; Sequence 2185, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2185
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2185

Query Match
Best Local Similarity 100.0%; Score 12; DB 4; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGAGCTGCT 26
DB 13 CCAGAGCTGCT 2

RESULT 11
US-09-866-108A-2186/C
; Sequence 2186, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
```

APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: FERN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOZIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: A60MICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeonica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 2186
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-2186

Query Match 9.1%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACTGCT 26
DB 12 CCAGGACTGCT 1

RESULT 12
US-08-379-078-717
Sequence 717, Application US/08379078
Patent No. 5639612
GENERAL INFORMATION:
APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
TITLE OF INVENTION: Gene Detection System
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBE, MARTENS, OLSON AND BEAR
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,078

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/974,406
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.011CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 717:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-379-078-717

Query Match 9.1%; Score 12; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACTGCT 26
DB 6 CCAGGACTGCT 17

RESULT 13
US-08-860-882A-52
Sequence 52, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGELTE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HUM
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-860-882A-52

Query Match 9.1%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGACCTGCTGCA 29
Db 1 GGACCTGCTGCA 12

RESULT 14

US-09-171-945-110
Sequence 110, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 110
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-110

Query Match 9.1%; Score 12; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGACCTGCTGCA 29
Db 1 GGACCTGCTGCA 12

RESULT 15

US-07-974-409C-289
Sequence 289, Application US/07974409C
Patent No. 6300058
GENERAL INFORMATION:
APPLICANT: Akitaya, Tatsuo
APPLICANT: Mitsuhashi, Masato
TITLE OF INVENTION: METHOD AND REAGENT
NUMBER OF INVENTION: FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 457
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/974,409C
FILING DATE: 12-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 289:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-974-409C-289

Query Match 9.1%; Score 12; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACCTGCT 26
Db 6 CCAGGACCTGCT 17

RESULT 16

US-09-011-769A-34
Sequence 34, Application US/09011769A
Patent No. 6436691
GENERAL INFORMATION:
APPLICANT: SLATER, Anthony M.
APPLICANT: BLAKLEY, David C.
APPLICANT: DAVIES, David H.
APPLICANT: HENNAM, John F.
APPLICANT: HENNEQUIN, Laurent F.A.
APPLICANT: MARSHAM, Peter R.
APPLICANT: DOWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, LLP
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 MB disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A
FILING DATE: 13-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996

APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AUG-1995
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-011-769A-34

Query Match 9.1%; Score 12; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGAAGCTGCTGCA 29
DB 1 GGAAGCTGCTGCA 12

RESULT 17
PCT-US93-00977-289
Sequence 289, Application PC/TUS9300977
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 711
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00977
FILING DATE: 19930129
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 289:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US93-00977-289

Query Match 9.1%; Score 12; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAAGAGCTGCT 26
DB 6 CCAAGAGCTGCT 17

RESULT 18
US-08-930-001-6/c
Sequence 6, Application US/08930001A

PATENT No. 6281412
GENERAL INFORMATION:
APPLICANT: MORITA, No. 628141210
TITLE OF INVENTION: METHOD FOR PRODUCING OSMOTOLERANT PLANTS
FILE REFERENCE: 0230-118P
CURRENT APPLICATION NUMBER: US/08/930,001A
EARLIER FILING DATE: 1997-09-26
EARLIER APPLICATION NUMBER: JAPAN 106819/1995
EARLIER FILING DATE: 1995-03-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-930-001-6

Query Match 9.1%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 GCTGATGAGC 97
DB 12 GCTGATGAGC 1

RESULT 19
US-09-640-101-99
Sequence 99, Application US/09640101
Patent No. 6448079
GENERAL INFORMATION:
APPLICANT: Wonda, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
APPLICANT: McKay, Robert
TITLE OF INVENTION: Antisense Modulation of p38 Mitogen
PROTEIN REFERENCE: Activated Protein Kinase Expression
FILE REFERENCE: ISPH-0488
CURRENT APPLICATION NUMBER: US/09/640,101
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 09/286,904
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 99
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-09-640-101-99

Query Match 9.1%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 AGCTTCTGCGCG 72
DB 3 AGCTTCTGCGCG 14

RESULT 20
US-09-920-759-53/c
Sequence 53, Application US/09920759
Patent No. 6537811
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Susan W. Freiler
TITLE OF INVENTION: ANTISENSE MODULATION OF SAP-1 EXPRESSION
FILE REFERENCE: RTS-0267
CURRENT APPLICATION NUMBER: US/09/920,759

; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-920-759-53

Query Match 9.1%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 GCGCTGATGGA 95
|||
Db 15 GCGCTGATGGA 4

RESULT 21
US-09-198-452A-5153
; Sequence 5153, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifflaß, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5153
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5153

Query Match 9.1%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TGCCAGGACCTG 24
|||
Db 5 TGCCAGGACCTG 16

RESULT 22
US-09-198-452A-5261/C
; Sequence 5261, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifflaß, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5261
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5261

Query Match 9.1%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCATCATCTGCC 16
|||
Db 18 GCATCATCTGCC 7

RESULT 23
US-09-091-885-6/C
; Sequence 6, Application US/09091885
; Patent No. 6756525
; GENERAL INFORMATION:
; APPLICANT: MURATA, No. 675652510
; TITLE OF INVENTION: METHOD FOR PRODUCING TEMPERATURE-TOLERANT PLANTS
; FILE REFERENCE: 230-123P
; CURRENT APPLICATION NUMBER: US/09/091,885
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PRIMER
US-09-091-885-6

Query Match 9.1%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 GCTGATGAGC 97
|||
Db 12 GCTGATGAGC 1

RESULT 24
US-09-724-126A-29
; Sequence 29, Application US/09724126A
; Patent No. 6706505
; GENERAL INFORMATION:
; APPLICANT: Han, Hui-Quan
; APPLICANT: Kwak, Keilth
; TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase Family
; FILE REFERENCE: 01017/35966A
; CURRENT APPLICATION NUMBER: US/09/724,126A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,211
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 29
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-724-126A-29

Query Match 9.1%; Score 12; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 CCCTGATGCAC 60
|||
Db 5 CCCTGATGCAC 16

RESULT 25
US-09-329-515A-59
; Sequence 59, Application US/09329515A
; Patent No. 6740487
; GENERAL INFORMATION:
; APPLICANT: Schwartz, David A.
; APPLICANT: Schutte, Brian C.
; TITLE OF INVENTION: Variant TLR4 nucleic acid and uses thereof
; FILE REFERENCE: 875.010US1
; CURRENT APPLICATION NUMBER: US/09/329,515A

/ CURRENT FILING DATE: 1999-06-10
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 59
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-329-515A-59

Query Match 9.1%; Score 12; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GCAGCCTGCAT 56
DB 6 GCAGCCTGCAT 17

RESULT 26
US-09-339-775-4/c
Sequence 4, Application US/09339775
Patent No. 6063626
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
FILE REFERENCE: RTS-0069
CURRENT APPLICATION NUMBER: US/09/339,775
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 4
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Probe
US-09-339-775-4

Query Match 9.1%; Score 12; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCATCATCTGCC 16
DB 14 GCATCATCTGCC 3

RESULT 27
US-08-211-202-76/c
Sequence 76, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
APPLICANT: BAIER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202

/ FILING DATE: 23-SEP-1992
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9120252.3
/ FILING DATE: 23-SEP-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9120377.8
/ FILING DATE: 25-SEP-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9206318.9
/ FILING DATE: 24-MAR-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9206372.6
/ FILING DATE: 24-MAR-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GB92/00883
/ FILING DATE: 15-MAY-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: David W. Clough
/ REGISTRATION NUMBER: 36,107
/ REFERENCE/DOCKET NUMBER: 28111/31960
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 76:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 23 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-08-211-202-76

Query Match 9.1%; Score 12; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCTGAGT 42
DB 20 GACTGCTGAGT 9

RESULT 28
US-08-350-260A-554/c
Sequence 554, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nislin, Ahuva
APPLICANT: Johnson, Kevin Stuart
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A

FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 554:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-554

Query Match 9.1%; Score 12; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGA 42
Db 20 GACTGCGTGA 9

RESULT 29
US-08-860-882A-39/c
Sequence 39, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGELTE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HUIW
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-860-882A-39

Query Match 9.1%; Score 12; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GAACTGCTGCA 29
Db 19 GAACTGCTGCA 8

RESULT 30
US-08-860-882A-51/c
Sequence 51, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGELTE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HUIW
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:
LENGTH: 23 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-860-882A-51

Query Match 9.1%; Score 12; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGACCTGCTGCA 29
DB 19 GGACCTGCTGCA 8

RESULT 31
US-09-011-769A-6/C
Sequence 6, Application US/09011769A
Patent No. 6436691

GENERAL INFORMATION:
APPLICANT: SLATER, Anthony M.

BLAKEY, David C.
DAVIES, David H.
HENNAM, John F.

HENNEQUIN, Laurent F.A.
MARSHAM, Peter R.
DOWELL, Robert I.

TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, LLP

STREET: 1100 New York Ave., N.W.
CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A

FILING DATE: 13-Feb-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975

FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7

FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2

FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0

FILING DATE: 16-AUG-1995
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-011-769A-6

Query Match 9.1%; Score 12; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGACCTGCTGCA 29
DB 19 GGACCTGCTGCA 8

RESULT 32

US-09-011-769A-33/C
Sequence 33, Application US/09011769A
Patent No. 6436691

GENERAL INFORMATION:
APPLICANT: SLATER, Anthony M.

BLAKEY, David C.
DAVIES, David H.
HENNAM, John F.

HENNEQUIN, Laurent F.A.
MARSHAM, Peter R.
DOWELL, Robert I.

TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, LLP

STREET: 1100 New York Ave., N.W.
CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A

FILING DATE: 13-Feb-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975

FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7

FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2

FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0

FILING DATE: 16-AUG-1995
INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-011-769A-33

Query Match 9.1%; Score 12; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGACCTGCTGCA 29
DB 19 GGACCTGCTGCA 8

RESULT 33

US-09-104-337A-554/C
Sequence 554, Application US/09104337A
Patent No. 6492160

GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul

Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter

Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond

TITLE OF INVENTION: Methods for producing members of specific
binding pairs

NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104.337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 554:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 554:
US-09-104-37A-554
Query Match 9.1%; Score 12; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9
RESULT 34
US-10-067-443-48/c
Sequence 48, Application US/10067443
Patent No. 6642041
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALLOPROTEASE HIGHLY EXPRESSED IN
FILE REFERENCE: D0073 NP
CURRENT FILING DATE: 2002-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0

SEQ ID NO 48
LENGTH: 23
TYPE: DNA
ORGANISM: Homo sapiens
US-10-067-443-48
Query Match 9.1%; Score 12; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9
RESULT 35
US-10-153-064-48/c
Sequence 48, Application US/10153064
Patent No. 6653485
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: P556
CURRENT APPLICATION NUMBER: US/10/153,064
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/293,212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Degenerate Vkapppa forward primer useful for
US-10-153-064-48
Query Match 9.1%; Score 12; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 31 GACTGCGTGAGT 42
DB 20 GACTGCGTGAGT 9
RESULT 36
US-09-724-126A-28
Sequence 28, Application US/09724126A
Patent No. 6706505
GENERAL INFORMATION:
APPLICANT: Han, Hui-Quan
TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase Family
FILE REFERENCE: 01017/35966A
CURRENT APPLICATION NUMBER: US/09/724,126A
CURRENT FILING DATE: 2000-11-28
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
SEQ ID NO 28
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-724-126A-28
Query Match 9.1%; Score 12; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 CCCTGCATGCAC 60
|||||
Db 4 CCCTGCATGCAC 15

RESULT 37
US-09-123-030-33
Sequence 33, Application US/09123030
Patent No. 6365337
GENERAL INFORMATION:
APPLICANT: Letts, Verity A.
APPLICANT: Frankel, Wayne N.
APPLICANT: Campbell, Kevin P.
APPLICANT: Felix, Ricardo
APPLICANT: Biddlecome, Gloria
TITLE OF INVENTION: Genes Encoding Neuronal Voltage-Gated Calcium Channel
FILE REFERENCE: US App. 09/123,030
CURRENT APPLICATION NUMBER: US/09/123,030
CURRENT FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-123-030-33

Query Match 9.1%; Score 12; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 AGGACCTGCTGC 28
|||||
Db 6 AGGACCTGCTGC 17

RESULT 38
US-09-866-108A-5110/c
Sequence 5110, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOmica-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: AboMica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 5110
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-5110

Query Match 9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 CCAGGACCTGCT 26
|||||
Db 25 CCAGGACCTGCT 14

RESULT 39
US-09-866-108A-5111/c
Sequence 5111, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOmica-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: AboMica Sequence Listing Engine
SEQ ID NO 5111
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-5111

Query Match 9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 CCAGGACCTGCT 26

Db 24 CCAGACTGCT 13

RESULT 40

US-09-866-108A-5112/c
; Sequence 5112, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5112
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5112

Query Match 9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGACTGCT 26
Db 23 CCAGACTGCT 12

RESULT 41

US-09-866-108A-5113/c
; Sequence 5113, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 5113
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-5113

Query Match 9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGACTGCT 26
Db 22 CCAGACTGCT 11

RESULT 42

US-09-866-108A-5114/c
; Sequence 5114, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

```

; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5114
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-5114
```

```

Query Match          9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      15 CCAGGACCTGCT 26
Db      21 CCAGGACCTGCT 10
```

```

RESULT 43
; US-09-866-108A-5115/c
; Sequence 5115, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5115
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-5115
```

```

Query Match          9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      15 CCAGGACCTGCT 26
Db      20 CCAGGACCTGCT 9
```

```

RESULT 44
; US-09-866-108A-5116/c
; Sequence 5116, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5116
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-5116
```

```

Query Match          9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      15 CCAGGACCTGCT 26
Db      19 CCAGGACCTGCT 8
```

```

RESULT 45
; US-09-866-108A-5117/c
; Sequence 5117, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
```

```
FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: AEWICA Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5117
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5117
```

```
Query Match          9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 15 CCAGACTGCT 26
Db 18 CCAGACTGCT 7
```

```
RESULT 46
US-09-866-108A-5118/c
; Sequence 5118, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
```

```
PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: AEWICA Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5118
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5118
```

```
Query Match          9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 15 CCAGACTGCT 26
Db 17 CCAGACTGCT 6
```

```
RESULT 47
US-09-866-108A-5119/c
; Sequence 5119, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: AEWICA Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5119
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5119
```

QY 15 CCAGGACCTGCT 26
| | | | | | | | | |
Db 16 CCAGGACCTGCT 5
| | | | | | | | | |

RESULT 48
US-09-866-108A-5120/c
; Sequence 5120, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5120
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5120

Query Match 9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACCTGCT 26
| | | | | | | | | |
Db 15 CCAGGACCTGCT 4
| | | | | | | | | |

RESULT 49
US-09-866-108A-5121/c
; Sequence 5121, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5121
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5121

Query Match 9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACCTGCT 26
| | | | | | | | | |
Db 14 CCAGGACCTGCT 3
| | | | | | | | | |

RESULT 50
US-09-866-108A-5122/c
; Sequence 5122, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 5122
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-5122

Query Match 9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACTGCT 26
DB 13 CCAGGACTGCT 2

RESULT 51
US-09-866-108A-5123/c
Sequence 5123, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yongang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 5123
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-5123

Query Match 9.1%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CCAGGACTGCT 26
DB 12 CCAGGACTGCT 1

RESULT 52
US-08-859-998-358/c
Sequence 358, Application US/0885998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jekhadze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 358:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-358

Query Match 9.1%; Score 12; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 TGTCCTACTGCTGC 120
DB 19 TGTCCTACTGCTGC 8

RESULT 53
US-08-486-857-3/c
Sequence 3, Application US/08486857
Patent No. 6075181
GENERAL INFORMATION:
APPLICANT: Kuchariapati, Raju
APPLICANT: Jakobovite, Aya
APPLICANT: Klapholz, Sue
APPLICANT: Brenner, Daniel G.

APPLICANT: Capon, Daniel J.
TITLE OF INVENTION: HUMAN ANTIBODIES DERIVED FROM IMMUNIZED
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,857
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halliwin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7639-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-486-857-3

Query Match 9.1%; Score 12; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGAGT 42
|||||
Db 20 GACTGCGTGAGT 9

RESULT 54
US-08-724-752-19/c
Sequence 19, Application US/08724752
Patent No. 6150584
GENERAL INFORMATION:
APPLICANT: Kucheralapati, Raju
APPLICANT: Jakobovits, Aya
APPLICANT: Brenner, Daniel G.
APPLICANT: Capon, Daniel J.
APPLICANT: Klapholz, Sue
TITLE OF INVENTION: HUMAN ANTIBODIES DERIVED FROM IMMUNIZED
TITLE OF INVENTION: XENOMICE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,752

FILING DATE: 02-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05928
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cell 4.17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-724-752-19

Query Match 9.1%; Score 12; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGAGT 42
|||||
Db 20 GACTGCGTGAGT 9

RESULT 55
US-09-225-928-358/c
Sequence 358, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95.
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 358:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 358:
US-09-225-928-358

Query Match 9.1%; Score 12; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 TGCTCTACTGTC 120
DB 19 TGCTCTACTGTC 8

RESULT 56
US-09-225-201B-358/c
Sequence 358, Application US/09225201B
Patent No. 648945
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Biblashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225.201B
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 358:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 358:
US-09-225-201B-358

Query Match 9.1%; Score 12; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 TGCTCTACTGTC 120
DB 19 TGCTCTACTGTC 8

RESULT 57
US-08-923-138-3/c
Sequence 3, Application US/08923138
Patent No. 6657103
GENERAL INFORMATION:
APPLICANT: KUCHERLAPATI, RAJU
APPLICANT: JAKOBOVITS, AYA
APPLICANT: KLAPHOLZ, SUB
APPLICANT: BRENNER, DANIEL G.
APPLICANT: CAPON, DANIEL J.

TITLE OF INVENTION: HUMAN ANTIBODIES DERIVED FROM IMMUNIZED XENOMICE
FILE REFERENCE: CELL 4.8 FMC CPA

CURRENT APPLICATION NUMBER: US/08/923,138
CURRENT FILING DATE: 1997-09-16
PRIOR APPLICATION NUMBER: 08/430,938
PRIOR FILING DATE: 1995-04-27
PRIOR APPLICATION NUMBER: 08/234,145
PRIOR FILING DATE: 1994-04-28
PRIOR APPLICATION NUMBER: 08/112,848
PRIOR FILING DATE: 1993-08-27
PRIOR APPLICATION NUMBER: 08/031,801
PRIOR FILING DATE: 1993-03-15
PRIOR APPLICATION NUMBER: 07/919,297
PRIOR FILING DATE: 1992-07-24
PRIOR APPLICATION NUMBER: 07/610,515
PRIOR FILING DATE: 1990-11-08
PRIOR APPLICATION NUMBER: 07/466,008
PRIOR FILING DATE: 1990-01-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-08-923-138-3

Query Match 9.1%; Score 12; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GACTGCGTGACT 42
DB 20 GACTGCGTGACT 9

RESULT 58
US-09-614-092A-19/c
Sequence 19, Application US/09614092A
Patent No. 6713610
GENERAL INFORMATION:
APPLICANT: KUCHERLAPATI, RAJU
APPLICANT: JAKOBOVITS, AYA
APPLICANT: BRENNER, DANIEL G.
APPLICANT: CAPON, DANIEL J.
APPLICANT: KLAPHOLZ, SUB
TITLE OF INVENTION: HUMAN ANTIBODIES DERIVED FROM IMMUNIZED XENOMICE
FILE REFERENCE: Cell 4.17 DIV2
CURRENT APPLICATION NUMBER: US/09/614,092A
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 08/724,752
PRIOR FILING DATE: 1996-10-02
PRIOR APPLICATION NUMBER: 08/430,938
PRIOR FILING DATE: 1995-04-27
PRIOR APPLICATION NUMBER: 08/234,145
PRIOR FILING DATE: 1994-04-28
PRIOR APPLICATION NUMBER: 08/112,848
PRIOR FILING DATE: 1993-08-27
PRIOR APPLICATION NUMBER: 08/031,801
PRIOR FILING DATE: 1993-03-15
PRIOR APPLICATION NUMBER: 07/919,297
PRIOR FILING DATE: 1992-07-24

PRIOR APPLICATION NUMBER: 07/610,515
PRIOR FILING DATE: 1990-11-08
PRIOR APPLICATION NUMBER: 07/466,008
PRIOR FILING DATE: 1990-01-12
PRIOR APPLICATION NUMBER: PCT/US96/05928
PRIOR FILING DATE: 1996-04-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 19
LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-614-092A-19

Query Match 9.1%; Score 12; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 GACTGCTGAGT 42
DB 20 GACTGCTGAGT 9

RESULT 59

US-08-911-894-25/c
Sequence 25, Application US/08911894
Patent No. 6030830

GENERAL INFORMATION:

APPLICANT: Saxon, Andrew

APPLICANT: Zhang, Ke

APPLICANT: Fujieda, Shigeharu

TITLE OF INVENTION: IMMUNOGLOBULIN TRANS-SPLICED TRANSCRIPTS

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 90

CORRESPONDENCE ADDRESSES:

ADDRESSES: Aktin, Gump, Strauss, Hauer & Feld

STREET: 816 Congress Avenue, Suite 1900

CITY: Austin

STATE: Texas

COUNTRY: USA

ZIP: 78701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/911,894

FILING DATE: Concurrently Herewith

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/023,579

FILING DATE: 19-AUG-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Mayfield, Denise L.

REGISTRATION NUMBER: 33,732

REFERENCE/DOCKET NUMBER: 43496.0006

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 499-6200

TELEFAX: (512) 499-6290

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-911-894-25

Query Match 9.1%; Score 12; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 TCATCTGCCAGG 19
DB 27 TCATCTGCCAGG 16

RESULT 60

US-09-180-109A-47/c
Sequence 47, Application US/09180109A
Patent No. 6410293

GENERAL INFORMATION:

APPLICANT: MUKIMOTO, Fujio

APPLICANT: NISHIO, Shoichi

APPLICANT: AKIMARU, Uiro

APPLICANT: MITSUDA, Satoshi

TITLE OF INVENTION: DNA Fragments Containing Biotin Biosynthetase Gene and

TITLE OF INVENTION: Use of the Same

FILE REFERENCE: 0152-0490P

CURRENT APPLICATION NUMBER: US/09/180,109A

CURRENT FILING DATE: 1998-12-03

PRIOR APPLICATION NUMBER: 09/047838 JAPAN

PRIOR FILING DATE: 1997-03-03

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 47

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer F3

US-09-180-109A-47

Query Match 9.1%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 CACAGCTCTGC 69
DB 19 CACAGCTCTGC 8

RESULT 61

US-09-304-232-669/c
Sequence 669, Application US/09304232
Patent No. 6525185

GENERAL INFORMATION:

APPLICANT: Fan, Jian Bing

APPLICANT: Chakravarti, Aravinda

APPLICANT: Halubek, Marc Kenneth

APPLICANT: Case Western Reserve University School of Medicine

APPLICANT: Altimetrix, Inc.

TITLE OF INVENTION: Polymorphisms Associated with

TITLE OF INVENTION: Hypertension

FILE REFERENCE: 018547-034210US

CURRENT APPLICATION NUMBER: US/09/304,232

CURRENT FILING DATE: 1999-05-03

EARLIER APPLICATION NUMBER: US 60/084,641

EARLIER FILING DATE: 1998-05-07

NUMBER OF SEQ ID NOS: 909

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 669

LENGTH: 29

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: NETEX9 56

US-09-304-232-669

Query Match 9.1%; Score 12; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TCATCTGCCAGG 19
Db 29 TCATCTGCCAGG 18

RESULT 62

US-07-931-473B-27
Sequence 27, Application US/07931473B
Patent No. 5270163
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/931,473B
FILING DATE: 19920817
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-931-473B-27

Query Match 9.1%; Score 12; DB 1; Length 30;
Best Local Similarity 83.3%; Pred. No. 4.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 91 ATGAGGCGCTCG 102
Db 5 AUGAGGCGCUCG 16

RESULT 63

US-07-714-131C-27
Sequence 27, Application US/07714131C
Patent No. 5475096
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 344
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage

COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/714,131C
FILING DATE: June 10, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-714-131C-27

Query Match 9.1%; Score 12; DB 1; Length 30;
Best Local Similarity 83.3%; Pred. No. 4.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 91 ATGAGGCGCTCG 102
Db 5 AUGAGGCGCUCG 16

RESULT 64
US-08-412-110-27
Sequence 27, Application US/08412110
Patent No. 5670637
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 344
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,110
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
US-08-412-110-27

Query Match 9.1%; Score 12; DB 1; Length 30;
Best Local Similarity 83.3%; Pred. No. 4.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 91 ATGAGCGCTCG 102
|:|||||:
Db 5 AUGAGCGCUCG 16

RESULT 65
US-08-409-442A-27
Sequence 27, Application US/08409442A
Patent No. 5696249
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,442A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-409-442A-27

Query Match 9.1%; Score 12; DB 1; Length 30;
Best Local Similarity 83.3%; Pred. No. 4.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 91 ATGAGCGCTCG 102
|:|||||:
Db 5 AUGAGCGCUCG 16

RESULT 66
US-08-469-609A-27
Sequence 27, Application US/08469609A
Patent No. 5843653
GENERAL INFORMATION:
APPLICANT: Larry Gold

APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,609A
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-609A-27

Query Match 9.1%; Score 12; DB 2; Length 30;
Best Local Similarity 83.3%; Pred. No. 4.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 91 ATGAGCGCTCG 102
|:|||||:
Db 5 AUGAGCGCUCG 16

RESULT 67
US-09-143-190-27
Sequence 27, Application US/09143190
Patent No. 6110900
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

```

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WordPerfect 8.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/143,190
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/469,609
/ FILING DATE: June 6, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/428,964
/ FILING DATE: April 25, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/412,110
/ FILING DATE: March 27, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/409,442
/ FILING DATE: March 24, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/714,131
/ FILING DATE: June 10, 1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/536,428
/ FILING DATE: June 11, 1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Barry J. Swanson
/ REGISTRATION NUMBER: 33,215
/ REFERENCE/DOCKET NUMBER: NEX01/C6
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (303) 793-3333
/ TELEFAX: (303) 793-3433
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 30 nucleotides
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-143-190-27

Query Match          9.1%; Score 12; DB 3; Length 30;
Best Local Similarity 83.3%; Pred. No. 4.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy      91 ATGGAGCGCTCG 102
      ||:|||||:|
Db      5 AUGGAGCGCUCG 16

RESULT 68
US-09-502-344-27
/ Sequence 27, Application US/09502344
/ Patent No. 6331398
/ GENERAL INFORMATION:
/ APPLICANT: Larry Gold
/ APPLICANT: Craig Turk
/ TITLE OF INVENTION: Nucleic Acid Ligands
/ NUMBER OF SEQUENCES: 374
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Swanson & Bratschun, L.L.C.
/ STREET: 8400 E. Prentice Avenue, Suite 200
/ CITY: Englewood
/ STATE: Colorado
/ COUNTRY: USA
/ ZIP: 80111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WordPerfect 8.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/502,344
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/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/143,190
/ FILING DATE: August 27, 1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/469,609
/ FILING DATE: June 6, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/428,964
/ FILING DATE: April 25, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/412,110
/ FILING DATE: March 27, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/409,442
/ FILING DATE: March 24, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/714,131
/ FILING DATE: June 10, 1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/536,428
/ FILING DATE: June 11, 1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Barry J. Swanson
/ REGISTRATION NUMBER: 33,215
/ REFERENCE/DOCKET NUMBER: NEX01/C7
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (303) 793-3333
/ TELEFAX: (303) 793-3433
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 30 nucleotides
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-502-344-27

Query Match          9.1%; Score 12; DB 3; Length 30;
Best Local Similarity 83.3%; Pred. No. 4.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy      91 ATGGAGCGCTCG 102
      ||:|||||:|
Db      5 AUGGAGCGCUCG 16

RESULT 69
US-09-937-832-16/C
/ Sequence 16, Application US/09937832
/ Patent No. 6586200
/ GENERAL INFORMATION:
/ APPLICANT: OMURA, SATOSHI
/ APPLICANT: ABE, AKIO
/ TITLE OF INVENTION: METHOD FOR DETECTING SUBSTANCES INHIBITING THE
/ TITLE OF INVENTION: BACTERIAL TYPE III SECRETION MECHANISM AND FUNCTION OF
/ FILE REFERENCE: KP-9106
/ CURRENT APPLICATION NUMBER: US/09/937,832
/ CURRENT FILING DATE: 2002-05-21
/ PRIOR APPLICATION NUMBER: PCT/JP01/00377
/ PRIOR FILING DATE: 2001-01-22
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 30
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
/ US-09-937-832-16

Query Match          9.1%; Score 12; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGCATCATCTGC 15
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Db 22 TGCATCATCTGC 11

RESULT 70

US-09-419-212-4
; Sequence 4, Application US/09419212
; Patent No. 6203992
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Grunados, E.
; APPLICANT: Scheffell, C.
; TITLE OF INVENTION: Nucleic Acid Primers And Probes For
; FILE REFERENCE: 6589, US.O1
; CURRENT APPLICATION NUMBER: US/09/419,212
; CURRENT FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 15.
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-419-212-4

Query Match 8.3%; Score 11; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACCTGC 25
|||||
Db 5 CCAGGACCTGC 15

RESULT 71

US-09-419-212-6/C
; Sequence 6, Application US/09419212
; Patent No. 6203992
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Scheffell, C.
; APPLICANT: Grunados, E.
; TITLE OF INVENTION: Nucleic Acid Primers And Probes For
; FILE REFERENCE: 6589, US.O1
; CURRENT APPLICATION NUMBER: US/09/419,212
; CURRENT FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-419-212-6

Query Match 8.3%; Score 11; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCAGGACCTGC 25
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Db 11 CCAGGACCTGC 1

RESULT 72
US-09-060-299-454/C

; Sequence 454, Application US/09060299

; Patent No. 6545137
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hees, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko
; APPLICANT: Merriman, Tony R
; APPLICANT: Metzker, Michael L
; TITLE OF INVENTION: No. 6545137el Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Nixon and Vanderhye
; STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,299
; FILING DATE: 15-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B. J. Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-35
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4091
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 454:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-060-299-454

Query Match 8.3%; Score 11; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 TGTCTACTCTG 119
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Db 14 TGTCTACTCTG 4

RESULT 73

US-09-402-923A-454/C
; Sequence 454, Application US/09402923A
; Patent No. 655654
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hees, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko

Meritman, Tony R
Meizker, Michael L
TITLE OF INVENTION: No. 6555654e1 LDL-Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
ZIP: VA 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,923A
FILING DATE: 14-Feb-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01102
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: B.J. Sadoff
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4100
TELEFAX: (703)816-4091
INFORMATION FOR SEQ ID NO: 454:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 454:
US-09-402-923A-454
Query Match 8.3%; Score 11; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 109 TGTCTACTG 119
DB 14 TGTCTACTG 4
RESULT 74
US-07-990-297-13
Sequence 13, Application US/07990297
Patent No. 5340728
GENERAL INFORMATION:
APPLICANT: GROSZ, RON
APPLICANT: JENSEN, MARK A
TITLE OF INVENTION: IMPROVED METHOD FOR
TITLE OF INVENTION: APPLICATION OF TARGETED
TITLE OF INVENTION: SEGMENTS OF NUCLEIC ACID USING
TITLE OF INVENTION: NESTED POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Macintosh

OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/990,297
FILING DATE: 19921209
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GEIGER, KATHLEEN W
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: MD-0103
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-990-297-13
Query Match 8.3%; Score 11; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 2 CATGCATCATC 12
DB 4 CATGCATCATC 14
RESULT 75
US-08-373-124A-1749/C
Sequence 1749, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327

```

; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1749:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-373-124A-1749

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Query Match      8.3%; Score 11; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      91 ATGAGGCGCTC 101
Db      12 ATGAGGCGCTC 2

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Search completed: February 2, 2005, 23:37:50
 Job time : 14.6615 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:07:30 : Search time 1529.28 Seconds

(without alignments)
11866.381 Million cell updates/sec

Title: US-10-048-046-1_COPY_1516_2013

Perfect score: 498

Sequence: 1 tgcctctgcaggaagca.....gtactggggccgaactgc 498

Scoring table: OLIGO_NUC

Searched: 32822875 seqs, 18219865908 residues

Word size: 0

Total number of hits satisfying chosen parameters: 46458

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

Database:

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
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6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 3	13	2.6	26	8	A2762572 1M0557P02
C 4	13	2.6	28	1	AU255721 AU255721
C 5	13	2.6	30	8	A2364675 AU255721
C 6	12	2.4	22	8	A2304010 1M0003023
C 7	12	2.4	23	8	A2785667 2M0029T15
C 8	12	2.4	23	6	CF303555 ABFL-02-
C 9	12	2.4	26	8	A2436027 1M0233C06
C 10	12	2.4	28	1	AA906876 C120e05.8
C 11	12	2.4	29	8	A2421270 1M0190C02
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C 13	12	2.4	30	8	A2623010 1M0460E14
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C 17	11	2.2	19	8	A2361152 1M0104A16
C 18	11	2.2	19	8	A2643124 1M0506P02
C 19	11	2.2	19	8	A2648404 1M0517T23
C 20	11	2.2	19	8	A2595149 2M0280D22
C 21	11	2.2	22	1	AA989077 OR88e03.8
C 22	11	2.2	22	9	TA312810P
C 23	11	2.2	23	6	CD531171 09L20 Ara
C 24	11	2.2	24	8	A2331594 1M0059D12

C 25	11	2.2	25	1	AT123486
C 26	11	2.2	25	7	H30582
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C 31	11	2.2	29	5	BX557759
C 32	11	2.2	29	8	A2316600
C 33	11	2.2	29	8	A2602874
C 34	11	2.2	30	1	AJ796976
C 35	11	2.2	30	6	CF300184
C 36	11	2.2	30	8	B2382659
C 37	11	2.2	31	6	CF325654
C 38	10	2.0	14	9	CL436292
C 39	10	2.0	15	4	BM397934
C 40	10	2.0	15	9	AJ590969
C 41	10	2.0	16	4	BM401104
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C 43	10	2.0	17	4	BM397514
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C 53	10	2.0	19	8	A2481973
C 54	10	2.0	19	8	A2501453
C 55	10	2.0	19	8	A2625779
C 56	10	2.0	19	8	A2647364
C 57	10	2.0	19	8	A2688730
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C 59	10	2.0	20	5	BX551623
C 60	10	2.0	20	6	CF307053
C 61	10	2.0	20	8	A2303903
C 62	10	2.0	20	8	A2307491
C 63	10	2.0	20	8	A2407675
C 64	10	2.0	20	8	A2484701
C 65	10	2.0	20	8	A2659783
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C 83	10	2.0	21	8	A2810730
C 84	10	2.0	21	8	A2812949
C 85	10	2.0	21	8	A2820163
C 86	10	2.0	21	8	A2828828
C 87	10	2.0	22	1	A1040053
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C 91	10	2.0	22	8	A2602332
C 92	10	2.0	22	8	A2770300
C 93	10	2.0	22	8	A2786587
C 94	10	2.0	22	8	BH854069
C 95	10	2.0	22	9	AJ594415
C 96	10	2.0	22	9	TA326E020
C 97	10	2.0	22	9	TA375C030

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H30582 y124e12.r1
H93534 y008g12.r1
CG712540 1119027E0
AU256278 AU256278
CF325420 JMT1--03-
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A2316600 1M0037G14
A2602874 1M0421B21
AJ796976 AJ796976
CF300184 7LEAF--04
B2382659 SALK_1186
CF325654 JMT1--03-
CL436292 PST2678-N
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AJ590969 Arabidops
BM401104 5009-0-82
BM397034 5009-0-28
BM397514 5009-0-33
BM398743 5009-0-49
BO590149 E012845-0
A1049374 ub33a03.x
A1042746 DXEP434C
BM395679 5009-0-10
CD532073 13104 Ara
CF305339 CLD1--01-
A2314110 1M0030E16
A2394490 1M0158005
A2481973 1M0306J12
A2501453 1M0340M13
A2625779 1M0467B14
A2647364 1M0513016
A2688730 2M0164104
AU060510 AU060510
BX551623 BX551623
CF307053 HDAL--06-
A2303903 1M0003B18
A2307491 1M0009C13
A2407675 1M0178E04
A2484701 1M0311C24
A2659783 1M0537M23
A2809111 2M0072B23
A2835099 2M0129T07
AG188183 Pan tceg1
AG191409 Pan tceg1
AG197503 Pan tceg1
AG201573 Pan tceg1
AU013419 AU013419
AU013601 AU013601
AU013625 AU013625
AU013662 AU013662
AU013714 AU013714
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A2783428 2M0025F10
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A2812949 2M0080D02
A2820163 2M0092M12
A2828828 2M0106C04
A1040053 qx28B01.x
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A2506740 1M0348I06
A2579341 1M0363F16
A2602332 1M0421I04
A2770300 1M057JL15
A2786587 2M0032J12
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AJ491048 T. brucei
AL495448 T. brucei

C 98	10	2.0	22	9	AG192935	AG192935 Pan treg1
C 99	10	2.0	23	1	AJ791120	AJ791120
100	10	2.0	23	8	AJ317066	AJ317066 IM0035C09
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102	10	2.0	23	8	AJ368791	AJ368791 IM0119H06
C 103	10	2.0	23	8	AJ451117	AJ451117 IM0250A16
104	10	2.0	23	8	AZ486802	AZ486802 IM0315H02
105	10	2.0	23	8	AZ582153	AZ582153 IM0374B24
106	10	2.0	23	9	TA265A03P	TA265A03P
107	10	2.0	24	1	AJ645986	AJ645986 T. brucei
108	10	2.0	24	6	CD744129	CD744129 IRB17.D11
109	10	2.0	24	8	AJ324350	AJ324350 IM0046F14
110	10	2.0	24	8	AJ363658	AJ363658 IM0109H16
111	10	2.0	24	8	AZ403810	AZ403810 IM0171M11
112	10	2.0	24	8	AZ478673	AZ478673 IM0298J20
C 113	10	2.0	24	8	AZ602206	AZ602206 IM0420B22
114	10	2.0	24	8	AZ647926	AZ647926 IM0514N12
115	10	2.0	24	8	AZ762000	AZ762000 IM0556F08
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C 118	10	2.0	25	1	AI081705	AI081705 CW81d01.8
C 119	10	2.0	25	1	AJ676853	AJ676853 AJ576853
C 120	10	2.0	25	1	AJ797003	AJ797003 AJ576853
C 121	10	2.0	25	5	BQ592774	BQ592774 E012124-0
C 122	10	2.0	25	6	CA587523	CA587523 LBE13P44P
C 123	10	2.0	25	7	R89803	R89803 YP91B12.r1
124	10	2.0	25	8	AZ346856	AZ346856 IM0082J15
C 125	10	2.0	25	8	AZ419335	AZ419335 IM0195J17
126	10	2.0	25	8	AZ759839	AZ759839 IM0535B02
C 127	10	2.0	25	8	AZ828697	AZ828697 2M0105O15
128	10	2.0	25	8	AZ944762	AZ944762 2M0205N19
C 129	10	2.0	25	8	BH900958	BH900958 K507822-3
C 130	10	2.0	26	1	AJ684340	AJ684340 AJ684340
C 131	10	2.0	26	1	AJ685260	AJ685260 AJ685260
C 132	10	2.0	26	6	CD746276	CD746276 S6_E09_S6
C 133	10	2.0	26	8	AZ314210	AZ314210 IM0030H23
C 134	10	2.0	26	8	AZ352412	AZ352412 IM0090M13
C 135	10	2.0	26	8	AZ482170	AZ482170 IM0146H24
C 136	10	2.0	26	8	AZ482112	AZ482112 IM0307J06
C 137	10	2.0	26	8	AZ760191	AZ760191 IM0553P10
138	10	2.0	26	8	AZ763044	AZ763044 IM0558P17
C 139	10	2.0	26	8	AZ765240	AZ765240 IM0565K11
C 140	10	2.0	26	8	BH909796	BH909796 SALX_0560
141	10	2.0	26	8	BZ353872	BZ353872 SALX_1223
C 142	10	2.0	26	9	TA126F02Q	TA126F02Q
143	10	2.0	26	9	TA23A040	TA23A040
C 144	10	2.0	27	1	AJ651227	AJ651227 T. brucei
C 145	10	2.0	27	1	AJ747128	AJ747128 AJ747128
C 146	10	2.0	27	6	CA587630	CA587630 LBE08P73
C 147	10	2.0	27	8	AZ338876	AZ338876 IM0070D11
C 148	10	2.0	27	8	AZ456744	AZ456744 IM0259H14
149	10	2.0	27	8	AZ472721	AZ472721 IM0286C08
C 150	10	2.0	27	8	AZ654711	AZ654711 IM0529J04

ALIGNMENTS

RESULT 1
AZ873829/c 21 bp DNA linear GSS 21-FEB-2001
LOCUS AZ873829 210187C15R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG2M0187C15 R, genomic survey sequence.

ACCESSION AZ873829
VERSION AZ873829.1 GI:13082289

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

TITLE Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A. and Wright, D., Weiss, R.
COMMENT Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0187 Row: C Column: 15
Seq primer: CACACAGAAACGCTATACCC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG2M0187C15"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1[4732114]gb[Af129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 CCTGACTGGGCG 144
Db 13 CCTGACTGGGCG 1

RESULT 2
BZ356062/c 24 bp DNA linear GSS 14-NOV-2002
LOCUS BZ356062 24022.33.70.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALX_128022.33.70.x, genomic survey sequence.

ACCESSION BZ356062
VERSION BZ356062.1 GI:24947395

KEYWORDS GSS.
SOURCE Arabidopsis thaliana (chale crese)

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 24) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gedrich,B.C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,J.,
Shim,P., Zimmerman,J., and Ecker,J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome

JOURNAL
COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is a single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At5g05540.
Class: TDNA tagged.

FEATURES

source Location/Qualifiers

1..24
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_128022.33.70.x"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html"

ORIGIN

Query Match 2.6%; Score 13; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 TTCTGCTGTCTGA 347
|||||
Db 16 TTCTGCTGTCTGA 4

RESULT 3

LOCUS

AZ762572 26 bp DNA linear GSS 16-FEB-2001

DEFINITION clone UUCG1M057P02 R, genomic survey sequence.

ACCESSION

AZ762572 GI:12872712

VERSION

KEYWORDS GSS.

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Jelam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiser,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0557 row: P column: 02
Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES

source

1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M057P02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: pMD42ny. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF12972.1]) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 2.6%; Score 13; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 CCGTACTGGGGC 144
|||||
Db 14 CCGTACTGGGGC 2

RESULT 4

LOCUS

AU255721 28 bp mRNA linear EST 25-APR-2002

DEFINITION AU255721 3'-directed mouse cDNA library Mus musculus cDNA clone

ACCESSION

AU255721 GI:20318731

VERSION

KEYWORDS EST.

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Kato,K. and Watabe,R.
Generation of expressed sequence tags from mouse brain
Unpublished (2002)
Contact: Kikuya Karo
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkar@bs.nara.ac.jp.
Url: <http://love2.aist-nara.ac.jp/BSD/index.html>.
Location/Qualifiers

FEATURES

source

1..28
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0006262"
/issue_type="brain"

ORIGIN /clone_lib="3'-directed mouse cDNA library"

Query Match 2.6%; Score 13; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 CTGTGGCTGTGGC 396
DB 20 CTGTGGCTGTGGC 8

RESULT 5
AZ364675/c 30 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0110K20R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0110K20 R, genomic survey sequence.
ACCESSION AZ364675
VERSION AZ364675.1 GI:10478291
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0110 row: K column: 20
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0110K20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

ORIGIN and selected for ampicillin resistance."

Query Match 2.6%; Score 13; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 378 TTACTGCTGTGGC 390
DB 28 TTACTGCTGTGGC 16

RESULT 6
AZ304010/c 22 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0003023R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0003023 R, genomic survey sequence.
ACCESSION AZ304010
VERSION AZ304010.1 GI:10339557
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: O column: 23
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source
1. 22
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0003023"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 2.4%; Score 12; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.3e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 GAGTCAGACATC 252
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15 GAGTCAGACATC 4

RESULT 7
A2785667 23 bp DNA linear GSS 16-FEB-2001
LOCUS 2M002901SR Mouse 10kb plasmid U0GC1M library Mus musculus genomic
DEFINITION clone U0GC2M0029015 R, genomic survey sequence.
ACCESSION A2785667
VERSION A2785667.1 GI:12922656
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Jellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
row: 7 column: 15
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U0GC2M0029015"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U0GC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 2.4%; Score 12; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.3e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 370 GTTCTGTGTTAC 381
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8 GTTCTGTGTTAC 19

RESULT 8
CP303555/c 25 bp mRNA linear EST 15-AUG-2003
LOCUS ABF1--02-J13.g1 ABF3-overexpressing transgenic rice lambda phage
DEFINITION cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA
clone ABF1--02-J13, mRNA sequence.
ACCESSION CP303555
VERSION CP303555.1 GI:33675316
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriocaulaceae; Oryzaceae; Oryza.
1 (bases 1 to 25)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF1--02-J13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABF1)"
/note="Vector: Bluescript SK(+); site 1: EcoRI; site 2:
XhoI; leaf was dried for 2hrs. cDNA was inserted into
lambda uni-zap XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN

Query Match 2.4%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 304 GAGAGCTCTG 315
|||||
13 GAGAGCTCTG 2

RESULT 9
AZ436027/c 26 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0233C06R Mouse 10kb plasmid U0GC1M library Mus musculus genomic
DEFINITION clone U0GC1M0233C06 R, genomic survey sequence.
ACCESSION AZ436027

```

VERSION      AZ436027.1 GI:10560040
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 26)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Bacorn,T., Duvall,B., Hamil,C.,
              Istaitieh,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
JOURNAL      Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
              84112, USA
              Tel.: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert length: 10000 Std Error: 0.00
              Plate: 0233 Row: C Column: 06
              Seq primer: CACACAGGAACGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 26.
FEATURES
  source
    1..26
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UDGCM0233C06"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UDGCM library"
        /note="Vector: PMD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pMDA2 (gi|4732114|gb|AF129072.1)' a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
ORIGIN
Query Match          2.4%; Score 12; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      313 GTGGCTCCAG 324
        ||||||||
        ||||||||
Db       22 GTGGCTTCAG 11

```

ACCESSION	AA906876
VERSION	AA906876.1
KEYWORDS	GI:3042120
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 28)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps-tdemail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 458 Std Error: 0.00 Seq primer: -40ml3 fwd. RT from Amersham High quality sequence stop: 1. location/Qualifiers
FEATURES	1..28
source	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1524032" /lab_host="DH10B" /clone_id="Soares NFL T GBC S1" /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NRT, and B-cell NCI CGAP GCBI) were mixed, and 86 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I M A G E clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
ORIGIN	
Query Match	2.4%; Score 12; DB 1; Length 28;
Best Local Similarity	100.0%; Pred. No. 6; 4e+05;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	423 TCGGCAGAACAT 434
Db	28 TCGGCAGAACAT 17
RESULT 11	
LOCUS	A2421270
DEFINITION	A2421270 29 bp DNA linear GSS 03-OCT-2000
ACCESSION	1M0199022F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0199022 F, genomic survey sequence.
VERSION	A2421270
KEYWORDS	A2421270.1 GI:10545283
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)
TITLE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
JOURNAL	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0199 row: 0 column: 22
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0408 row: M column: 09
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers

1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0139022"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114[g14732114]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 2.4%; Score 12; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 283 ACATGAAAAAC 294
|||
Db 18 ACATGAAAAAC 29

RESULT 12
AZ595520 29 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0408M09F Mouse 10kb plasmid UGC1M library Mus musculus genomic
DEFINITION Clone UGC1M0408M09 F, genomic survey sequence.
ACCESSION AZ595520
VERSION AZ595520.1 GI:11717710
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center

1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0408M09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114[g14732114]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 2.4%; Score 12; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 164 ACCGCTGCTGTG 175
|||
Db 6 ACCGCTGCTGTG 17

RESULT 13
AZ623010 30 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0460E14F Mouse 10kb plasmid UGC1M library Mus musculus genomic
DEFINITION Clone UGC1M0460E14 F, genomic survey sequence.
ACCESSION AZ623010
VERSION AZ623010.1 GI:11745200
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: E column: 14
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCM0460E14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 2.4%; Score 12; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 CTGCTCGACCC 122
Db 13 CTGCTCGACCC 2

RESULT 14
CF306933/c 12 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
HBA1--05-E05.g1 OSHDACL-overexpressing transgenic rice lambda phage
cDNA library 1 (HBA1) Oryza sativa (japonica cultivar-group) CDNA
clone HBA1--05-E05, mRNA sequence.
CF306933
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarthroideae; Oryzaceae; Oryza.
1 (bases 1 to 12)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim, J.S., Yun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003).
Contact: Nahm B.H.
Genetics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .12
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HBA1--05-E05"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E. coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage CDNA library 1 (HBA1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. CDNA
was inserted into lambda uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 2.2%; Score 11; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 305 AGAGCCTCGTG 315
Db 12 AGAGCCTCGTG 2

RESULT 15
A1017839 16 bp mRNA linear EST 16-JUN-1998
LOCUS
DEFINITION
ov06e12.x1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1636750 3',
similar to TR_035993 Q35993 CYTOCHROME C OXIDASE III; contains
element 11 11 repetitive element; mRNA sequence.
A1017839
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1636750"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid3"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 2.2%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 AACACACACAG 236
|||||
1 AACACACACAG 11

RESULT 16
BM400383/c 19 bp mRNA linear EST 17-JAN-2002
LOCUS 5009-0-72-B01.c.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM400383
VERSION BM400383.1 GI:18200436

SOURCE EST.
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 19)
Turkewitz,A.P., Karer,K.M., Jahm,C., Orlas,E., Kirk,K.E.,
Frankel,J., and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apurkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source Location/Qualifiers

1..19
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript 2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 2.2%; Score 11; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 GTGAGCTCAAC 195
|||||
11 GTGAGCTCAAC 1

RESULT 17
AZ361152

LOCUS 19 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M010416R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UUGCG1M010416 R, genomic survey sequence.
ACCESSION AZ361152
VERSION AZ361152.1 GI:10474852

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rally,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A., and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0104 row: A column: 16
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source Location/Qualifiers

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M010416"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42nv. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 2.2%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 CCAGCCCATGC 52
|||||
2 CCAGCCCATGC 12

RESULT 18
AZ643124/c

LOCUS 19 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0506P02R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UUGCG1M0506P02 R, genomic survey sequence.
ACCESSION AZ643124
VERSION AZ643124.1 GI:11770578

KEYWORDS GSS.

SOURCE
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weiser, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiser
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0506 row: P column: 02
Seq primer: CACACAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source 1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0506P02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCGM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 2.2%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 CCTGTACTGGG 142
|||||
|||||

Db 12 CCTGTACTGGG 2

RESULT 19
AZ648404 19 bp DNA linear GSS 14-DEC-2000
LOCUS
DEFINITION 1M0517123F Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGM0517123 F, genomic survey sequence.
ACCESSION AZ648404
VERSION AZ648404.1 GI:11780837
KEYWORDS GSS.

SOURCE
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weiser, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiser
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0517 row: I column: 23
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source 1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0517123"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCGM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 2.2%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 AACACAAACAG 236
|||||
|||||

Db 1 AACACAAACAG 11

RESULT 20
AZ995149 19 bp DNA linear GSS 27-APR-2001
LOCUS
DEFINITION 2M0280D22R Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGM0280D22 R, genomic survey sequence.
ACCESSION AZ995149
VERSION AZ995149.1 GI:13866376
KEYWORDS GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Rolly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhuesern,A. and Wright,D., Weiss,R.
Niederhuesern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0280 row: D column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C2M0280D22"
/sex="female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid U08C2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 2.2%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCT 40
|||||
1 CACCTGCTGCT 11

Db 1 CACCTGCTGCT 11

RESULT 21
LOCUS AA89077/c 22 bp mRNA linear EST 27-JUL-1998
DEFINITION or88e03.at NCI-CGAP LUS Homo sapiens cDNA clone IMAGE:1602940 3' similar to TR:Q15816 Q15816 TRANSMEMBRANE PROTEIN JACGED 1. [2]
TR:Q14902 ; contains TARI.b2 MSRI repetitive element ;, mRNA sequence.
AA89077
ACCESSION AA89077

VERSION
AA89077.1 GI:3174648

KEYWORDS
EST

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINT at: www.bio.1inl.gov/bdtp/image/image.html

FEATURES
Location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1602940"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_1lb="NCI CGAP LUS"
/note="Organ: lung; Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from a neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 2.2%; Score 11; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 CCCGACCGCG 159
|||||
13 CCCGACCGCG 3

Db 13 CCCGACCGCG 3

RESULT 22
LOCUS TA312B10P/c 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 312b10, forward sequence, genomic survey sequence.
ACCESSION AT490359
VERSION AT490359.1 GI:11866449
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE
1 (bases 1 to 22)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Ackin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton.

COMMENT Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

Location/Qualifiers
1..22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TRU927"
/db_xref="taxon:5691"
/clone="312b10"

ORIGIN

Query Match 2.2%; Score 11; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 484 TGGGGCCGTAA 494
|||||

Db 22 TGGGGCCGTAA 12

RESULT 23

CD531171 23 bp mRNA linear EST 31-DEC-2003
LOCUS 09L20 Arabidopsis leaf Senescence Library Arabidopsis thaliana CDNA
DEFINITION CD531171
3', mRNA sequence.

ACCESSION CD531171.1 GI:40451183
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 23)

REFERENCE
AUTHORS Guo, Y., Cai, Z. and Gan, S.
TITLE Transcriptome of Arabidopsis leaf senescence
JOURNAL Plant Cell Environ. 27 (5), 521-549 (2004)
COMMENT Contact: Sueheng Gan
Department of Horticulture
Cornell University
119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
Tel: 607 254 5418
Fax: 607 255 0599
Email: sg288@cornell.edu
Insert Length: 23 Std Error: 0.00
Seq Primer: T7
POLYA-No.

FEATURES

source

Location/Qualifiers
1..23
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecoli_type="landberg erecta"
/db_xref="taxon:3702"
/tissue_type="leaf"
/dev_stage="yellow leaf with Greenish Base Area"
/lab_host="E. coli"
/clone_lib="Arabidopsis leaf Senescence Library"
/note="Organ: Rosette leaf; Vector: pBluescript SKIT+;
Site_1: EcorI; Site_2: EcorI; Senescent rosette leaves #5
and #6 (counted from the bottom) were harvested and
immediately frozen in liquid N2. The leaves were visibly

ORIGIN

Yellow excised for the leaf base areas that were still
greenish.

Query Match 2.2%; Score 11; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 GACTGCTACTG 485
|||||

Db 10 GACTGCTACTG 20

RESULT 24

AZ331594/c 24 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0059D12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0059D12 R, genomic survey sequence.
ACCESSION AZ331594
A2331594.1 GI:10394437
KEYWORDS GSS.

SOURCE
ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
plate: 0059 row: D column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

source

Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0059D12"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gblAF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

ORIGIN chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 2.2%; Score 11; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 326 GGGAGCTGTTT 336
|||||
Db 21 GGGAGCTGTTT 11

RESULT 25
LOCUS A1123486 25 bp mRNA linear EST 01-OCT-1998
DEFINITION ga01e11.x1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone
IMAGE:1683596.3 similar to SW:BAT2_HUMAN P48634 LARGE PROLINE-RICH
PROTEIN BAT2 ;, mRNA sequence.

ACCESSION A1123486

VERSION A1123486.1 GI:3539252

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 25)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
cDNA library preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E.B. Consortium/LNL at:
www-bio.lnl.gov/bdtp/image/image.html

Insert Length: 495 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amerham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source 1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1683596"
/issue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_id="Soares parathyroid tumor NBHPA"
/note="Organ: parathyroid gland; Vector: pRTT3D
(Pharmacia) with a modified polylinker; Site 1: Not I,
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGGCCGACCAATTTTTTTTTTTTTTTT
TTTT-3'] , double-stranded cDNA was size selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pRTT3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

ORIGIN

Query Match 2.2%; Score 11; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 450 GCCAGTGCCG 460
|||||
Db 13 GCCAGTGCCG 3

RESULT 26
LOCUS H30582 25 bp mRNA linear EST 17-JUL-1995
DEFINITION y124e12.r1 Soares breast 2NBHST Homo sapiens cDNA clone
IMAGE:159214.5 similar to gb:U19686.rn1 MACROPHAGE MIGRATION
INHIBITORY FACTOR (HUMAN) ;, mRNA sequence.

ACCESSION H30582

VERSION H30582.1 GI:901492

KEYWORDS EST.

SOURCE Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 25)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, D., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

JOURNAL The Wash-Merck EST Project
Unpublished (1995)

COMMENT Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGS Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGS Consortium (info@image.lnl.gov) for further information.
Seq primer: M13rev
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source 1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:573305"
/db_xref="taxon:9606"
/clone="IMAGE:159214"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_id="Soares breast 2NBHST"
/note="Organ: breast; Vector: pRTT3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGGCCGCTTTTTTTTTTTTTTTT 3'] ,
double-stranded cDNA was ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pRTT3 vector (Pharmacia).
Library went through one round of normalization to a Cot =
230. Library constructed by Bento Soares and M. Fatima
Bonaldo."

ORIGIN

Query Match 2.2%; Score 11; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 386 GTGACCTGCGC 396
|||||
Db 13 GTGACCTGCGC 3

RESULT 27

H93534/c
LOCUS H93534 25 bp mRNA linear EST 01-DEC-1995
DEFINITION YV08912.r1 Soares fetal liver INFES Homo sapiens cDNA clone
IMAGE:24182.5' similar to gb|87933|HUMALU364 Human carcinoma
cell-derived Alu RNA transcript, (rRNA);, mRNA sequence.
H93534
ACCESSION H93534.1 GI:1099862
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 25)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
TITLE The Washu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LBNL
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbnl.gov) for further information.
Trace considered overall poor quality
Seq primer: M13Kp1
High quality sequence stop: 1.
Location/Qualifiers
1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3791315"
/db_xref="taxon:9606"
/clone="IMAGE:24182"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFES"
/note="Organ: Liver and Spleen; Vector: pTR73D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' ACTGAGAGATTAATTAAGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pTR73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bernaldo."

ORIGIN
Query Match 2.2%; Score 11; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 195 CCTGGGTGACA 205
|||||
Db 15 CCTGGGTGACA 5

RESULT 28
CG12540 25 bp DNA linear GSS 20-OCT-2003
LOCUS CG12540
DEFINITION 1119027B01.2EL.y2 1119 - Rescueu Grid AA Zea mays genomic, genomic
survey sequence.
ACCESSION CG12540
VERSION GSS.
KEYWORDS GSS.
GSS. 37738446

SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 25)
AUTHORS Walbot, V.
TITLE Maize genomic sequences found using engineered Rescueu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119027 row: B column: 01
Class: transposon-tagged.
Location/Qualifiers
1..25
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al88/B73/K55"
/db_xref="taxon:4577"
/issue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - Rescueu Grid AA"
/note="Organ: leaf; Vector: Rescueu (engineered from
Bluescript backbone); Site 1: BamHI; Site 2: BglII;
Rescueu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescueu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'Rescueu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN
Query Match 2.2%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 60 GAGAGCGGAGC 70
|||||
Db 10 GAGAGCGGAGC 20

RESULT 29
AU256278 26 bp mRNA linear EST 25-APR-2002
LOCUS AU256278
DEFINITION AU256278.3'-directed mouse cDNA library Mus musculus cDNA clone
BED0007861 3', mRNA sequence.
ACCESSION AU256278
VERSION AU256278.1 GI:20319813
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
AUTHORS Kato, K. and Matoba, R.
TITLE Generation of expressed sequence tags from mouse brain
JOURNAL Unpublished (2002)
COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581
Fax: 81-743-72-5589

Email: kkatoo@ds.aisc-nara.ac.jp,
URL: http://love2.aisc-nara.ac.jp/BED/index.html.

FEATURES

SOURCE

1. .26
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED007961"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"

ORIGIN

Query Match 2.2%; Score 11; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 315 GGCTCTCCAGC 325
|||||
9 GGCTCTCCAGC 19

Db 9 GGCTCTCCAGC 19

RESULT 30

CF325420 27 bp mRNA linear EST 18-AUG-2003
LOCUS CF325420/c
DEFINITION JMT1--03-D02.g1 AtJMT-overexpressing transgenic rice lambda phage
cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA
clone JMT1--03-D02, mRNA sequence.

ACCESSION CF325420
VERSION CF325420.1 GI:33799120

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

SOURCE

1. .27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39847"
/clone="JMT1--03-D02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda
phage cDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasminate Carboxyl
methyltransferase overexpression line."

ORIGIN

Query Match 2.2%; Score 11; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 305 AGAGCTCGTG 315

4 |||||
12 AGAGCTCGTG 2

Db 12 AGAGCTCGTG 2

RESULT 31

BX557759 29 bp mRNA linear EST 10-OCT-2003
LOCUS BX557759
DEFINITION BX557759 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse34e06_glc, mRNA sequence.

ACCESSION BX557759
VERSION BX557759.1 GI:33428934

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2NW
All clones with suffix gic are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
Location/Qualifiers

FEATURES

SOURCE

1. .29
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse34e06_glc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.Brucei"

ORIGIN

Query Match 2.2%; Score 11; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 348 TTACAGAGTCA 358
|||||
11 TTACAGAGTCA 21

Db 11 TTACAGAGTCA 21

RESULT 32

AZ318600 29 bp DNA linear GSS 29-SEP-2000
LOCUS AZ318600/c
DEFINITION IM003G14R Mouse 10kb plasmid UNGCM library Mus musculus genomic
clone tUCGCM003G14 R, genomic survey sequence.

ACCESSION AZ318600
VERSION AZ318600.1 GI:10368531

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0037 row: G column: 14
 Seq primer: CACACAGGAAACACCTATGACC
 Class: plasmid ends
 High quality sequence stop: 29.
 Location/Qualifiers
 1..29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM0037G14"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 2.2%; Score 11; DB 8; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 132 CCTGTACTGGG 142
 Db 28 CCTGTACTGGG 18

RESULT 33
 AZ602874 29 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0421B21R Mouse 10kb plasmid UGGCM library Mus musculus genomic
 DEFINITION
 AZ602874
 ACCESSION AZ602874.1 GI:11725064
 VERSION
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0421 row: B column: 21
 Seq primer: CACACAGGAAACACCTATGACC
 Class: plasmid ends
 High quality sequence stop: 29.
 Location/Qualifiers
 1..29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM0421B21"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 2.2%; Score 11; DB 8; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 46 CCCATGCCCGA 56
 Db 22 CCCATGCCCGA 12

RESULT 34
 AJ796976 30 bp mRNA linear EST 11-AUG-2004
 LOCUS AJ796976 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
 DEFINITION
 AJ796976
 ACCESSION AJ796976.1 GI:5112304
 VERSION
 KEYWORDS EST.
 SOURCE Antirrhinum majus (snapdragon)
 ORGANISM Antirrhinum majus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterides; lamids; Lamiales; Plantaginaceae; Antirrhineae;
Antirrhinum.
1 (bases 1 to 30)
Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
Antirrhinum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforchung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
1. .30
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_3_12_103"
/issue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

ORIGIN
Query Match 2.2%; Score 11; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 289 AAAACATGTT 239
|||||
8 AAAACATGTT 18

RESULT 35
LOCUS CF300184 30 bp mRNA linear EST_15-AUG-2003
DEFINITION 7LEAF--04-H21.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-H21, mRNA sequence.
ACCESSION CF300184.1 GI:33671945
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 30)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .30
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-H21"
/issue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOP0, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN
Query Match 2.2%; Score 11; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.3e+06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 476 ACTGCTACTG 486
|||||
1 ACTGCTACTG 11

RESULT 36
LOCUS B2382659 30 bp DNA linear GSS 26-NOV-2002
DEFINITION SALK_118628.15.45.x Arabidopsis thaliana TDNA insertion lines survey sequence.
ACCESSION B2382659
VERSION B2382659.1 GI:25477906
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 30)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadinh, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At2g06280.
Class: TDNA tagged.
Location/Qualifiers
1. .30
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_118628.15.45.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocol.html

ORIGIN
Query Match 2.2%; Score 11; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 371 TTCTGCTTAC 381
|||||
4 TTCTGCTTAC 14

RESULT 37
LOCUS CF325654/c 11 bp mRNA linear EST_18-AUG-2003
DEFINITION UMT1--03-N04.g1 AluMT-overexpressing transgenic rice lambda phage cDNA library (UMT1) Oryza sativa (japonica cultivar-group) cDNA clone UMT1--03-N04, mRNA sequence.
ACCESSION CF325654
VERSION CF325654.1 GI:33799587
KEYWORDS

SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiaceae; Oryzae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..11
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT1--03-N04"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli SOLR"
/clone_lib="AluMT-overexpressing transgenic rice lambda phage cDNA library (JMT1)"
/note="Vector: Bluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis thaliana cDNA library. methyltransferase overexpression line."

ORIGIN
Query Match 2.0%; Score 10; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 306 GAGCTGCTG 315
DB 11 GAGCTGCTG 2

RESULT 38
CL436292/c
LOCUS
DEFINITION CL436292 14 bp DNA linear GSS 18-MAR-2004
PST2678-NR.Seg MICE1 Mus musculus genomic clone PST2678-NR.Seg,
genomic survey sequence.
ACCESSION CL436292
VERSION CL436292.1 GI:45570949
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 14)
Hicks,G.G.
www.fscells.ca
Unpublished (2002)
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicks@gcc.umanitoba.ca
U3NeosVI gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. RS cell line harboring insertion mutation of target gene is available. Sequence analysis available from
http://140.193.242.7/seed/public_search_frame.php?PST=PST2678-NR.Se

FEATURES
Class: Gene Trap.
source
1..14
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="PST2678-NR.Seg"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (11 subclone)"
/clone_lib="MICE1"
/note="Vector: U3NeosVI"

ORIGIN
Query Match 2.0%; Score 10; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.5e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 383 GCTGTGCTT 392
DB 10 GCTGTGCTT 1

RESULT 39
BM397934/c
LOCUS
DEFINITION BM397934 15 bp mRNA linear EST 17-JAN-2002
5009-0-39-C05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397934
VERSION BM397934.1 GI:18197987
KEYWORDS EST.
SOURCE Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 15)
Frankel,J., Karter,K.M., Jahn,C., Orlas,E., Kirk,K.E., Turkewitz,A.P., Karter,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apurkew@midway.uchicago.edu
Seq primer: 73.

FEATURES
source
1..15
Location/Qualifiers
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match 2.0%; Score 10; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 82 CCGCTGCTG 91
DB 11 CCGCTGCTG 2

RESULT 40
AUS90969/c

LOCUS AU590969 15 bp DNA linear GSS 15-JAN-2004
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 577F01 genomic survey sequence.
 ACCESSION AU590969
 VERSION AU590969.1 GI:37940593
 KEYWORDS GSS; left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1
 AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Legnietec, L., Caboche, M., and Leclercq, A.
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
 JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
 MEDLINE 22363535
 PUBMED 12446565
 REFERENCE 2 (bases 1 to 15)
 AUTHORS Balzerque, S.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publicines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).
 FEATURES
 source
 1. 15
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultiivar="Wassiliwskij1a"
 /db_xref="taxon:3702"
 /clone="577F01"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 1. 15
 /note="T-DNA flanking sequence left border"
 ORIGIN
 Query Match 2.0%; Score 10; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.6e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 289 AAAACATGT 298
 |||||
 |||||
 Db 15 AAAAAGCTGT 6
 |||||
 |||||
 RESULT 41
 BM401104 16 bp mRNA linear EST 17-JAN-2002
 LOCUS BM401104/c
 DEFINITION 5009-0-82-F06.c.1 Chilcoat/Turkewitz cDNA (large fraction)
 ACCESSION BM401104
 VERSION BM401104 GI:18201157
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE 1 (bases 1 to 16)
 AUTHOR Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobutcher, L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 Location/Qualifiers
 1. 16
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 ORIGIN
 Query Match 2.0%; Score 10; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.6e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 185 GTGAGCTCAA 194
 |||||
 |||||
 Db 10 GTGAGCTCAA 1
 |||||
 |||||
 RESULT 42
 BM397034 17 bp mRNA linear EST 17-JAN-2002
 LOCUS BM397034/c
 DEFINITION 5009-0-28-C07.c.2 Chilcoat/Turkewitz cDNA (large fraction)
 ACCESSION BM397034
 VERSION BM397034 GI:18197087
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE 1 (bases 1 to 17)
 AUTHOR Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 Location/Qualifiers
 1. 17
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 ORIGIN
 Query Match 2.0%; Score 10; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.6e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 185 GTGAGCTCAA 194

Db 10 GTGAGCTCAA 1

RESULT 43
BM397514/c
LOCUS
DEFINITION 17 bp mRNA linear EST 17-JAN-2002
5009-0-33-H05.t.1 Chlcoact/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM397514
VERSION
BM397514.1 GI:18197567
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS
Turkewitz, A.P., Karrer, K.M., Jahn, C., Ortas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172

FEATURES
source
1. .17
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_1lb="Chlcoact/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chlcoact and Turkewitz (2001).
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 2.0%; Score 10; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 185 GTGAGCTCAA 194
|||||
10 GTGAGCTCAA 1

Db 10 GTGAGCTCAA 1

RESULT 44
BM398743
LOCUS
DEFINITION 18 bp mRNA linear EST 17-JAN-2002
5009-0-49-F05.t.1 Chlcoact/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM398743
VERSION
BM398743.1 GI:18198796
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS
Turkewitz, A.P., Karrer, K.M., Jahn, C., Ortas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu
Seq primer: T3
Location/Qualifiers
1. .18
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_1lb="Chlcoact/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chlcoact and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 2.0%; Score 10; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 184 TGTGAGCTCA 193
|||||
1 TGTGAGCTCA 10

Db 1 TGTGAGCTCA 10

RESULT 45
B0590149
LOCUS
DEFINITION 18 bp mRNA linear EST 06-DEC-2002
E012845-024-019-B19-T7 MP12-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-B19 3-PRIME, mRNA sequence.
ACCESSION
B0590149
VERSION
B0590149.1 GI:26119732
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS
Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wronck, W., Menze, A., O'Brien, J., Lehnach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weishaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp12-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
Plate: 19 row: B column: 19
Seq primer: T7; GATATCGATCTCACTATGAGGC.
Location/Qualifiers
1. .18
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="RWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189975"
/db_xref="taxon:161934"
/clone_024-019-B19"
/clone_1lb="MP12-ADIS-024-storage root"
/clone_1lb="EMDH108"
/clone_1lb="MP12-ADIS-024-storage root"
/note="Vector: PCWVS-PORT6; Site 1: Salt; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinmanlebenser Saatrucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NoI, primer sites and
orientation:
SP6-SalI-CCAGCGGTCG-5prime-cDNA-polyA-CC-NoI-T7; Note:
Sequencing granted in the context of the GABI-Beet

FEATURES
source
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1.19

/organism="Tetrahymena thermophila"
/mol_type="rRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_1lb="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 2.0%; Score 10; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 GTGAGCTCAA 194
|||||
Db 12 GTGAGCTCAA 3

RESULT 49

CD532073 19 bp mRNA linear EST 31-DEC-2003
LOCUS 13104 Arabidopsis leaf Senescence library Arabidopsis thaliana cDNA
DEFINITION 3', mRNA sequence.
ACCESSION CD532073
VERSION CD532073.1 GI:40452085

KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 19)

AUTHORS Guo, Y., Cai, Z. and Gan, S.
TITLE Transcriptome of Arabidopsis leaf senescence
JOURNAL Plant Cell Environ. 27 (5), 521-549 (2004)
COMMENT Contact: Susheng Gan
Department of Horticulture
Cornell University
119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
Tel: 607 254 5418
Fax: 607 255 0599
Email: sg28@cornell.edu
Insert Length: 19 Std Error: 0.00
Seq primer: T7
POLYA-No.

FEATURES

source

1.19 Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotYPE="Landsberg erecta"
/db_xref="taxon:3702"
/clone_1lb="Yellow leaf with Greenish Base Area"
/dev_stage="E. coli"
/note="Organ: Rosette leaf; Vector: pBluescript SKII+; Site 1: EcoRI; Site 2: EcoRI; Senescent rosette leaves #5 and #6 (counted from the bottom) were harvested and immediately frozen in liquid N2. The leaves were visibly yellow excepted for the leaf base areas that were still greenish."

ORIGIN

Query Match 2.0%; Score 10; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TGCGCTTCC 43

Db 4 TCGCTCTCC 13
|||||

RESULT 50
CF305339/c 19 bp mRNA linear EST 15-AUG-2003
LOCUS CLD1--01-H03.b1 Rice cold treated leaf plasmid cDNA library (CLD1)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone CLD1--01-H03, mRNA sequence.

ACCESSION CF305339
VERSION CF305339.1 GI:33677100
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)

REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm, B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1.19 Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone_1lb="CLD1--01-H03"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice cold treated leaf plasmid cDNA library (CLD1)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

ORIGIN

Query Match 2.0%; Score 10; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 CAGAGTCACG 360
|||||
Db 15 CAGAGTCACG 6

RESULT 51

AZ314110 19 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0030E16R Mouse 10kb plasmid UUGCM library Mus musculus genomic
DEFINITION clone UUGCM0030E16 R, genomic survey sequence.
ACCESSION AZ314110
VERSION AZ314110.1 GI:10359675
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
1 (bases 1 to 19)

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0306 row: J column: 12
Seq primer: CACACAGAAACACGATATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0306J12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 2.0%; Score 10; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 475 GACTGCTACT 484
DB 14 GACTGCTACT 5

RESULT 54
AZ501453/c 19 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0340M13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0340M13 F, genomic survey sequence.
ACCESSION AZ501453
VERSION AZ501453.1 GI:10682769
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE
AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0340 row: M column: 13
Seq primer: CGTGTGAAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0340M13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 2.0%; Score 10; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 43 CAGCCCATGC 52
DB 18 CAGCCCATGC 9

RESULT 55
AZ626779/c 19 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0677A14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0677A14 F, genomic survey sequence.
ACCESSION AZ626779
VERSION AZ626779.1 GI:11748969
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE
AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0467 row: A column: 14
Seq primer: CGTGTAAACGACGCCACG
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0467A14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 2.0%; Score 10; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 108 GGTCGTGCTG 117
|||
Db 19 GGTCGTGCTG 10

RESULT 56
AZ647364/c 19 bp DNA linear GSS 14-DEC-2000
LOCUS 1M051301R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0513016 R, genomic survey sequence.
ACCESSION AZ647364
VERSION AZ647364.1 GI:11778756
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0513 row: O column: 16
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0513016"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 2.0%; Score 10; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 358 ACCGGAGACA 367
|||
Db 19 ACCGGAGACA 10

RESULT 57
AZ858730 19 bp DNA linear GSS 21-FEB-2001
LOCUS 2M014104F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC2M014104 F, genomic survey sequence.
ACCESSION AZ858730
VERSION AZ858730.1 GI:13052133
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SVC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdum@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0164 row: 1 column: 04
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UTGCM0164104"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UTGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (G14732114|GB|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 2.0%; Score 10; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 115 CTGACGCTT 124
DB 9 CTGACGCTT 18

RESULT 58
A0060510 20 bp mRNA linear EST 20-MAY-1999
LOCUS A0060510 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
DEFINITION A0060510 Dictyostelium discoideum SLK222, mRNA sequence.
VERSION A0060510
KEYWORDS A0060510 GI:4881614
SOURCE EST.
ORGANISM Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
REFERENCE 1 (bases 1 to 20)
Mori, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M.,
Yoshino, R., Mitera, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H.,
Williams, J., Meade, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
Developmental cDNA in Dictyostelium discoideum
Unpublished (1998)

COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.
Location/Qualifiers
1..20
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLK222"
/dev_stage="slug"
/clone_1lb="Dictyostelium discoideum SL (H.Urushihara)"

ORIGIN
Query Match 2.0%; Score 10; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 AACACACACA 235
DB 11 AACACACACA 20

RESULT 59
BX551623 20 bp mRNA linear EST 10-OCT-2003
LOCUS BX551623 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION BX551623 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse119f08_glc, mRNA sequence.
VERSION BX551623
KEYWORDS BX551623.1 GI:33375933
SOURCE EST.
ORGANISM Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 20)
Lehane, M.J., Aksoy, S., Gibson, M., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
JOURNAL MEDLINE
PUBMED 22861942
COMMENT 14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix glc are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
Location/Qualifiers
1..20
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse119f08_glc"
/tissue_type="adult infected gut"
/clone_1lb="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with

ORIGIN T.brucei"

Query Match 2.0%; Score 10; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 TTGACATCG 288
|||||
Db 7 TTGACATCG 16

RESULT 60

CF307503 20 bp mRNA linear EST 15-AUG-2003
LOCUS CF307503/c

DEFINITION HD1--06-007.g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library 1 (HD1) Oryza sativa (japonica cultivar-group) cDNA

CF307503

ACCESSION CF307503.1 GI:33679264

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretaceae; Oryzaeae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
Source

1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD1--06-007"
/cvsue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage cDNA library 1 (HD1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 2.0%; Score 10; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 CAGCGGGAG 331
|||||
Db 16 CAGCGGGAG 7

RESULT 61

LOCUS

DEFINITION AZ303903 20 bp DNA linear GSS 29-SEP-2000
1M0003B18r Mouse 10kb plasmid UGCG1M library Mus musculus genomic

ACCESSION AZ303903
VERSION AZ303903.1 GI:10339339

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

REFERENCE

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: B column: 18
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0003B18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g1473214[gB]AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 2.0%; Score 10; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 AAGGAGCCA 20
|||||
Db 17 AAGGAGCCA 8

RESULT 62

LOCUS

DEFINITION AZ307491 20 bp DNA linear GSS 29-SEP-2000
1M0009C13f Mouse 10kb plasmid UGCG1M library Mus musculus genomic

ACCESSION AZ307491
VERSION AZ307491.1 GI:10346544

KEYWORDS
GSS.
Mus musculus (house mouse)

SOURCE
Mus musculus

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE
Unpublished (2000)

JOURNAL
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: C column: 13
Seq primer: GGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source
1..20
location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M009C13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U06C1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 2.0%; Score 10; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 CATCTGAAG 258
|||||||
Db 7 CATCTGAAG 16

RESULT 63
AZ407675 20 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0178804R Mouse 10kb plasmid U06C1M library Mus musculus genomic
DEFINITION clone U06C1M0178804 R, genomic survey sequence.
ACCESSION AZ407675
VERSION AZ407675.1 GI:10531688

KEYWORDS
GSS.
Mus musculus (house mouse)

SOURCE
Mus musculus

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE
Unpublished (2000)

JOURNAL
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0178 row: E column: 04
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source
1..20
location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0178E04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U06C1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 2.0%; Score 10; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 ATGGAAC 294
|||||||
Db 8 ATGGAAC 17

RESULT 64
AZ484701 20 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0311C24F Mouse 10kb plasmid U06C1M library Mus musculus genomic
DEFINITION clone U06C1M0311C24 F, genomic survey sequence.
ACCESSION AZ484701
VERSION AZ484701.1 GI:10649799

KEYWORDS
GSS.
Mus musculus (house mouse)

SOURCE
Mus musculus

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

REFERENCE
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

TITLE
Unpublished (2000)

JOURNAL
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row: P column: 23
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source
1. 20
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U062M0072P23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid U062M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|pb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 2.0%; Score 10; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 370 GTTCTGTGTT 379
|||||
18 GTTCTGTGTT 9

RESULT 67
AZ835099 20 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0129107F Mouse 10kb plasmid U062M library Mus musculus genomic
DEFINITION clone U062M0129107 F, genomic survey sequence.
ACCESSION AZ835099
VERSION AZ835099.1 GI:13005007

KEYWORDS
GSS.
Mus musculus (house mouse)

SOURCE
Mus musculus

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

REFERENCE
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

TITLE
Unpublished (2000)

JOURNAL
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0128 row: I column: 07
Seq primer: CATTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source
1. 20
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U062M0129107"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid U062M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|pb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 2.0%; Score 10; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 177 CCCGTTTGT 186
|||||
DB 9 CCCGTTTGT 18

RESULT 68
AG188183 20 bp DNA linear GSS 06-MAR-2004
LOCUS AG188183
DEFINITION Pan troglodytes DNA, clone: RP43-061M08.T7, genomic survey sequence.
ACCESSION AG188183
VERSION AG188183.1 GI:45220352

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

GSS.
Pan troglodytes (chimpanzee)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
1
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W., and Yoo, H.
BAC end sequences of library RP-43
2 (bases 1 to 20)
Unpublished
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W., and Yoo, H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. 20
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-061M08.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC library"

ORIGIN
Query Match 2.0%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred.No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 CTGGGTACA 205
Db 1 CTGGGTACA 10
|||||
|||||

RESULT 69
AG191409 20 bp DNA linear GSS 06-MAR-2004
LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-067F16.T7, genomic survey
sequence.
AG191409
AG191409.1 GI:45223585
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
1
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W., and Yoo, H.
BAC end sequences of library RP-43
2 (bases 1 to 20)
Unpublished
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W., and Yoo, H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. 20
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-077L17.T7"
/sex="male"
/cell_type="lymphocytes"

COMMENT
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-067F16.T7"
/sex="male"
/cell_type="lymphocytes"

FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred.No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 AGACCCCGC 86
Db 6 AGACCCCGC 15
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|||||

RESULT 70
AG197503 20 bp DNA linear GSS 06-MAR-2004
LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-077L17.T7, genomic survey
sequence.
AG197503
AG197503.1 GI:45229679
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
1
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W., and Yoo, H.
BAC end sequences of library RP-43
2 (bases 1 to 20)
Unpublished
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W., and Yoo, H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. 20
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-077L17.T7"
/sex="male"
/cell_type="lymphocytes"

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

ORIGIN /clone_11b="RP-43 Chimpanzee Male BAC Library"

Query Match 2.0%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 AGGACCGCGC 86
Db 7 AGGACCGCGC 16

RESULT 71
AG201573/c
LOCUS AG201573
DEFINITION Pan troglodytes DNA, clone: RP43-084C17.T7, genomic survey
sequence.
ACCESSION AG201573
VERSION AG201573.1 GI:45233748
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
BAC end sequences of library RP-43
TITLE Unpublished
JOURNAL 2 (bases 1 to 20)
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Hong-Seong Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yuseong-gu, Daejeon 305-313, Korea
(E-mail: redstone@mail.kribb.re.kr, URL: <http://pns.grc.kribb.re.kr/>,
Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : DBAC3.6
R.Site 1 : ECORI
R.Site 2 : ECORI
FEATURES
source
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-084C17.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_11b="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 2.0%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 AGTCAGACAT 251
Db 10 AGTCAGACAT 1

RESULT 72
AU013419/c
LOCUS AU013419
DEFINITION 21 bp mRNA linear EST 03-AUG-1998
Schizosaccharomyces pombe cDNA clone spc08126, mRNA sequence.
ACCESSION AU013419

VERSION AU013419.1 GI:3368210
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
REFERENCE 1 (bases 1 to 21)
Moriyomo, M. and Mita, K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces
pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsuoki Moriyomo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.
FEATURES
source
1. .21
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc08126"
/sex="h minus"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, <http://www.nirs.go.jp/>)"

ORIGIN

Query Match 2.0%; Score 10; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.8e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 TGTCGTGATTA 350
Db 13 TGTCGTGATTA 4

RESULT 73
AU013601/c
LOCUS AU013601
DEFINITION 21 bp mRNA linear EST 03-AUG-1998
Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc08394, mRNA sequence.
ACCESSION AU013601
VERSION AU013601.1 GI:3368392
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
REFERENCE 1 (bases 1 to 21)
Moriyomo, M. and Mita, K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces
pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsuoki Moriyomo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.
FEATURES
source
1. .21
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc08394"

/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, <http://www.nirs.go.jp>)"

ORIGIN

Query Match 2.0%; Score 10; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.8e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 TGTCTGATTA 350
|||||
13 TGTCTGATTA 4

RESULT 74

AU013625/c

AU013625 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc08421, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

EST.
Schizosaccharomyces pombe (fission yeast)
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
1 (bases 1 to 21)
Morimyo, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomyces
pombe

REFERENCE
AUTHORS
TITLE

Unpublished (1998)
Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
1..21
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
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/clone="spc08421"
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/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, <http://www.nirs.go.jp>)"

FEATURES
Source

ORIGIN

Query Match 2.0%; Score 10; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.8e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 TGTCTGATTA 350
|||||
13 TGTCTGATTA 4

RESULT 75
AU013662/c
LOCUS
DEFINITION

AU013662 21 bp mRNA linear EST 03-AUG-1998
AU013662 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc08470, mRNA sequence.

ACCESSION AU013662
VERSION AU013662.1 GI:3368453
KEYWORDS "EST"
SOURCE Schizosaccharomyces pombe (fission yeast)
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
1 (bases 1 to 21)
Morimyo, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomyces
pombe

REFERENCE

AUTHORS

TITLE

JOURNAL

Unpublished (1998)
Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
1..21
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc08470"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, <http://www.nirs.go.jp>)"

FEATURES
Source

ORIGIN

Query Match 2.0%; Score 10; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.8e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 TGTCTGATTA 350
|||||
13 TGTCTGATTA 4

Search completed: February 2, 2005, 23:32:11
Job time : 1535.28 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:06:25 ; Search time 234.038 Seconds
(without alignments)
11170.029 Million cell updates/sec

Title: US-10-048-046-1_COPY_1516_2013

Perfect score: 498

Sequence: 1 tgcctctgcgaaggaagcca.....gtcactcggggccgtaactgc 498

Scoring table: OLIGO-NUC

Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 0

Total number of hits satisfying chosen parameters: 336436

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

Database :

1: Genesegq.23Sep04:*
2: genesegq1980s:*
3: genesegq1990s:*
4: genesegq2000s:*
5: genesegq2001as:*
6: genesegq2002as:*
7: genesegq2002bs:*
8: genesegq2003as:*
9: genesegq2003bs:*
10: genesegq2003cs:*
11: genesegq2003ds:*
12: genesegq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	3.6	18	5	AAEF30374 Human che
2	18	3.6	18	5	AAEF30360 Human che
3	18	3.6	18	5	AAEF30364 Human che
4	18	3.6	18	5	AAEF30366 Human che
5	18	3.6	18	5	AAEF30370 Human che
6	17	3.4	17	5	AAEF30362 Human che
7	17	3.4	17	5	AAEF30372 Human che
8	17	3.4	17	5	AAEF30368 Human che
9	16	3.2	20	12	AD125055 Human ABR
10	16	3.2	25	5	AAEF30375 Human che
11	15	3.0	20	6	ABK69194 Human pho
12	15	3.0	21	10	ADB61552 Hepatocyte
13	15	3.0	22	6	ABSF74300 Human cal
14	15	3.0	22	9	ACD25698 Human cal
15	15	3.0	25	4	AA500234 Afx trans
16	15	3.0	25	9	ACT20807 Human mic
17	15	3.0	25	9	ACH57351 DNA target
18	14	2.8	15	2	AAK65296 Mouse B7-
19	14	2.8	15	2	AAK65298 Mouse B7-
20	14	2.8	15	2	AAK65297 Mouse B7-
21	14	2.8	19	6	ABL95963 Probe #40

22	14	2.8	19	10	ADL25029	Adl25029 Intestina
23	14	2.8	20	4	AAH75338	Aah75338 Mouse ind
24	14	2.8	20	6	AAK98349	Aak98349 High mobi
25	14	2.8	20	10	ADD98605	Add98605 Hamster h
26	14	2.8	20	12	ADM36243	Adm36243 3' RACE p
27	14	2.8	21	10	ADG29799	Adg29799 EGFR-targ
28	14	2.8	21	11	ADL80074	Adl80074 Human HER
29	14	2.8	21	12	ADM36242	Adm36242 5' RACE p
30	14	2.8	22	12	ADM24728	Adm24728 Expressio
31	14	2.8	23	2	AAH10330	Aah10330 Anti-p-ae
32	14	2.8	23	10	ADG29798	Adg29798 EGFR-targ
33	14	2.8	23	11	ADL80073	Adl80073 Human HER
34	14	2.8	23	12	ADG25209	Adg25209 N. gonorr
35	14	2.8	23	12	ADG25212	Adg25212 N. gonorr
36	14	2.8	24	2	AAQ78839	Aaq78839 HCMV Ab 1
37	14	2.8	24	2	ADG77626	Adg77626 Canine di
38	14	2.8	24	3	AAV68558	Aav68558 Lambda ch
39	14	2.8	24	3	AAZ60776	Aaz60776 5' PCR pr
40	14	2.8	24	6	ABZ30677	Abz30677 Candida a
41	14	2.8	25	6	AAI42621	Aai42621 Mouse inh
42	14	2.8	25	6	AAK99746	Aak99746 Mouse INO
43	14	2.8	25	9	ACK25054	Ack25054 Human mic
44	14	2.8	25	9	ACH63234	Ach63234 DNA target
45	14	2.8	26	8	ABV74186	Abv74186 Murine FI
46	14	2.8	30	4	AAAC3911	Aaac3911 Chromobac
47	13	2.6	15	2	AAH34531	Aah34531 Human Fas
48	13	2.6	15	3	AAH34533	Aah34533 Human Fas
49	13	2.6	17	3	AAA38405	Aaa38405 Pseudomon
50	13	2.6	17	4	AA512968	Aa512968 Familial
51	13	2.6	17	6	ABN07848	Abn07848 Human GDM
52	13	2.6	17	6	ABN07850	Abn07850 Human GDM
53	13	2.6	17	6	ABN07851	Abn07851 Human GDM
54	13	2.6	17	6	ABN07847	Abn07847 Human GDM
55	13	2.6	17	8	ABN07849	Abn07849 Human GDM
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58	13	2.6	18	2	AAQ26547	Aaq26547 Control p
59	13	2.6	18	2	AAV48442	Aav48442 Transform
60	13	2.6	18	3	AAZ77336	Aaz77336 Human bia
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62	13	2.6	18	4	AAEF3133	Aaef3133 Sequence
63	13	2.6	18	4	AAEF3133	Aaef3133 Sequence
64	13	2.6	18	4	AA502440	Aa502440 Human TSR
65	13	2.6	18	4	AA502441	Aa502441 Human TSR
66	13	2.6	18	5	ABA82453	Ab82453 Zmxi1 gen
67	13	2.6	18	6	ABK23250	Abk23250 Human Zma
68	13	2.6	18	8	ACC45833	Acc45833 Human HBV
69	13	2.6	18	10	ADB98531	Adb98531 Sequence
70	13	2.6	19	6	ABZ75622	Abz75622 STR mark
71	13	2.6	19	6	ABK11325	Abk11325 Arabidops
72	13	2.6	19	9	ACH66467	Ach66467 Sense PCR
73	13	2.6	19	11	ADO14975	Ado14975 Human PDG
74	13	2.6	19	11	ADO14664	Ado14664 Human PDG
75	13	2.6	19	12	ADM82819	Adm82819 PGK RT-PC
76	13	2.6	19	12	ADG62436	Adg62436 Anti-MYB
77	13	2.6	20	2	AAH33593	Aah33593 HIV-1 gen
78	13	2.6	20	2	AAH18316	Aah18316 BRCA1 gen
79	13	2.6	20	2	AAH17532	Aah17532 Primer #2
80	13	2.6	20	2	AAH32603	Aah32603 BRCA1 gen
81	13	2.6	20	2	AAV57180	Aav57180 Human Not
82	13	2.6	20	2	AAV57099	Aav57099 Human Not
83	13	2.6	20	2	AAK03558	Aak03558 Reverse p
84	13	2.6	20	4	AAAD04633	Aaad04633 Human ins
85	13	2.6	20	9	ACC84367	Acc84367 Human aro
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87	13	2.6	20	10	ABZ85105	Abz85105 Human oli
88	13	2.6	20	10	ABZ85104	Abz85104 Human oli
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90	13	2.6	20	11	ABD21335	Abd21335 Human tra
91	13	2.6	20	12	ADH48235	Adh48235 Human GRK
92	13	2.6	20	12	ADH19153	Adh19153 Human PCT
93	13	2.6	20	12	ADH19230	Adh19230 Human PCT
94	13	2.6	20	12	ADL72135	Adl72135 Murine tu

95	13	2.6	20	12	ADP10870	Adp10870 Set 1 lcf
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97	13	2.6	20	12	ADQ94693	Adg94693 Human pto
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109	13	2.6	22	9	ACD06338	AcD06338 Forward R
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111	13	2.6	23	3	AAZ94779	Aaz94779 ATP bindi
112	13	2.6	23	12	ADM918934	Adm918934 Human G-P
113	13	2.6	23	12	ADM918934	Adm918934 Primer #2
114	13	2.6	24	2	AAH4850	Aah4850 Human end
115	13	2.6	24	2	AAH44451	Aah44451 SPINK5 5'
116	13	2.6	24	6	ABK49042	Abk49042 PCR prime
117	13	2.6	24	6	ABK6679	Abk6679 Human gen
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119	13	2.6	24	6	ABK6679	Abk6679 Human gen
120	13	2.6	24	8	ACF30912	Acf30912 Rice chro
121	13	2.6	24	10	ABX94708	Abx94708 A. liquef
122	13	2.6	24	12	ADI09971	Adi09971 Rice chro
123	13	2.6	24	12	ADO47959	Ado47959 Human HIP
124	13	2.6	25	4	AAQ10052	Aaq10052 P4 primer
125	13	2.6	25	4	AAH38963	Aah38963 SNP speci
126	13	2.6	25	5	AAH38735	Aah38735 SNP speci
127	13	2.6	25	5	AAF79936	Aaf79936 PCR prime
128	13	2.6	25	6	ABN12741	Abn12741 Human GDM
129	13	2.6	25	6	ABN12746	Abn12746 Human GDM
130	13	2.6	25	6	ABN12748	Abn12748 Human GDM
131	13	2.6	25	6	ABN12739	Abn12739 Human GDM
132	13	2.6	25	6	ABN12749	Abn12749 Human GDM
133	13	2.6	25	6	ABN12747	Abn12747 Human GDM
134	13	2.6	25	6	ABN12750	Abn12750 Human GDM
135	13	2.6	25	6	ABN12740	Abn12740 Human GDM
136	13	2.6	25	6	ABN12744	Abn12744 Human GDM
137	13	2.6	25	6	ABN12751	Abn12751 Human GDM
138	13	2.6	25	6	ABN12745	Abn12745 Human GDM
139	13	2.6	25	6	ABN12742	Abn12742 Human GDM
140	13	2.6	25	6	ABN12743	Abn12743 Human GDM
141	13	2.6	25	6	ACC43282	Acc43282 Nucleotid
142	13	2.6	25	9	ACI44632	AcI44632 Human mic
143	13	2.6	25	9	ACI25820	AcI25820 Human mic
144	13	2.6	25	9	ACI32483	AcI32483 Human mic
145	13	2.6	25	9	ACI6758	AcI6758 Human mic
146	13	2.6	25	9	ACI91640	AcI91640 Human mic
147	13	2.6	25	9	ACK01374	Ack01374 Human mic
148	13	2.6	25	9	ACK08731	Ack08731 Human mic
149	13	2.6	25	9	ACK10671	Ack10671 Human mic
150	13	2.6	25	9	ACI97680	AcI97680 Human mic

ALIGNMENTS

RESULT 1
AAAF30374/c
ID AAF30374 standard; DNA; 18 BP.
XX AAF30374;
AC
XX
DT 14-MAY-2001 (first entry)
XX
DE Human checkpoint gene chr 3' PCR primer.
XX
KM Checkpoint with forkhead associated domain and ring finger; Chr; human;
KM mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;

KW	ubiquitin-protein ligase; PCR primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200109150-A2.
XX	
PD	08-FEB-2001.
XX	
PF	14-JUN-2000; 2000WO-US016391.
XX	
PR	29-JUL-1999; 99US-0146194P.
XX	
PA	(WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX	
PI	Halazonecic T, Scolnick D;
XX	
DR	WPI; 2001-182927/18.
XX	
PT	Novel nucleic acid sequence of mitotic checkpoint gene encoding a
PT	checkpoint with forkhead-associated domain and ring finger protein, for
PT	diagnosing tumorigenic cells and in screening for anticancer drugs.
XX	
PS	Example 3; Page 38; 85pp; English.
XX	
CC	The present sequence is that of a 3' PCR primer, used with the 5' primer
CC	given in AAF30373, to amplify a cDNA fragment corresponding to
CC	nucleotides 1214-1902 of the human chr sequence given in AAF30352. The
CC	chr gene encodes the human mitotic checkpoint protein Chr (see
CC	AAAB20219), which is required for regulation of the transition of cells
CC	from prophase to metaphase during mitosis. Loss of expression of Chr is
CC	associated with a predisposition to tumorigenesis upon exposure to
CC	mitotic stress. A set of primers (see AAF30353-76) was used to amplify
CC	regions spanning the entire chr coding region in order to determine
CC	whether the chr gene is mutated in any of the human cancer cell lines
CC	SW480, DLD1, HCT116, SAOS2, U2OS, IMR5 and NCP. A mutation leading
CC	to a Val-580 to Met amino acid substitution was identified in the chr
CC	gene of U2OS cells. Chr polypeptides and chr nucleic acids are used in
CC	methods of diagnosing tumorigenic cells and of screening for drugs which
CC	can inhibit the activity of Chr in a cancer cell, rendering it more
CC	sensitive to additional antitumour therapies
XX	
SQ	Sequence 18 BP; 8 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
XX	
QY	Query Match 3.6%; Score 18; DB 5; Length 18;
XX	Best Local Similarity 100.0%; Pred. No. 1.2e+02;
XX	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	328 GGAGTGTTCCTGCTGCT 345
XX	
XX	18 GGAGTGTTCCTGCTGCT 1
XX	
RESULT 2	
AAAF30360/c	
ID AAF30360 standard; DNA; 18 BP.	
XX AAF30360;	
AC	
XX	
DT 14-MAY-2001 (first entry)	
XX	
DE Human checkpoint gene chr 3' PCR primer.	
XX	
KW Checkpoint with forkhead associated domain and ring finger; Chr; human;	
KW mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;	
XX ubiquitin-protein ligase; PCR primer; ss.	
XX	
OS Homo sapiens.	
XX	
PN WO200109150-A2.	
XX	
PD 08-FEB-2001.	
XX	
PF 14-JUN-2000; 2000WO-US016391.	

```

XX 29-JUL-1999; 99US-0146194P.
PR (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Halazonetis T, Scolnick D;
XX WPI; 2001-182927/18.
XX
XX Novel nucleic acid sequence of mtotic checkpoint gene encoding a
PT checkpoint with forkhead-associated domain and ring finger protein, for
PT diagnosing tumorigenic cells and in screening for anticancer drugs.
XX
XX Example 3; Page 38; 85pp; English.
XX
XX The present sequence is that of a 3' PCR primer, used with the 5' primer
CC given in AAF30359, to amplify a cDNA fragment corresponding to
CC nucleotides 904-1753 of the human chr sequence given in AAF30352. The
CC chr gene encodes the human mitotic checkpoint protein Chfr (see
CC AAB20219), which is required for regulation of the transition of cells
CC from prophase to metaphase during mitosis. Loss of expression of Chfr is
CC associated with a predisposition to tumourigenesis upon exposure to
CC mitotic stress. A set of primers (see AAF30353-76) was used to amplify
CC regions spanning the entire chr coding region in order to determine
CC whether the chr gene is mutated in any of the human cancer cell lines
CC SM480, DDD1, HT29, HCT116, SMO2, U2OS, IMR5 and NGP. A mutation leading
CC to a Val-580 to Met amino acid substitution was identified in the chr
CC gene of U2OS cells. Chfr polypeptides and chr nucleic acids are used in
CC methods of diagnosing tumorigenic cells and of screening for drugs which
CC can inhibit the activity of Chfr in a cancer cell, rendering it more
CC sensitive to additional antitumour therapies
XX
XX Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 3.6%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 179 CGTTTGTGAGCTCAACC 196
Db 18 CGTTTGTGAGCTCAACC 1
RESULT 3
AAF30364/c
ID AAF30364 standard; DNA; 18 BP.
XX
XX AAF30364;
XX
XX 14-MAY-2001 (first entry)
XX
XX Human checkpoint gene chr 3' PCR primer.
XX
XX Checkpoint with forkhead associated domain and ring finger; Chfr; human;
KM mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;
KM ubiquitin-protein ligase; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200109150-A2.
XX
XX 08-FEB-2001.
XX
XX 14-JUN-2000; 2000WO-US016391.
XX
XX 29-JUL-1999; 99US-0146194P.
XX
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Halazonetis T, Scolnick D;
XX WPI; 2001-182927/18.
XX

```

```

PT Novel nucleic acid sequence of mitotic checkpoint gene encoding a
PT checkpoint with forkhead-associated domain and ring finger protein, for
PT diagnosing tumorigenic cells and in screening for anticancer drugs.
XX
XX Example 3; Page 38; 85pp; English.
XX
XX The present sequence is that of a 3' PCR primer, used with the 5' primer
CC given in AAF30363, to amplify a cDNA fragment corresponding to
CC nucleotides 904-1902 of the human chr sequence given in AAF30352. The
CC chr gene encodes the human mitotic checkpoint protein Chfr (see
CC AAB20219), which is required for regulation of the transition of cells
CC from prophase to metaphase during mitosis. Loss of expression of Chfr is
CC associated with a predisposition to tumourigenesis upon exposure to
CC mitotic stress. A set of primers (see AAF30353-76) was used to amplify
CC regions spanning the entire chr coding region in order to determine
CC whether the chr gene is mutated in any of the human cancer cell lines
CC SM480, DDD1, HT29, HCT116, SMO2, U2OS, IMR5 and NGP. A mutation leading
CC to a Val-580 to Met amino acid substitution was identified in the chr
CC gene of U2OS cells. Chfr polypeptides and chr nucleic acids are used in
CC methods of diagnosing tumorigenic cells and of screening for drugs which
CC can inhibit the activity of Chfr in a cancer cell, rendering it more
CC sensitive to additional antitumour therapies
XX
XX Sequence 18 BP; 8 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
SQ
Query Match 3.6%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 328 GGAAGTGTCTGCTGCT 345
Db 18 GGAAGTGTCTGCTGCT 1
RESULT 4
AAF30366/c
ID AAF30366 standard; DNA; 18 BP.
XX
XX AAF30366;
XX
XX 14-MAY-2001 (first entry)
XX
XX Human checkpoint gene chr 3' PCR primer.
XX
XX Checkpoint with forkhead associated domain and ring finger; Chfr; human;
KM mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;
KM ubiquitin-protein ligase; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200109150-A2.
XX
XX 08-FEB-2001.
XX
XX 14-JUN-2000; 2000WO-US016391.
XX
XX 29-JUL-1999; 99US-0146194P.
XX
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Halazonetis T, Scolnick D;
XX WPI; 2001-182927/18.
XX
XX Novel nucleic acid sequence of mitotic checkpoint gene encoding a
PT checkpoint with forkhead-associated domain and ring finger protein, for
PT diagnosing tumorigenic cells and in screening for anticancer drugs.
XX
XX Example 3; Page 38; 85pp; English.
XX
XX The present sequence is that of a 3' PCR primer, used with the 5' primer
CC given in AAF30365, to amplify a cDNA fragment corresponding to
CC nucleotides 1187-1753 of the human chr sequence given in AAF30352. The

```

CC chr gene encodes the human mitotic checkpoint protein Chfr (see
CC AAB20219), which is required for regulation of the transition of cells
CC from prophase to metaphase during mitosis. Loss of expression of Chfr is
CC associated with a predisposition to tumorigenesis upon exposure to
CC mitotic stress. A set of primers (see AAF30353-76) was used to amplify
CC regions spanning the entire chfr coding region in order to determine
CC whether the chfr gene is mutated in any of the human cancer cell lines
CC SW480, DLD1, HT29, HCT116, SAOS2, U2OS, IMR5 and NCP. A mutation leading
CC to a Val-580 to Met amino acid substitution was identified in the chfr
CC gene of U2OS cells. Chfr polypeptides and chfr nucleic acids are used in
CC methods of diagnosing tumorigenic cells and of screening for drugs which
CC can inhibit the activity of Chfr in a cancer cell, rendering it more
CC sensitive to additional anticancer therapies

SO Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 3.6%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 CGTTTGAGCTCAACC 196
Db 18 CGTTTGAGCTCAACC 1

RESULT 5
ID AAF30370/c
AAAF30370 standard; DNA; 18 BP.

AC AAF30370;

DT 14-MAY-2001 (first entry)

DE Human checkpoint gene chfr 3' PCR primer.

XX Checkpoint with forkhead associated domain and ring finger; Chfr; human;
KM mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;
KW ubiquitin-protein ligase; PCR primer; ss.

OS Homo sapiens.

PN WO200109150-A2.

PD 08-FEB-2001.

PF 14-JUN-2000; 2000WO-US016391.

PR 29-JUL-1999; 99US-0146194P.

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.

PI Halazonetis T, Scolnick D;

DR WPI; 2001-182927/18.

PT Novel nucleic acid sequence of mitotic checkpoint gene encoding a
PT checkpoint with forkhead-associated domain and ring finger protein, for
PT diagnosing tumorigenic cells and in screening for anticancer drugs.

PS Example 3; Page 38; 85pp; English.

XX The present sequence is that of a 3' PCR primer, used with the 5' primer
XX given in AAF30361, to amplify a cDNA fragment corresponding to
XX nucleotides 1215-1753 of the human chfr sequence given in AAF30352. The
XX chfr gene encodes the human mitotic checkpoint protein Chfr (see
XX AAB20219), which is required for regulation of the transition of cells
XX from prophase to metaphase during mitosis. Loss of expression of Chfr is
XX associated with a predisposition to tumorigenesis upon exposure to
XX mitotic stress. A set of primers (see AAF30353-76) was used to amplify
XX regions spanning the entire chfr coding region in order to determine
XX whether the chfr gene is mutated in any of the human cancer cell lines
XX SW480, DLD1, HT29, HCT116, SAOS2, U2OS, IMR5 and NCP. A mutation leading
XX to a Val-580 to Met amino acid substitution was identified in the chfr

CC gene of U2OS cells. Chfr polypeptides and chfr nucleic acids are used in
CC methods of diagnosing tumorigenic cells and of screening for drugs which
CC can inhibit the activity of Chfr in a cancer cell, rendering it more
CC sensitive to additional anticancer therapies

SO Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 3.6%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 CGTTTGAGCTCAACC 196
Db 18 CGTTTGAGCTCAACC 1

RESULT 6
ID AAF30362/c
AAAF30362 standard; DNA; 17 BP.

AC AAF30362;

DT 14-MAY-2001 (first entry)

DE Human checkpoint gene chfr 3' PCR primer.

XX Checkpoint with forkhead associated domain and ring finger; Chfr; human;
KM mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;
KW ubiquitin-protein ligase; PCR primer; ss.

OS Homo sapiens.

PN WO200109150-A2.

PD 08-FEB-2001.

PF 14-JUN-2000; 2000WO-US016391.

PR 29-JUL-1999; 99US-0146194P.

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.

PI Halazonetis T, Scolnick D;

DR WPI; 2001-182927/18.

PT Novel nucleic acid sequence of mitotic checkpoint gene encoding a
PT checkpoint with forkhead-associated domain and ring finger protein, for
PT diagnosing tumorigenic cells and in screening for anticancer drugs.

PS Example 3; Page 38; 85pp; English.

XX The present sequence is that of a 3' PCR primer, used with the 5' primer
XX given in AAF30361, to amplify a cDNA fragment corresponding to
XX nucleotides 904-1772 of the human chfr sequence given in AAF30352. The
XX chfr gene encodes the human mitotic checkpoint protein Chfr (see
XX AAB20219), which is required for regulation of the transition of cells
XX from prophase to metaphase during mitosis. Loss of expression of Chfr is
XX associated with a predisposition to tumorigenesis upon exposure to
XX mitotic stress. A set of primers (see AAF30353-76) was used to amplify
XX regions spanning the entire chfr coding region in order to determine
XX whether the chfr gene is mutated in any of the human cancer cell lines
XX SW480, DLD1, HT29, HCT116, SAOS2, U2OS, IMR5 and NCP. A mutation leading
XX to a Val-580 to Met amino acid substitution was identified in the chfr
XX gene of U2OS cells. Chfr polypeptides and chfr nucleic acids are used in
XX methods of diagnosing tumorigenic cells and of screening for drugs which
XX can inhibit the activity of Chfr in a cancer cell, rendering it more
XX sensitive to additional anticancer therapies

SO Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 3.4%; Score 17; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 GGTGACAAGTGTCTGGA 215
 |||||
 DB 17 GGTGACAAGTGTCTGGA 1

RESULT 7

AAAF30372/c
 ID AAAF30372 standard; DNA; 17 BP.

AC AAAF30372;
 XX

DT 14-MAY-2001 (first entry)
 XX

DE Human checkpoint gene chr 3' PCR primer.
 XX

KM Checkpoint with forkhead associated domain and ring finger; Chfr; human;
 KM mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;
 KM ubiquitin-protein ligase; PCR primer; ss.

OS Homo sapiens.
 XX

PN W0200109150-A2.
 XX

PD 08-FEB-2001.
 XX

PF 14-JUN-2000; 2000WO-US016391.
 XX

PR 29-JUL-1999; 99US-0146194P.
 XX

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 XX

PI Halazonecis T, Scolnick D;
 XX

DR WPI; 2001-182927/18.
 XX

PT Novel nucleic acid sequence of mitotic checkpoint gene encoding a
 PT checkpoint with forkhead-associated domain and ring finger protein, for
 PT diagnosing tumorigenic cells and in screening for anticancer drugs.
 XX

PS Example 3; Page 38; 85pp; English.
 XX

CC The present sequence is that of a 3' PCR primer, used with the 5' primer
 CC given in AAF30371, to amplify a cDNA fragment corresponding to
 CC nucleotides 1215-1772 of the human chr sequence given in AAF30352. The
 CC chr gene encodes the human mitotic checkpoint protein Chfr (see
 CC AAB20219), which is required for regulation of the transition of cells
 CC from prophase to metaphase during mitosis. Loss of expression of Chfr is
 CC associated with a predisposition to tumorigenesis upon exposure to
 CC mitotic stress. A set of primers (see AAF30353-76) was used to amplify
 CC regions spanning the entire chr coding region in order to determine
 CC whether the chr gene is mutated in any of the human cancer cell lines
 CC SW480, DDD1, HRT9, HCT116, SAOS2, U2OS, IMR5 and NGP. A mutation leading
 CC to a Val-580 to Met amino acid substitution was identified in the chr
 CC gene of U2OS cells. Chr polypeptides and chr nucleic acids are used in
 CC methods of diagnosing tumorigenic cells and of screening for drugs which
 CC can inhibit the activity of Chfr in a cancer cell, rendering it more
 CC sensitive to additional antitumour therapies
 CC

SQ Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 3.4%; Score 17; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 GGTGACAAGTGTCTGGA 215
 |||||
 DB 17 GGTGACAAGTGTCTGGA 1

RESULT 8
 AAF30368/c

ID AAF30368 standard; DNA; 17 BP.

AC AAF30368;
 XX

DT 14-MAY-2001 (first entry)
 XX

DE Human checkpoint gene chr 3' PCR primer.
 XX

KM Checkpoint with forkhead associated domain and ring finger; Chfr; human;
 KM mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;
 KM ubiquitin-protein ligase; PCR primer; ss.

OS Homo sapiens.
 XX

PN W0200109150-A2.
 XX

PD 08-FEB-2001.
 XX

PF 14-JUN-2000; 2000WO-US016391.
 XX

PR 29-JUL-1999; 99US-0146194P.
 XX

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 XX

PI Halazonecis T, Scolnick D;
 XX

DR WPI; 2001-182927/18.
 XX

PT Novel nucleic acid sequence of mitotic checkpoint gene encoding a
 PT checkpoint with forkhead-associated domain and ring finger protein, for
 PT diagnosing tumorigenic cells and in screening for anticancer drugs.
 XX

PS Example 3; Page 38; 85pp; English.
 XX

CC The present sequence is that of a 3' PCR primer, used with the 5' primer
 CC given in AAF30367, to amplify a cDNA fragment corresponding to
 CC nucleotides 1187-1772 of the human chr sequence given in AAF30352. The
 CC chr gene encodes the human mitotic checkpoint protein Chfr (see
 CC AAB20219), which is required for regulation of the transition of cells
 CC from prophase to metaphase during mitosis. Loss of expression of Chfr is
 CC associated with a predisposition to tumorigenesis upon exposure to
 CC mitotic stress. A set of primers (see AAF30353-76) was used to amplify
 CC regions spanning the entire chr coding region in order to determine
 CC whether the chr gene is mutated in any of the human cancer cell lines
 CC SW480, DDD1, HRT9, HCT116, SAOS2, U2OS, IMR5 and NGP. A mutation leading
 CC to a Val-580 to Met amino acid substitution was identified in the chr
 CC gene of U2OS cells. Chr polypeptides and chr nucleic acids are used in
 CC methods of diagnosing tumorigenic cells and of screening for drugs which
 CC can inhibit the activity of Chfr in a cancer cell, rendering it more
 CC sensitive to additional antitumour therapies
 CC

SQ Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 3.4%; Score 17; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 GGTGACAAGTGTCTGGA 215
 |||||
 DB 17 GGTGACAAGTGTCTGGA 1

RESULT 9
 ADI25055

ID ADI25055 standard; DNA; 20 BP.

AC ADI25055;
 XX

DT 22-APR-2004 (first entry)
 XX

DE Human ATR1 exon 3 reverse PCR primer.
 XX

KM dominant negative mutant RAB7; dominant negative mutant ARHGAP10;
 XX

KM peripheral neuropathy, human; AATB1, PCR; primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN W02004005541-A1.
 XX
 PD 15-JAN-2004.
 XX
 PF 08-JUL-2003; 2003WO-EP050290.
 XX
 PR 09-JUL-2002; 2002EP-00077724.
 PR 08-APR-2003; 2003EP-00076033.
 XX
 PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 XX
 PI Van Broeckhoven C, De Jonghe P, Timmerman V, Verhoeven K,
 XX
 DR WPI; 2004-091384/09.
 XX
 PT New isolated nucleic acid coding for a dominant negative, mutant RAB7
 PT polypeptide and/or a dominant negative, mutant ARHGAP10 polypeptide,
 PT useful for detecting the presence of peripheral neuropathy in a human.
 XX
 PS Example; Page 22; 38pp; English.
 XX
 CC The present invention describes an isolated nucleic acid (1) coding for a
 CC dominant negative, mutant RAB7 polypeptide and/or a dominant negative,
 CC mutant ARHGAP10 polypeptide. (1) contains in comparison to the wild type
 CC RAB7 encoding sequence comprising 624 bp (SEQ ID NO: 1, AD125025) and/or
 CC to the wild type ARHGAP10 encoding sequence comprising 3366 bp (SEQ ID
 CC NO: 3, AD125027), one or more mutations, where the presence of the
 CC nucleic acid is indicative for a predisposition or presence of a
 CC peripheral neuropathy. Also described: (1) a nucleic acid probe which is
 CC a fragment of (1); (2) a recombinant vector comprising (1); (3) a host
 CC cell comprising a recombinant vector of (2); (4) a method for the
 CC preparation of a diagnostic assay to detect the presence of a peripheral
 CC neuropathy in a human; and (5) a transgenic non-human animal comprising
 CC the vector of (2). (1) is useful for isolating and detecting human
 CC peripheral neuropathy causing or predisposing genes. The diagnostic assay
 CC is useful for detecting the presence of peripheral neuropathy in a human.
 CC The present sequence represents a PCR primer for human AATB1, which is
 CC used in an example from the present invention.
 XX
 SQ Sequence 20 BP; 2 A; 10 C; 3 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 3.2%; Score 16; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 111 CTGCTGACGACCTTTTC 126
 DB 3 CTGCTGACGACCTTTTC 18
 XX
 RESULT 10
 AAF30375
 ID AAF30375 standard; DNA; 25 BP.
 XX
 AC AAF30375;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Human checkpoint gene chr 5; PCR primer.
 XX
 KM Checkpoint with forkhead associated domain and ring finger; Chfr, human;
 KM mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;
 KM ubiquitin-protein ligase; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS
 XX
 PN W0200109150-A2.
 XX

PD 08-FEB-2001.
 XX
 XX
 PF 14-JUN-2000; 2000WO-US016391.
 XX
 PR 29-JUL-1999; 99US-0146194P.
 XX
 XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 XX
 PI Halazonetis T, Scolnick D;
 XX
 DR WPI; 2001-182927/18.
 XX
 PT Novel nucleic acid sequence of mitotic checkpoint gene encoding a
 PT checkpoint with forkhead-associated domain and ring finger protein, for
 PT diagnosing tumorigenic cells and in screening for anticancer drugs.
 XX
 PS Example 3; Page 38; 85pp; English.
 XX
 CC The present sequence is that of a 5' PCR primer, used with the 3' primer
 CC given in AAF30376, to amplify a cDNA fragment corresponding to
 CC nucleotides 1625-2279 of the human chr sequence given in AAF30352. The
 CC chr gene encodes the human mitotic checkpoint protein Chfr (see
 CC AAB20219), which is required for regulation of the transition of cells
 CC from prophase to metaphase during mitosis. Loss of expression of Chfr is
 CC associated with a predisposition to tumourigenesis upon exposure to
 CC mitotic stress. A set of primers (see AAF30353-76) was used to amplify
 CC regions spanning the entire chr coding region in order to determine
 CC whether the chr gene is mutated in any of the human cancer cell lines
 CC SW480, DLD1, HT29, HCT116, SMO2, U2OS, IMR5 and NCP. A mutation leading
 CC to a Val-350 to Met amino acid substitution was identified in the chr
 CC gene of U2OS cells. Chfr polypeptides and chr nucleic acids are used in
 CC methods of diagnosing tumorigenic cells and of screening for drugs which
 CC can inhibit the activity of chr in a cancer cell, rendering it more
 CC sensitive to additional anticancer therapies
 XX
 SQ Sequence 25 BP; 7 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 3.2%; Score 16; DB 5; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 118 CAGCCTTCTGCCACC 133
 DB 10 CAGCCTTCTGCCACC 25
 XX
 RESULT 11
 ABR69194/C
 ID ABR69194 standard; DNA; 20 BP.
 XX
 AC ABR69194;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human phosphotyrase kinase alpha 2 antisense oligonucleotide ISIS 118748.
 XX
 KM Antisense; phosphotyrase kinase alpha 2; metabolic disorder; ss;
 KM antidiabetic; antiinflammatory; antimicrobial; cytostatic; diabetes;
 KM infection; inflammation; tumour; human.
 XX
 OS Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FH 1..20
 FT modified_base /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "All cytosines are 5-methylcytosine"
 FT 1..5
 FT /tag= c

PF 22-DEC-1999; 99US-00470443.
 XX
 PR 30-DEC-1998; 98US-0114359P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Lerman MI, Latif F, Wei M, Duh F, Minna JD, Sekido Y, Gao B;
 DR WPI; 2002-730574/79.
 XX
 PT Novel purified nucleic acid sequence encoding human calcium channel
 PT alpha2delta subunit protein, useful for detecting, preventing and
 PT treating cancer, stroke, brain trauma, Huntington's disease, myocardial
 PT infarction.
 XX
 PS Example 7; Col 47; 77pp; English.
 XX
 CC The invention relates to a purified nucleic acid sequence (referred as
 CC CACNA2D2 gene which encodes human calcium channel alpha2delta-2 subunit
 CC protein) comprising a fully defined alpha2delta splice isoform 1, 2 or 3
 CC nucleic acid sequence, or its complement and the encoded protein. Also
 CC include are: (1) a method of producing a calcium channel protein which
 CC involves introducing a recombinant expression vector comprising the
 CC CACNA2D2 nucleic acid and encoding the calcium channel protein, into a
 CC cultured host cell under conditions such that the host cell expresses the
 CC amino acid sequences; and (2) a method for co-expressing calcium channel
 CC proteins, comprising carrying out the method of (1), but with one or more
 CC than one expression vector comprising one or more nucleic acid sequences
 CC encoding the splice variants. CACNA2D2 nucleic acid is useful for
 CC producing a calcium channel protein. The recombinantly expressed
 CC polypeptide is useful for treating patients with Lambert-Eaton myasthenic
 CC syndrome (LEMS) (an autoimmune disease) and for identifying compounds
 CC useful for treating other diseases associated with abnormal calcium
 CC channel protein activity (e.g. epilepsy, migraine, episodic ataxia,
 CC cancer, stroke, brain trauma, Alzheimer's disease, multifactor dementia,
 CC Korsakoff's disease, amyotrophic lateral sclerosis, convulsions, angina
 CC seizures, Huntington's disease, amnesia, cardiac arrhythmia, angina
 CC pectoris, hypoxic damage to the cardiovascular system, ischaemic heart
 CC disease, muscular dystrophy and hypertension) CACNA2D2 nucleic acid is
 CC useful as primers and probes for detecting presence of nucleic acid
 CC sequence encoding at least a portion of calcium channel protein, in
 CC detection, identification and isolation of alpha2delta sequences
 CC diagnosing and typing of preneoplasias and cancers, since genetic
 CC disruption of 3p21.3 region (in which the alpha 2delta gene is located)
 CC is common in cancer (e.g. lung cancer and breast cancer) and
 CC preneoplastic lesion (e.g. hyperplasia, dysplasia, carcinoma in situ).
 CC The present is an SSCP (single strand change polymorphism) PCR primer
 CC used to detect polymorphisms in sequences encoding a human calcium
 CC channel alpha2delta splice isoform protein
 XX
 SQ Sequence 22 BP; 3 A; 5 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 3.0%; Score 15; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 377 GTTACTGCTGGAGCC 391
 Db 6 GTTACTGCTGGAGCC 20
 ACDD25698
 ACDD25698 standard; DNA; 22 BP.
 AC ACD25698;
 XX
 DT 26-AUG-2003 (first entry)
 XX
 DE Human calcium channel alpha2delta SSCP primer MUR7R.
 XX
 KW Human; 66; PCR; calcium channel alpha2delta; chromosome 3p21.3; primer;

KW transgenic; cancer; lung cancer; small cell carcinoma; epilepsy; stroke;
 KW non-small cell carcinoma; breast cancer; nasopharyngeal cancer;
 KW cervical cancer; head and neck cancer; neurological disease;
 KW brain trauma; Alzheimer's disease; multifactor dementia; seizure;
 KW amyotrophic lateral sclerosis; convulsions; Huntington's disease;
 KW amnesia; cardiovascular disease; cardiac arrhythmia; angina pectoris;
 KW hypoxic damage; ischaemia; myocardial infarction; SSCP;
 KW congestive heart failure; Lambert-Eaton myasthenic syndrome;
 KW single strand conformation polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN US2003044911-A1.
 XX
 PD 06-MAR-2003.
 XX
 PF 05-APR-2002; 2002US-00116949.
 XX
 PR 30-DEC-1998; 98US-0114359P.
 PR 22-DEC-1999; 99US-00470443.
 XX
 PA (LEHM/) LERMAN M I.
 PA (LATI/) LATIF F.
 PA (WEIM/) WEI M.
 PA (DUHF/) DUH F.
 PA (MINN/) MINNA J D.
 PA (SEKI/) SEKIDO Y.
 PA (GAOB/) GAO B.
 XX
 PI Lerman MI, Latif F, Wei M, Duh F, Minna JD, Sekido Y, Gao B;
 DR WPI; 2003-492262/46.
 XX
 PT New substantially pure human calcium channel alpha2delta subunit splice
 PT isoform 1, 2 and 3 sequence useful in preventing, treating and diagnosing
 PT cancer, neurological disorders and cardiovascular disease.
 XX
 PS Example 7; Page 25; 79pp; English.
 XX
 CC The invention relates to a substantially purified amino acid sequence
 CC comprising at least a portion of human calcium channel alpha2delta
 CC subunit splice isoform 1, splice isoform 2 sequence or splice isoform 3,
 CC or their variants, and their encoding nucleic acids (or their
 CC complements, variants, or homologues). Also included are screening a test
 CC compound for modulating calcium channel activity, an antibody which binds
 CC to the calcium channel or its variants and producing a transgenic non-
 CC human animal (where the animal expresses a reduced level of calcium
 CC channel alpha 2delta subunit relative to a corresponding wild-type
 CC animal). The calcium channel proteins are useful for generating an
 CC antibody (which is useful for detecting the proteins or their portions).
 CC The transgenic animal (preferably a rodent e.g. mouse) is useful for
 CC identifying a therapeutic compound for treating a transgenic animal
 CC having cancer, especially lung cancer, nasopharyngeal cancer, cervical
 CC cell carcinoma, breast cancer, cancer (small cell carcinoma or non-small
 CC head and neck cancer, a neurological disease, especially epilepsy,
 CC stroke, brain trauma, Alzheimer's disease, multifactor dementia,
 CC amyotrophic lateral sclerosis, convulsions, seizures, Huntington's
 CC disease, and amnesia, a cardiovascular disease, especially cardiac
 CC arrhythmia, angina pectoris, hypoxic damage to the cardiovascular system,
 CC ischaemic damage to the cardiovascular system, myocardial infarction, and
 CC congestive heart failure, or Lambert-Eaton myasthenic syndrome. The
 CC proteins and nucleic acids are useful in the diagnosis, prevention and
 CC treatment of the above mentioned diseases. The human gene for the calcium
 CC channel is located on chromosome 3p21.3. The present sequence is an SSCP
 CC (single strand conformation polymorphism) primer used to detect
 CC polymorphisms in the calcium channel alpha2delta subunit gene
 XX
 SQ Sequence 22 BP; 3 A; 5 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 3.0%; Score 15; DB 9; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 GTTACTGCTGTGCC 391
|||||
Db 6 GTTACTGCTGTGCC 20

RESULT 15
AAS00234/c
ID AAS00234 standard; DNA; 25 BP.

XX AAS00234;

DT 09-MAY-2001 (first entry)

DE Afx transcription factor response element, selected sequence #12.

KM DNA binding domain; Afx; transcription factor; drug target; insulin;
KW human fork head transcription factor; Afx response element; human;
XX diabetes; insulin receptor signalling pathway; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
FH protein_bind 12..19

FT /tag= A
FT /note= "Binding site for human fork head transcription
factor Afx"

XX MO200114544-A1.

XX 01-MAR-2001.

XX 22-AUG-2000; 2000MO-SE001603.

XX 26-AUG-1999; 99SE-00003009.
PR 31-AUG-1999; 99US-0151867P.
PR 25-NOV-1999; 99SE-00004269.

XX (PHAA) PHARMACIA & UPJOHN AB.

PI Climent-Johansson I, Dahlman-Wright K, Lake S, Maeserman W;

DR WPI; 2001-218446/22.

XX New Afx response element with a nucleotide sequence comprising a DNA
PT binding site for the human fork head transcription factor Afx, useful in
XX screening for genes or in bioinformatic analysis of the human genome.

XX Example 3; Fig 3; 34pp; English.

XX The sequence represents the Afx transcription factor response element,
CC selected sequence #12. Human fork head transcription factor, Afx, was
CC expressed and the protein used to select a response element comprising an
CC 8 base pair (bp) nucleotide sequence. The nucleotide sequence comprises
CC AACATGTT, the Afx response element, and is useful in bioinformatic
CC analysis e.g. of the human genome. Employing the Afx response element is
CC also useful for screening for genes that may be used as diabetes drug
CC targets. This can provide a subset of genes transcriptionally responsive
CC to insulin and may lead to development of assays that facilitate the
CC analysis of genes interacting with the insulin receptor pathway. The
CC genes found in such screening may also be employed in further screening
CC methods for compounds which modify the insulin receptor signalling
CC pathway

XX Sequence 25 BP; 5 A; 6 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 3.0%; Score 15; DB 4; Length 25;

Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 AAAACATGTTGACCG 304
|||||

Db 21 AAAACATGTTGACCG 7

RESULT 16
AC120807 standard; DNA; 25 BP.
ID AC120807

XX AC120807;

DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 20798.

KM EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
XX cross-species comparison.

OS Homo sapiens..

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

PI Miltmann MP;

DR WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 20798; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 7 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 3.0%; Score 15; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 4.1e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 TGATTACAGAGTAC 359
|||||

Db 4 TGATTACAGAGTAC 18

RESULT 17

ACH57351
ID ACH57351 standard; DNA; 25 BP.
XX
AC ACH57351;
XX
DT 16-OCT-2003 (first entry)
XX
DE DNA target sequence #6487 useful in array for genetic analyses.
XX
KW Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
PN US2003082596-A1.
XX
PD 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
XX
PA (MITT/) MITTMANN M.
XX
PI Miltmann M;
XX
DR WPI; 2003-576608/54.
XX
PT New probe array useful e.g. for monitoring gene expression levels, for
PT analysing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
XX
PS Claim 1; SEQ ID NO 6487; 9pp; English.
XX
XX The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived sublibraries) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH5260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/pa1pdiDIDEntry.html
XX
SQ Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 3.0%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1e+33;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 CGGCTGTACGGCTG 170
Db 8 CGGCTGTACGGCTG 22

RESULT 18

AAK65296
ID AAK65296 standard; RNA; 15 BP.
XX
AC AAK65296;
XX
DT 20-JUL-1999 (first entry)
XX
DE Mouse B7-1 hammerhead ribozyme target SEQ ID NO:1928.
XX
KW Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW streptolysin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX
OS Mus sp.
XX
PN WO9618736-A2.
XX
PD 20-JUN-1996.
XX
PF 22-NOV-1995; 95WO-US015516.
XX
PR 13-DEC-1994; 94US-00354920.
PR 23-DEC-1994; 94US-00363250.
PR 17-FEB-1994; 94US-00363254.
PR 20-FEB-1995; 95US-00390850.
PR 02-APR-1995; 95US-00426124.
PR 02-MAY-1995; 95US-00432874.
PR 04-MAY-1995; 95US-00434509.
PR 07-JUL-1995; 95US-0000951P.
PR 07-JUL-1995; 95US-0000974P.
PR 07-AUG-1995; 95US-00512861.
PR 05-OCT-1995; 95US-00541365.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Beiglmann L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
PI Mowbrigen J, Gustofson J, Ueman N, Wincott F, Matulic-Adamic J;
PI Karpelsty A, Thompson JD, Modak A, Burgin A;
XX
DR WPI; 1996-300653/30.
XX
PT Enzymatic nucleic acid molecules having a hammer-head motif - used for
PT the treatment of arthritis, induction of graft tolerance or treatment of
PT auto-immune diseases.
XX
XX Claim 10; Page 179; 307pp; English.
XX
XX The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
CC; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
CC can inhibit collagenase and stromelysin production in the synovial
CC membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC be used to treat antigen presenting cells of a donor to induce tolerance
CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC streptolysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention
XX
SQ Sequence 15 BP; 5 A; 3 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 2.8%; Score 14; DB 2; Length 15;
Best Local Similarity 78.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 257 AGAATTACTCGCA 270
 ||||:|||||
 DB 2 AGAATUACCGGCA 15

RESULT 19
 AAX65297
 ID AAX65298 standard; RNA; 15 BP.
 XX AAX65298;
 AC
 XX 20-JUL-1999 (first entry)
 DT
 XX Mouse B7-1 hammerhead ribozyme target SEQ ID NO:1930.
 DE
 XX Arthritic condition; graft tolerance; immune response; target; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
 KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
 KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
 KW diagnosis; ss.
 XX
 OS Mus sp.
 XX
 PN WO9618736-A2.
 XX
 PD 20-JUN-1996.
 XX
 PF 22-NOV-1995; 95WO-US015516.
 XX
 PR 13-DEC-1994; 94US-00354920.
 PR 23-DEC-1994; 94US-00363253.
 PR 23-DEC-1994; 94US-00363254.
 PR 17-FEB-1995; 95US-00390850.
 PR 20-APR-1995; 95US-00426124.
 PR 02-MAY-1995; 95US-00432874.
 PR 04-MAY-1995; 95US-00434509.
 PR 07-JUL-1995; 95US-0000951P.
 PR 07-JUL-1995; 95US-0000974P.
 PR 07-AUG-1995; 95US-00512861.
 PR 05-OCT-1995; 95US-00541365.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
 PI McWiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;
 PI Karpelsky A, Thompson JD, Modak A, Burgin A;
 XX
 DR WPI; 1996-300653/30.
 XX
 PT Enzymatic nucleic acid molecules having a hammer-head motif - used for
 PT the treatment of arthritis, induction of graft tolerance or treatment of
 PT auto-immune diseases.
 XX
 PS Claim 10; Page 179; 307pp; English.
 XX
 CC The present invention describes a novel enzymatic nucleic acid (ENA)
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
 CC at (iii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
 CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
 CC can inhibit collagenase and stromelysin production in the synovial
 CC membrane of joints for the treatment or prevention of arthritis.
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
 CC be used to treat antigen presenting cells of a donor to induce tolerance
 CC in a recipient to an alloantigen of a donor. They can also be used for
 CC enhancing graft tolerance or for treating autoimmune disease, and for
 CC treating allergies and other inflammatory conditions. The ENA's can also
 CC be used in diagnosis. Ribozyme therapy impacts on the expression of
 CC stromelysin without introducing the non-specific effects upon gene
 CC expression which accompany treatment with retinoids and dexamethasone.
 CC The concentration of ribozyme required to affect a therapeutic treatment
 CC is lower than that required of antisense molecules, and is highly
 CC specific. The present sequence is used in the exemplification of the

CC present invention
 XX
 SQ Sequence 15' BP; 5 A; 3 C; 4 G; 0 T; 3 U; 0 Other:
 Query Match 2.8%; Score 14; DB 2; Length 15;
 Best Local Similarity 78.6%; Pred. No. 1.3e+04;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 257 AGAATTACTCGCA 270
 ||||:|||||
 DB 2 AGAATUACCGGCA 15

RESULT 20
 AAX65297
 ID AAX65297 standard; RNA; 15 BP.
 XX AAX65297;
 AC
 XX 20-JUL-1999 (first entry)
 DT
 XX Mouse B7-1 hammerhead ribozyme target SEQ ID NO:1929.
 DE
 XX Arthritic condition; graft tolerance; immune response; target; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
 KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
 KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
 KW diagnosis; ss.
 XX
 OS Mus sp.
 XX
 PN WO9618736-A2.
 XX
 PD 20-JUN-1996.
 XX
 PF 22-NOV-1995; 95WO-US015516.
 XX
 PR 13-DEC-1994; 94US-00354920.
 PR 23-DEC-1994; 94US-00363253.
 PR 23-DEC-1994; 94US-00363254.
 PR 17-FEB-1995; 95US-00390850.
 PR 20-APR-1995; 95US-00426124.
 PR 02-MAY-1995; 95US-00432874.
 PR 04-MAY-1995; 95US-00434509.
 PR 07-JUL-1995; 95US-0000951P.
 PR 07-JUL-1995; 95US-0000974P.
 PR 07-AUG-1995; 95US-00512861.
 PR 05-OCT-1995; 95US-00541365.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
 PI McWiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;
 PI Karpelsky A, Thompson JD, Modak A, Burgin A;
 XX
 DR WPI; 1996-300653/30.
 XX
 PT Enzymatic nucleic acid molecules having a hammer-head motif - used for
 PT the treatment of arthritis, induction of graft tolerance or treatment of
 PT auto-immune diseases.
 XX
 PS Claim 10; Page 179; 307pp; English.
 XX
 CC The present invention describes a novel enzymatic nucleic acid (ENA)
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
 CC at (iii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
 CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
 CC can inhibit collagenase and stromelysin production in the synovial
 CC membrane of joints for the treatment or prevention of arthritis.
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
 CC be used to treat antigen presenting cells of a donor to induce tolerance
 CC in a recipient to an alloantigen of a donor. They can also be used for
 CC enhancing graft tolerance or for treating autoimmune disease, and for

treating allergies and other inflammatory conditions. The ENA's can also be used in diagnosis. Ribozyme therapy impacts on the expression of streptomycin without introducing the non-specific effects upon gene expression which accompany treatment with retinoids and dexamethasone. The concentration of ribozyme required to affect a therapeutic treatment is lower than that required of antisense molecules, and is highly specific. The present sequence is used in the exemplification of the present invention

Sequence 15 BP; 5 A; 3 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 2.8%; Score 14; DB 2; Length 15;
Best Local Similarity 78.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

257 AGAATTACCTGGCA 270
|||||:|||||
2 AGAATUACUGGCA 15

RESULT 21
ABL95963/C
ID ABL95963 standard; DNA; 19 BP.
XX ABL95963;
AC
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe #40 for assaying nucleic acids.
XX
XX Probe; polymorphism detection; mutation detection; disease diagnosis;
KM microbial identification; ss.
XX
OS Unidentified.
XX
XX WO200208414-A1.
XX
XX 31-JAN-2002.
XX
XX 27-JUN-2001; 2001WO-1B001147.
XX
XX 27-JUN-2000; 2000JP-00193133.
XX 03-AUG-2000; 2000JP-00236115.
XX 26-SEP-2000; 2000JP-00292483.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (KANK-) KANKYO ENG CO LTD.
XX
XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
XX WPI; 2002-195876/25.
XX
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
XX Example 41; Page 103; 152pp; Japanese.
XX
XX The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridizing with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridization reaction system is increased after completion of the
CC hybridization but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 19 BP; 2 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 14; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

304 GAGAGCCTGCTGAC 317
|||||:|||||
18 GAGAGCCTGCTGAC 5

RESULT 22
ADL25029
ID ADL25029 standard; DNA; 19 BP.
XX
XX
AC ADL25029;
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Intestinal epithelium/peyer's patch M cell-associated PCR primer #174.
DE
XX
XX Intestinal epithelium cell development; peyer's patch M cell development;
KM inflammatory bowel disease; glutenenteropathy; infectious disease;
KM autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KM Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;
KM immune system disorder; hypersensitivity; anaphylaxis;
KM blood group incompatibility; ss; human; PCR; primer.
XX
XX Homo sapiens.
OS
XX
XX WO200208052-A2.
XX
XX 17-OCT-2002.
XX
XX 04-APR-2002; 2002WO-US010873.
XX
XX 04-APR-2001; 2001US-0281416P.
XX
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
XX Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;
PI WPI; 2003-075470/07.
XX
XX Novel isolated or purified polypeptide encoded by genes associated with
PT intestinal epithelium or M cell development, differentiation or function,
PT useful for treating autoimmune diseases and infectious diseases.
XX
XX Disclosure; SEQ ID NO 539; 152pp; English.
XX
XX The invention comprises DNA sequences which are associated with
CC intestinal epithelium and peyer's patch M cells. The DNA sequences of the
CC invention are useful for assessing, modifying, modulating or regulating
CC intestinal epithelium or M cell development. The DNA sequences of the
CC invention are also useful in the treatment of: inflammatory bowel
CC disease, glutenenteropathy, infectious diseases, autoimmune diseases
CC (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's
CC disease, multiple sclerosis, allergy, asthma and diabetic mellitus),
CC diseases or disorders of the immune system, hypersensitivity,
CC anaphylaxis, and blood group incompatibility. The present DNA sequence
CC represents a PCR primer that was used to amplify an intestinal
XX epithelium/peyer's patch M cell-associated DNA sequence of the invention.
XX
SQ Sequence 19 BP; 5 A; 5 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 2.8%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 CCTTCGACGAGG 17
|||||:|||||
1 CCTTCGACGAGG 14

RESULT 23

AAH75338
ID AAH75338 standard; DNA; 20 BP.
AC AAH75338;
XX
XX 02-OCT-2001 (first entry)
XX
DE Mouse inducible NOS antisense oligonucleotide SEQ ID NO 182.
XX
XX Antisense oligonucleotide; inducible nitric oxide synthase; NOS;
KM modulate expression; immunomodulator; antidiabetic; cardiovascular;
KM cardiac; neuroprotective; vasotropic; ischaemia; reperfusion injury;
KM 2'-O-methoxyethyl; phosphorothioate; mouse; ss.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone, 5' and 3' five
FT nucleotide 2'-MOE (2'-O-methoxyethyl) wings, all cytidine
FT residues are 5-methylcytidines and a deoxy gap"
XX
XX WO200152902-A1.
XX
XX 26-JUL-2001.
XX
XX 15-JAN-2001; 2001WO-US001381.
XX
XX 24-JAN-2000; 2000US-00490208.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dean NM, Cowse LM;
XX
XX WPI; 2001-465340/50.
XX
XX
XX New antisense oligonucleotides for modulating the expression of inducible
PT nitric oxide synthase in cells or tissues, particularly useful for
PT treating e.g. immunological, cardiovascular or neurological disorders, or
PT ischemia.
XX
XX
XX Example 17; Page 87; 14pp; English.
XX
XX The invention relates to antisense compounds, especially
CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
CC nitric oxide synthase and which specifically hybridize to and modulate
CC expression of inducible nitric oxide synthase. The antisense compounds
CC have immunomodulator, antidiabetic, cardiovascular, cardiac,
CC neuroprotective, disorder and vasotropic activity. The antisense
CC oligonucleotides are useful for inhibiting the expression of inducible
CC nitric oxide synthase in cells or tissues. In particular, the antisense
CC oligonucleotides are useful for treating diseases or disorders associated
CC with inducible nitric oxide synthase, e.g. diabetes, immunological
CC disorder, cardiovascular disorder, neurological disorder or
CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
CC useful for research and diagnostics. The present sequence is that of an
CC antisense 2'-O-methoxyethyl gapmer oligonucleotide with a
CC phosphorothioate backbone, a central "gap" region of ten nucleotides
CC flanked by five nucleotide 2'-MOE (2'-methoxyethyl) wings and 5-
CC methylcytidine residues throughout the oligonucleotide. The antisense
CC oligonucleotide is targeted to mouse inducible nitric oxide synthase (NOS)
CC mRNA (AAH47974)
XX
SQ Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 2.8%; Score 14; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 AGAGCTCGTGCT 318
|||||

Db 1 AGAGCTCGTGCT 14

RESULT 24

AAK98349/c
ID AAK98349 standard; DNA; 20 BP.
XX

AAK98349;
XX

08-MAY-2002 (first entry)
XX

High mobility group nonhistone chromatin protein EMSA probe PCR primer 2.

XX Expression augmenting sequence element; EASE; ss; HMG; HMG-I(Y);
KM recombinant protein expression; mammalian host cell; PCR; primer;
KM high mobility group; nonhistone chromatin protein;
KM architectural transcription factor; EMSA;
KM electrophoretic mobility shift assay.

XX Unidentified.

XX US6309841-B1.
XX

30-OCT-2001.
XX

12-SEP-2000; 2000US-00660299.
XX

11-JAN-1996; 96US-00586509.
XX

13-JAN-1997; 97US-00785150.
XX

05-NOV-1999; 99US-00435377.
XX

(IMGV) IMMUNEX CORP.
XX

Morris AE, Thomas JN;
XX

WPI; 2002-033281/04.
XX

New expression augmenting sequence elements isolated from a Chinese
PT hamster ovary cell line improve expression of recombinant proteins in
PT host mammalian cells.
XX

Example 15; Col 20; 25pp; English.
XX

The invention comprises Chinese hamster expression augmenting sequence
CC elements (EASEs; AAK98343-AAK98344) that can be used to improve
CC expression of recombinant proteins in mammalian host cells. The EASE
CC sequences of the invention contain numerous binding sites for members of
CC the HMG-I(Y) ("high mobility group") family of nonhistone chromatin
CC proteins, a group of minor groove-binding architectural transcription
CC factors which are thought to be involved in the mechanisms by which EASE
CC sequences improve expression of transgenes. The EASEs of the invention
CC can also be used in the identification of additional EASE sequences (e.g.
CC from other transformed cell lines which exhibit high levels of expression
CC not attributable to a high gene copy number). Expression of recombinant
CC therapeutic proteins in mammalian cells is often preferable to expression
CC in microbial (prokaryotic) cells, since the post-translational
CC modification found in mammalian cells are more likely to resemble those
CC found in a mammal. Sequences AAK98348 - AAK98353 represent PCR primers
CC used to create electrophoretic mobility shift assay (EMSA) probes
CC specific for HMG proteins
XX

SQ Sequence 20 BP; 10 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 14; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 TGTTCGTGCTGCT 345
|||||

Db 18 TGTTCGTGCTGCT 5
|||||

RESULT 25

```

ADD98905/c
ID ADD98905 standard; DNA; 20 BP.
XX
AC ADD98905;
XX
DT 29-JAN-2004 (first entry)
XX
DE Hamster high mobility group, HMG-I(Y) gene EMSA probe #2.
XX
KW Hamster; high mobility group; HMG-I(Y); ss; probe;
KW expression augmenting sequence element; EASE; EMSA;
KW electrophoretic shift mobility assay.
XX
OS Cricetus griseus.
XX
PN US2003008345-A1.
XX
PD 09-JAN-2003.
XX
PF 09-OCT-2001; 2001US-00973928.
XX
PR 11-JAN-1996; 96US-00586509.
PR 13-JAN-1997; 97US-00785150.
PR 05-NOV-1999; 99US-00435377.
PR 02-MAR-2000; 2000US-0186537P.
PR 12-SEP-2000; 2000US-0060299.
XX
PA (MORR/) MORRIS A E.
PA (THOM/) THOMAS J N.
XX
PI Morris AE, Thomas JN;
XX
DR WPI; 2003-863362/80.
XX
PT New isolated polynucleotide used for producing recombinant protein by
PT culturing mammalian host cell.
XX
PS Example 15; Page 12; 27pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a nucleic
CC acid molecule comprising nucleotides 11538-11692; nucleotides 11538-
CC 11760; nucleotides 11673-12165; nucleotides 11813-12165 or nucleotides
CC 11899-12165 of AD89798, the hamster high mobility group, HMG-I(Y) gene,
CC fragments of the DNA having expression augmenting activity (an expression
CC augmenting sequence element, EASE) or their combinations or complementary
CC DNA. Also included are a mammalian host cell which comprises the
CC polynucleotide, and production of a recombinant protein which comprises
CC culturing the cell under conditions promoting expression of the protein.
CC The polynucleotides are used for production of recombinant protein,
CC particularly in eukaryotic cells for research and therapeutic
CC applications. The method is also used for identifying expression
CC augmenting sequence elements e.g. from other transformed cell lines. High
CC expression of recombinant proteins is facilitated in a short period. The
CC present sequence is an EMSA (electrophoretic shift mobility assay) probe
CC for the hamster HMG-I(Y) protein.
XX
SQ Sequence 20 BP; 10 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX
Query Match 2.8%; Score 14; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 332 TGTTCGTGCTGCT 345
DB 18 TGTTCGTGCTGCT 5
XX
RESULT 26
ADM36243
ID ADM36243 standard; DNA; 20 BP.
XX
AC ADM36243;
XX

```

```

DT 03-JUN-2004 (first entry)
XX
DE 3' RACE PCR primer used to amplify murine SST8-5 cDNA SeqID 38.
XX
KW PCR; ss; mouse; murine; differentiation; metabolic function; adipocyte;
KW obesity; hypertension; hyperlipaemia; diabetes; arteriosclerosis;
KW anorectic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;
KW primer.
XX
OS Mus musculus.
XX
PN WO2004007711-A1.
XX
PD 22-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-JP008690.
XX
PR 10-JUL-2002; 2002JP-00201856.
XX
PA (TAKEDA) TAKEDA CHEM IND LTD.
XX
PI Matsuzawa Y, Funahashi T, Shimomura C, Furuyama N;
XX
DR WPI; 2004-122943/12.
XX
PT Mouse membrane and secretory proteins of adipocyte origin and
PT polynucleotides encoding them for screening compounds as remedies for
PT obesity, diabetes, arteriosclerosis, hypertension and hyperlipemia.
XX
PS Example 3; SEQ ID NO 38; 195pp; Japanese.
XX
CC This invention relates to novel membrane proteins that are associated
CC with differentiation and/or metabolic function of adipocytes, in
CC particular of mouse origin. Specifically, it refers to the isolated
CC nucleic acid molecules encoding all or part of these proteins,
CC appropriate antibodies and screening assays useful for the development of
CC drug compositions derived thereof. The present invention describes these
CC compositions as useful for the treatment of diseases associated with
CC abnormalities of adipocyte function, such that they can be used to
CC prevent, treat or diagnose obesity, hypertension, hyperlipaemia, diabetes
CC and arteriosclerosis. Accordingly, they exhibit anorectic, antidiabetic,
CC antidiabetic, antidiabetic, antidiabetic and hypotensive activities. This
CC oligonucleotide is a 3' RACE gene specific PCR primer used to amplify
CC murine adipocyte-derived cDNA of the invention.
XX
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX
Query Match 2.8%; Score 14; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 28 TGCACCTGCTGCTT 41
DB 2 TGCACCTGCTGCTT 15
XX
RESULT 27
ADG29799/c
ID ADG29799 standard; RNA; 21 BP.
XX
AC ADG29799;
XX
DT 26-FEB-2004 (first entry)
XX
DE EGFR-targeted siNA DNA-RNA hybrid - SEQ ID 365.
XX
KW double-stranded short interfering nucleic acid; siNA;
KW antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW antiemetic; pulmonary disease; restenosis; arteriosclerosis;
KW Alzheimer's; Parkinson's; epilepsy; dementia; Huntington's;
KW amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; EGFR.
XX
OS Unidentified.
XX

```

OS Synthetic.
XX WO2003074654-A2.
XX
XX 12-SEP-2003.
PD
XX 20-FEB-2003; 2003WO-US005028.
PF
XX 20-FEB-2002; 2002US-0358580P.
PR
XX 11-MAR-2002; 2002US-0363124P.
PR
XX 06-JUN-2002; 2002US-0386782P.
PR
XX 29-AUG-2002; 2002US-0406784P.
PR
XX 05-SEP-2002; 2002US-0408378P.
PR
XX 09-SEP-2002; 2002US-0409293P.
PR
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX McSwiggen J, Beigelman L, Chowrira B, Pavco P, Fosnaugh K;
PI
XX Jamison S, Usman N, Thompson J;
XX
XX WPI; 2003-731676/69.
XX
XX
XX New double-stranded short interfering nucleic acid molecule, useful for
PT down-regulating the expression of an endogenous mammalian target gene or
PT for treating diseases that respond to modulation of gene expression or
PT activity.
XX
XX Example 24; SEQ ID NO 365; 593bp; English.
XX
XX The invention relates to a double-stranded short interfering nucleic acid
CC (siRNA) molecule that down-regulates expression of an endogenous mammalian
CC target gene comprising one or more chemical modifications and each strand
CC of the double-stranded siRNA comprises about 21 nucleotides. The siRNA of
CC the invention demonstrates antiarteriosclerotic, neuroprotective,
CC neurotropic, antiparkinsonian and anticonvulsant activities and may be
CC useful for down-regulating the expression of an endogenous mammalian
CC target gene and therefore in the treatment of any disease or condition
CC that responds to modulation of gene expression or activity in a cell,
CC tissue or organism. The disease or condition may include pulmonary
CC diseases such as asthma, atherosclerosis, Alzheimer's disease,
CC Parkinson's disease, epilepsy, dementia, Huntington's disease or
CC amyotrophic lateral sclerosis. Furthermore, the siRNA may be utilized for
CC gene therapy applications. The current sequence is that of the siRNA DNA-
CC RNA hybrid of the invention.
XX
XX Sequence 21 BP; 3 A; 2 C; 8 G; 2 T; 6 U; 0 Other;
SQ
Query Match 2.8%; Score 14; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 244 TCAGACATCCTGAA 257
Db 16 TCAGACATCCTGAA 3
RESULT 28
ADL80074/c
ID ADL80074 standard; RNA; 21 BP.
XX
XX ADL80074;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human HER1 (EGFR) chemically modified siRNA, SEQ ID NO:1241.
DE
XX RNA interference; short interfering nucleic acid; siRNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; cancer;
KW cytostatic; human; oncogene; epidermal growth factor receptor; EGFR;

KW HER1; c-erb-B-1; DNA-RNA hybrid; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 3..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro bases"
FT 10
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro bases"
FT 12..14
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro bases"
FT 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro base"
FT 20..21
FT modified_base
FT /*tag= e
FT /mod_base= OTHER
FT /note= "Ribothymidine. Also, the internucleotide linkage
FT is phosphorothioate"
XX
XX WO2003070912-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005045.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR
XX 11-MAR-2002; 2002US-0363124P.
PR
XX 29-MAY-2002; 2002WO-US015840.
PR
XX 06-JUN-2002; 2002US-0386782P.
PR
XX 29-AUG-2002; 2002US-0406784P.
PR
XX 05-SEP-2002; 2002US-0408378P.
PR
XX 09-SEP-2002; 2002US-0409293P.
PR
XX 19-SEP-2002; 2002US-00251117.
PR
XX 21-OCT-2002; 2002US-0027494.
PR
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX McSwiggen J, Pavco P, Beigelman L, Fosnaugh K, Jamison S;
PI
XX WPI; 2003-697612/66.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of the epidermal growth
PT factor receptor gene.
XX
XX Example 9; SEQ ID NO 1241; 171bp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of one or more human epidermal growth factor
CC receptor (EGFR) genes (including HER1, HER2 HER3 and HER4) by RNA
CC interference. The siNAs may or may not comprise ribonucleotides and may
CC be double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC can contain deoxyribonucleotides, and can be chemically synthesised,
CC expressed from a vector or enzymatically synthesised. The invention also
CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
CC used to modulate expression of EGFR genes in cells, tissue explants or

CC organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
CC for the treatment of a variety of conditions. They may be used for
CC treating a wide range of cancers such as breast and ovarian cancer. The
CC cDNAs are also useful for drug screening, diagnosis, therapeutic target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function, and gene mapping (e.g., of single nucleotide
CC polymorphisms). The present sequence represents a chemically modified
CC sRNA targeted to the human HER1 (EGFR) mRNA transcript.

XX
SQ Sequence 21 BP; 3 A; 2 C; 8 G; 2 T; 6 U; 0 Other;

Query Match 2.8%; Score 14; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 TCAGACATCCTGAA 257
Db 16 TCAGACATCCTGAA 3

RESULT 29
ADM36242/c
ID ADM36242 standard; DNA; 21 BP.

XX
AC ADM36242;
XX
DT 03-JUN-2004 (first entry)
XX

DE 5' RACE PCR primer used to amplify murine SSTR-5 cDNA SeqID 37.

XX
KM PCR; ss; mouse; murine; differentiation; metabolic function; adipocyte;
KM obesity; hypertension; hyperlipemia; diabetes; arteriosclerosis;
KM anorectic; antidiabetic; antiarteriosclerotic; antilipemic; hypotensive;
KM primer.

XX
OS Mus musculus.

XX
PN WO2004007711-A1.

XX
PD 22-JAN-2004.

XX
PF 09-JUL-2003; 2003MO-JP008690.

XX
PR 10-JUL-2002; 2002JP-00201856.

XX
PA (TAKE) TAKEDA CHEM IND LTD.

XX
PI Matsuzawa Y, Funahashi T, Shimomura C, Furuyama N;

XX
DR WPI, 2004-122943/12.

XX
PT Mouse membrane and secretory proteins of adipocyte origin and
PT polynucleotides encoding them for screening compounds as remedies for
PT obesity, diabetes, arteriosclerosis, hypertension and hyperlipemia.

XX
PS Example 3; SEQ ID NO 37; 195bp; Japanese.

XX
CC This invention relates to novel membrane proteins that are associated
CC with differentiation and/or metabolic function of adipocytes, in
CC particular of mouse origin. Specifically, it refers to the isolated
CC nucleic acid molecules encoding all or part of these proteins,
CC appropriate antibodies and screening assays useful for the development of
CC drug compositions derived thereof. The present invention describes these
CC compositions as useful for the treatment of diseases associated with
CC abnormalities of adipocyte function, such that they can be used to
CC prevent, treat or diagnose obesity, hypertension, hyperlipemia, diabetes
CC and arteriosclerosis. Accordingly, they exhibit anorectic, antidiabetic,
CC antidiabetic, antilipemic and hypotensive activities. This
CC oligonucleotide is a 5' RACE gene specific PCR primer used to amplify
CC murine adipocyte-derived cDNA of the invention.

XX
SQ Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 14; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 TGCACCTGCTGCTT 41
Db 20 TGCACCTGCTGCTT 7

RESULT 30
ADM24728
ID ADM24728 standard; DNA; 22 BP.

XX
AC ADM24728;

XX
DT 20-MAY-2004 (first entry)

XX
DE Expression vector library associated adaptor #1.

XX
KM expression vector library; adaptor-modified cDNA; cellular library;
KM retroviral vector library; cellular phenotype; cancer; immune response;
KM neurobiology; anti-apoptotic; neuronal function; neuronal death;
KM exocytosis; intracellular calcium cycling; sarcolemmal calcium cycling;
KM cardiomyocyte; arrhythmia; bone morphogenic protein; hormone mimetic;
KM bone formation; adaptor; ds.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

XX
FT misc_difference 20..22

XX
FT /tag= a

XX
FT /note= "This sequence overhangs the complementary strand

XX
FT forming a sticky end"

XX
EN US2003211462-A1.

XX
PD 13-NOV-2003.

XX
PF 08-MAY-2002; 2002US-00142662.

XX
PR 08-MAY-2002; 2002US-00142662.

XX
PA (SHEN/) SHEN M.

XX
PA (YUSS/) YU S.

XX
PA (MUKX/) MU X.

XX
PA (PAYA/) PAYAN D.

XX
PI Shen M, Yu S, Wu X, Payan D;

XX
DR WPI, 2004-010664/01.

XX
PT Producing expression vector library by synthesizing cDNA from mRNAs,

XX
PT ligating with adaptor, cleaving adaptor modified cDNA with endonuclease

XX
PT to provide first nucleic acid and cloning the nucleic acid with vector.

XX
PS Claim 6; Fig 1; 41bp; English.

XX
CC The invention describes a method of producing an expression vector
CC library by providing several mRNA, synthesizing first and second cDNA
CC strands from mRNAs, ligating a first adaptor to the 5' end and a second
CC adaptor to the 3' end of the double stranded cDNA to produce an adaptor-
CC modified cDNA, cleaving the adaptor-modified cDNA with restriction
CC endonuclease SfiI to produce first a nucleic acid and cloning the first
CC nucleic acid into an expression vector. Also described are: a cellular
CC library (1) comprising the retroviral vector library produced by (M1),
CC where the first nucleic acid is fused with 5' end of the second nucleic
CC acid; and screening (M2) for a bioactive agent capable of altering a
CC cellular phenotype involving introducing a retroviral expression vector
CC library, produced by (M1) into several cells, screening several cells for
CC a cell with an altered phenotype. (1) is useful for creating novel cell
CC lines from cancer patients, for identifying modulators of immune
CC response, in neurobiology for screening anti-apoptotics for preservation
CC of neuronal function and prevention of neuronal death, for screening

CC agents capable of modulating exocytosis. (1) is also useful in
CC conjunction with known cancer therapeutics to screen agonists to make the
CC therapeutics more effective or less toxic. (M1) is useful to identify
CC agents that regulate the intracellular and sarcolemmal calcium cycling in
CC cardiomyocytes, to prevent arrhythmias. (M2) is useful for screening
CC agonists of bone morphogenic proteins, hormone mimetics to stimulate,
CC regulate or enhance new bone formation, and for screening bioactive
CC agents capable of modulating various physiological processes or biochemical
CC activities. This sequence represents an adaptor associated with the
CC creation of an expression vector library.

XX Sequence 22 BP; 3 A; 9 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 14; DB 12; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.3e+04; Mismatches 0; Gaps 0;

Db 450 GCCAGTGGCCGCTAA 463
9 GCCAGTGGCCGCTAA 22

RESULT 31

AAT10330/C

ID AAT10330 standard; DNA; 23 BP.

XX AAT10330;

DT 18-JUL-1996 (first entry)

DE Anti-P.aeruginosa type B antibody VL region N-terminal 5'-primer.

XX Human, immunoglobulin, IgM, lambda light chain, variable region;
KM lipopolysaccharide; LPS; antigen; Pseudomonas aeruginosa; type B;
XX monoclonal antibody; PCR primer; ss.

OS Synthetic.

XX Key Location/Qualifiers

XX CDS 1..23

XX FT /*tag= a /note= "does not include start or stop codons"

XX JF07327677-A.

XX 19-DEC-1995.

XX 07-JUN-1994; 94JP-00125125.

XX 07-JUN-1994; 94JP-00125125.

XX (MITK) MITSUI TOATSU CHEM INC.

XX WPI: 1996-072335/08.

XX P-PsDB; AAR91912.

XX Gene(s) encoding human antibody variable regions against P.aeruginosa

XX type B - useful for prodn. of monoclonal antibody-producing cells.

XX Example 2; Page 11; 12pp; Japanese.

XX A cDNA fragment (see AAT10327) coding for the lambda light chain variable

XX region of a human antibody which specifically recognizes a

XX lipopolysaccharide (LPS) antigen from Pseudomonas aeruginosa was cloned

XX by PCR. The coding sequence can be used for preparing cell lines which

XX produce monoclonal antibodies against the LPS. The present sequence is

XX that of a 5'-primer used in the PCR amplification

XX Sequence 23 BP; 5 A; 9 C; 5 G; 4 T; 0 U; 0 Other;

Qy 185 GTGAGCTCAACCTG 198
14 GTGAGCTCAACCTG 1

RESULT 32

ID ADG29798 standard; RNA; 23 BP.

XX ADG29798;

DT 26-FEB-2004 (first entry)

DE EGFR-targeted siNA DNA-RNA hybrid - SEQ ID 364.

XX double-stranded short interfering nucleic acid; siNA;

KM antiarteriosclerotic; neuroprotective; neurotropic; antiparkinsonian;

KM anticonvulsant; pulmonary disease; restenosis; atherosclerosis;

KM Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;

KM amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; EGFR.

XX Unidentified.

OS Synthetic.

XX WO2003074654-A2.

XX 20-FEB-2003; 2003WO-US005028.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 06-JUN-2002; 2002US-0366782P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mergelgen J, Beigelman L, Chowrira B, Pavco P, Fosnaugh K;

XX Jamison S, Usman N, Thompson J;

XX WPI: 2003-731676/69.

XX New double-stranded short interfering nucleic acid molecule, useful for

XX down-regulating the expression of an endogenous mammalian target gene or

XX for treating diseases that respond to modulation of gene expression or

XX activity.

XX Example 24; SEQ ID NO 364; 593pp; English.

XX The invention relates to a double-stranded short interfering nucleic acid

XX (siNA) molecule that down-regulates expression of an endogenous mammalian

XX target gene comprising one or more chemical modifications and each strand

XX of the double-stranded siNA comprises about 21 nucleotides. The siNA of

XX the invention demonstrates antiarteriosclerotic, neuroprotective,

XX neurotropic, antiparkinsonian and anticonvulsant activities and may be

XX useful for down-regulating the expression of an endogenous mammalian

XX target gene and therefore in the treatment of any disease or condition

XX that responds to modulation of gene expression or activity in a cell,

XX disease or organism. The disease or condition may include pulmonary

XX diseases such as restenosis, atherosclerosis, Alzheimer's disease,

XX Parkinson's disease, epilepsy, dementia, huntington's disease or

XX amyotrophic lateral sclerosis. Furthermore, the siNA may be utilized for

XX gene therapy applications. The current sequence is that of the siNA DNA-

XX RNA hybrid of the invention.

XX Sequence 23 BP; 6 A; 8 C; 2 G; 2 T; 3 U; 2 Other;

Query Match 2.8%; Score 14; DB 10; Length 23;

Best Local Similarity 78.6%; Pred. No. 1.3e+04;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 244 TCAGACATCTCGAA 257
Db 5 UCAGACAUCCUGAA 18

RESULT 33
ADL80073
ID ADL80073 standard; RNA; 23 BP.
AC ADL80073;
XX
XX 20-MAY-2004 (first entry)
DT
XX
DE Human HER1 (EGFR) chemically modified siRNA, SEQ ID NO:1240.
XX
XX RNA interference; short interfering nucleic acid; siRNA;
KM short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KM short hairpin RNA; shRNA; expression modulation; gene therapy;
KM drug screening; diagnosis; therapeutic target identification;
KM pharmacogenomics; gene function analysis; gene mapping; cancer;
KM cytotoxic; human; oncogene; epidermal growth factor receptor; EGFR;
KM HER1; c-erb-B-1; DNA-RNA hybrid; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT modified_base
FT 1 Location/Qualifiers
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Inverted deoxy abasic"
FT 3. .6
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro bases"
FT 10
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro base"
FT 12. .15
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro bases"
FT 19. .20
FT /*tag= e
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro bases"
FT 21. .22
FT /*tag= f
FT /mod_base= OTHER
FT /note= "Ribothymidine"
FT 23
FT /*tag= g
FT /mod_base= OTHER
FT /note= "Inverted deoxy abasic"
XX
PN WO2003070912-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005045.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 29-MAY-2002; 2002WO-US016840.
PR 06-JUN-2002; 2002US-00163552.
PR 06-JUN-2002; 2002US-0386782P.
PR 03-JUL-2002; 2002US-0393924P.
PR 28-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

PR 19-SEP-2002; 2002US-00251117.
PR 21-OCT-2002; 2002US-00277494.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Pavco P, Beigelman L, Fossnaugh K, Jamison S;
PI WPI; 2003-697612/66.
DR
XX
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of the epidermal growth
PT factor receptor gene.
XX
XX
PS Example 9; SEQ ID NO 1240; 171pp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of one or more human epidermal growth factor
CC receptor (EGFR) genes (including HER1, HER2 HER3 and HER4) by RNA
CC interference. The siNAs may or may not comprise ribonucleotides and may
CC be double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC can contain deoxyribonucleotides, and can be chemically synthesized.
CC expressed from a vector or enzymatically synthesized. The invention also
CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
CC used to modulate expression of EGFR genes in cells, tissue explants or
CC organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
CC for the treatment of a variety of conditions. They may be used for
CC treating a wide range of cancers such as breast and ovarian cancer. The
CC siNAs are also useful for drug screening, diagnosis, therapeutic target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function, and gene mapping (e.g., of single nucleotide
CC polymorphisms). The present sequence represents a chemically modified
CC siRNA targeted to the human HER1 (EGFR) mRNA transcript.
XX
SQ Sequence 23 BP; 6 A; 8 C; 2 G; 2 T; 3 U; 2 Other;
XX

Query Match 2.8%; Score 14; DB 11; Length 23;
Best Local Similarity 78.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 244 TCAGACATCTCGAA 257
Db 5 UCAGACAUCCUGAA 18

RESULT 34
ADO25209
ID ADO25209 standard; DNA; 23 BP.
XX
XX ADO25209;
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX N. gonorrhoeae gyrB gene, oligonucleotide probe #1.
DE
XX
XX Bacterial species identification; bacterial infection;
KM hyper-variable region; conserved region; topoisomerase; gyrB; parE;
KM infection-causing bacteria; respiratory tract infection; probe; ss.
XX
XX Neisseria gonorrhoeae.
OS
XX
XX WO2004046379-A1.
PN
XX
XX 03-JUN-2004.
PD
XX
XX 19-NOV-2003; 2003WO-FI000888.
PF
XX
XX 19-NOV-2002; 2002FI-00002064.
PR

XX	(MOBI-) MOBIDIAG OY.
PA	
XX	
PI	Roth S, Jalava J, Nikkari S;
DR	WPI; 2004-420639/39.
XX	
PT	Diagnostic method for detecting and identifying bacterial species causing
PT	infections from clinical sample by contacting amplified DNA with a
XX	desired combination of oligonucleotide probe sequences.
PS	Claim 15; SEQ ID NO 30; 77pp; English.
XX	
CC	The present invention relates to a diagnostic method for detecting and
CC	identifying bacterial species that cause infections. The method comprises
CC	contacting amplified DNA from a clinical sample with a desired
CC	combination of oligonucleotide probe sequences that hybridise under
CC	normal hybridisation conditions with hyper-variable regions situated near
CC	the conserved regions of genes encoding topoisomerases, especially
CC	gyrB/parE, of bacterial species causing the infections. The invention
CC	also discloses broad-range primers originating from the conserved regions
CC	of the topoisomerase genes of infection-causing bacteria, and a
CC	diagnostic kit containing the oligonucleotide probes and primers of the
CC	invention. The combination of oligonucleotide probes is useful for
CC	detecting, identifying or classifying infection-causing bacterial
CC	species, such as those causing respiratory tract infections. The primers
CC	are useful for amplifying topoisomerase genes especially genes encoding
CC	gyrB and parE proteins. The present sequence represents an
CC	oligonucleotide probe of the invention.
XX	
SO	Sequence 23 BP; 11 A; 6 C; 2 G; 4 T; 0 U; 0 Other;
	Query Match 2.8%; Score 14; DB 12; Length 23;
	Best Local Similarity 100.0%; Pred.No. 1.3e+04;
	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	227 ACAACACACGCTAC 240
DB	5 ACAACACACGCTAC 18
RESULT 35	
ID	ADO25212 standard; DNA; 23 BP.
XX	ADO25212;
AC	
XX	
DT	26-AUG-2004 (first entry)
XX	
DE	N. gonorrhoeae gyrB gene, oligonucleotide probe #4.
XX	
KW	Bacterial species identification; bacterial infection;
KW	hyper-variable region; conserved region; topoisomerase; gyrB; parE;
KW	infection-causing bacteria; respiratory tract infection; probe; ss.
OS	Neisseria gonorrhoeae.
XX	
PN	WO2004046379-A1.
XX	
PD	03-JUN-2004.
XX	
PF	19-NOV-2003; 2003WO-FI000888.
XX	
PR	19-NOV-2002; 2002FI-00002064.
XX	
PA	(MOBI-) MOBIDIAG OY.
XX	
PI	Roth S, Jalava J, Nikkari S;
XX	
DR	WPI; 2004-420639/39.
XX	
PT	Diagnostic method for detecting and identifying bacterial species causing
PT	infections from clinical sample by contacting amplified DNA with a

PT	desired combination of oligonucleotide probe sequences.
XX	
PS	Claim 15; SEQ ID NO 33; 77bp; English.
CC	
CC	The present invention relates to a diagnostic method for detecting and
CC	identifying bacterial species that cause infections. The method comprises
CC	contracting amplified DNA from a clinical sample with a desired
CC	combination of oligonucleotide probe sequences that hybridise under
CC	normal hybridisation conditions with hyper-variable regions situated near
CC	the conserved regions of genes encoding topoisomerases, especially
CC	gyrB/parc, of bacterial species causing the infections. The invention
CC	also discloses broad-range primers originating from the conserved regions
CC	of the topoisomerases genes of infection-causing bacteria, and a
CC	diagnostic kit containing the oligonucleotide probes and primers of the
CC	invention. The combination of oligonucleotide probes is useful for
CC	detecting, identifying or classifying infection-causing bacterial
CC	species, such as those causing respiratory tract infections. The primers
CC	are useful for amplifying topoisomerase genes especially genes encoding
CC	gyrB and parC proteins. The present sequence represents an
CC	oligonucleotide probe of the invention.
XX	
SQ	Sequence 23 BP; 11 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
	Query March 2.8%; Score 14; DB 12; Length 23;
	Best Local Similarity 100.0%; Pred. No. 1.3e+04;
	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	227 ACAACAACAGCTAC 240
Db	2 ACAACACACGCTAC 15
RESULT 36	
AAQ78839/c	
ID	AAQ78839 standard; DNA; 24 BP.
XX	
AC	AAQ78839;
XX	
DT	25-MAR-2003 (revised)
DT	19-JUL-1995 (first entry)
XX	
DE	HCMV Ab lambda light chain variable domain PCR primer V(L7).
XX	
KW	Human cytomegalovirus; antibody lambda light chain variable domain;
KW	immunoassay; immunotherapy; HCMV; PCR primer; ss.
XX	
OS	Synthetic.
XX	
PN	WO9425490-A1.
XX	
PD	10-NOV-1994.
XX	
PF	29-APR-1994; 94MO-US004705.
XX	
PR	30-APR-1993; 93US-00055985.
XX	
PA	(SCRI) SCRIPPS RES INST.
XX	
PI	Burton DR, Barbas C, Burioni R, Williamson A;
XX	
DR	WPI; 1994-358194/44.
XX	
PT	Human monoclonal antibodies (MAbs) against human cytomegalovirus - also
PT	nucleic acids and cell lines producing the MAbs, useful in diagnosis and
PT	immunotherapy.
XX	
PS	Example 2b1; Page 84; 171pp; English.
XX	
CC	AAQ78833-Q78839 are 5' primers which separately pair with the 3' primer
CC	AAQ78840, for the PCR amplification of the human cytomegalovirus (HCMV)
CC	antibody lambda light chain variable regions. The complete antibodies
CC	could be used to detect HCMV, and anti-human HCMV Abs in human patients
CC	via a competitive immunoassay. The antibodies may also be useful in

CC Immunotherapy. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 24 BP, 5 A; 10 C; 5 G; 4 T; 0 U; 0 Other;

SQ

Query Match 2.8%; Score 14; DB 2; Length 24;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 GTGAGCTCAACCTG 198

DB 14 GTGAGCTCAACCTG 1

RESULT 37

ADG77626/C

ID ADG77626 standard; DNA; 24 BP.

AC ADG77626;

DT 11-MAR-2004 (first entry)

XX Canine disease marker-related PCR primer 470.

XX Genetic disease; genetic trait; dog; carrier of recessive disease;

XX copper toxicosis; CT; canine genome map; breed-specific profile;

XX DNA fingerprint; dog identification; PCR; primer; ss.

XX Canis familiaris.

XX WO9731011-A1.

XX 28-AUG-1997.

XX 18-FEB-1997; 97WO-US002396.

XX 22-FEB-1996; 96US-0012060P.

XX (UNMI) UNIV MICHIGAN.

XX (UNMS) UNIV MICHIGAN STATE.

XX Brewer GJ, Venta PJ, Yuzbasiyan-Gurkan V;

XX WPI; 1997-435082/40.

XX New oligonucleotide primers for diagnosis of genetic diseases and traits

XX in dogs - amplify specific regions of the genome containing

XX microsatellite repeats, especially for diagnosing copper toxicosis and

XX carriers.

XX Claim 1; Page 15; 40pp; English.

XX This invention relates to novel oligonucleotide PCR primers which may be

XX used to identify markers associated with genetic diseases and traits in

XX dogs, in particular to diagnose genetic diseases that are not

XX phenotypically visible and to identify carriers of recessive diseases. A

XX specific application is diagnosis of copper toxicosis (CT). The invention

XX can also be used to create a genetic map of the canine genome; to

XX generate breed-specific profiles; to establish paternity and to identify

XX dogs from DNA fingerprints. The method provides rapid analysis of the

XX target sequences from only a small sample of DNA. Diagnosis can be done

XX at any time in the dog's life. The present sequence is that of a PCR

XX primer of the invention.

XX Sequence 24 BP, 8 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

SQ

Query Match 2.8%; Score 14; DB 2; Length 24;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GAAGATTACTCTGG 268

DB 17 GAAGATTACTCTGG 4

RESULT 38

AAV68558/C

ID AAV68558 standard; DNA; 24 BP.

XX AAV68558;

DT 16-FEB-1999 (first entry)

XX Lambda chain fragment 5' PCR primer VL7.

XX Lambda chain fragment; human; receptor; antigen; tumour;

XX auto-immune disease; PCR; primer; graft rejection; allergy;

XX inflammatory disease; endocrine disease; degenerative disease;

XX amplification; ss.

XX Synthetic.

XX WO9646645-A2.

XX 22-OCT-1998.

XX 14-APR-1998; 98WO-EP002180.

XX 14-APR-1997; 97EP-00106109.

XX (KUFE/) KUFE P.

XX (RAUM/) RAUM T.

XX Kufer P, Raum T;

XX WPI; 1998-594564/50.

XX Production of anti-human antigen receptors - by selecting a combination

XX of functionally rearranged VH and VL immunoglobulin chains expressed from

XX a recombinant vector.

XX Example 1; Page 28; 84pp; English.

XX This is the nucleotide sequence of a lambda chain fragment used for

XX amplification in the method of the invention, for providing receptors

XX that can be used for targeting antigens in humans without being

XX immunogenic themselves. Such receptors can be used for treating diseases

XX such as tumours or auto-immune diseases, graft rejection after

XX transplantation, infectious diseases by targeting cellular receptors as

XX well as allergic, inflammatory, endocrine and degenerative diseases by

XX targeting key molecules involved in the pathological process

XX Sequence 24 BP, 5 A; 10 C; 5 G; 4 T; 0 U; 0 Other;

SQ

Query Match 2.8%; Score 14; DB 2; Length 24;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 GTGAGCTCAACCTG 198

DB 14 GTGAGCTCAACCTG 1

RESULT 39

AAZ60776/C

ID AAZ60776 standard; DNA; 24 BP.

AC AAZ60776;

DT 16-MAY-2000 (first entry)

XX 5' PCR primer VL7 for light chain variable region DNA.

XX Variable heavy chain; human anti-HCV antibody; chronic Hepatitis C;

XX conformation-dependent epitope; HCV glycoprotein E2; HCV infection;

XX liver transplantation; Tupaia-hepatocyte; HCV-infectious human sera;

XX PCR primer; ss.

```

XX OS Homo sapiens.
XX PN WO200005266-A1.
XX PD 03-FEB-2000.
XX PF 20-JUL-1999; 99MO-EP005173.
XX PR 21-JUL-1998; 98EP-00113595.
XX PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & B.
XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX PI Reiter C, Habersetzzer F, Fournillier A, Trepo C, Desgranges C,
XX PI Inchausti G;
XX DR WPI; 2000-182654/16.
XX PT Novel antibodies, antigens, for diagnosing and treating Hepatitis C
XX PT virus, comprising at least one complementarily determining region of the
XX PT variable domain of a human antibody.
XX PS Example 6; Page 40; 64pp; English.
XX CC PCR primers AAZ60770-78 were used to amplify DNA encoding the variable
XX CC light chain of a human anti-Hepatitis C virus (HCV) antibody. The
XX CC amplified sequence was used to construct antibodies of the invention.
XX CC These antibodies comprise at least one complementarily determining region
XX CC (CDR) of the variable domain of a human antibody that specifically
XX CC recognizes a conformation-dependent epitope of HCV glycoprotein E2 and is
XX CC capable of precipitating covalently or non-covalently associated E2/E1
XX CC complexes. The antibodies are useful for preventing (re)infection of HCV
XX CC and are useful for alleviating chronic Hepatitis C in a human or an
XX CC animal. The antibodies are useful for diagnosing chronic Hepatitis C for
XX CC the presence of neutralization of binding of HCV glycoprotein E2 on to
XX CC of target cells. The antibodies are useful for the treatment or prevention
XX CC of HCV infection or recurrence of HCV infection, in which they are
XX CC administered prior, during or after liver transplantation. Therapeutic
XX CC compositions containing the antibodies are also useful in liver
XX CC transplantation. The antibody is also useful for the prevention of
XX CC infection of Tupaia-hepatocyte with HCV-infectious human sera
XX SO Sequence 24 BP; 5 A; 10 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 2.8%; Score 14; DB 3; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+04;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 185 GTGAGCTCAACCTG 198
XX DB 14 GTGAGCTCAACCTG 1
XX
XX RESULT 40
XX ABZ20677
XX ID ABZ30677 standard; DNA; 24 BP.
XX AC ABZ30677;
XX XX
XX DT 30-JAN-2003 (first entry)
XX DE Candida albicans GRACE strain PCR primer SEQ ID NO 4828.
XX XX
XX KM Fungus; yeast; tetracycline promoter; GRACE strain; biosynthesis;
XX KM signal transduction; DNA replication; cell division; growth;
XX KM proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX OS Candida albicans.
XX XX
XX PN WO200253728-A2.
XX PD 11-JUL-2002.

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XX PF 26-DEC-2001; 2001MO-US049486.
XX XX
XX PR 29-DEC-2000; 2000US-0259128P.
XX PR 20-FEB-2001; 2001US-00792024.
XX PR 22-AUG-2001; 2001US-0314050P.
XX XX
XX PA (ELIT-) ELITRA PHARM INC.
XX XX
XX PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KJ;
XX DR WPI; 2002-566694/60.
XX PS Claim 36; SEQ ID NO 4828; 167pp + Sequence Listing; English.
XX CC The invention relates to constructing (M1) a strain of diploid fungal
XX CC cells in which both alleles of a gene are modified, comprising modifying
XX CC one allele by insertion or replacement by a cassette having an
XX CC expressible selectable marker and modifying other allele by
XX CC recombination, of a promoter replacement fragment with a heterologous
XX CC promoter, so that expression of the second allele is regulated by the
XX CC promoter. (M1) is useful for constructing a strain of diploid fungal
XX CC cells in which both alleles of a gene are modified. The diploid fungal
XX CC cells having both alleles modified are useful for identifying a gene that
XX CC is essential to the survival or growth of a fungus, a gene that
XX CC contributes to the virulence and/or pathogenicity of a fungus, a gene that
XX CC that contributes to the resistance of a diploid fungus to an antifungal
XX CC agent, an antifungal agent that inhibits the growth of a diploid fungus
XX CC and for identifying a therapeutic agent for treatment of a mammalian
XX CC disease. (M1) is useful for identifying a compound which modulates the
XX CC activity of a gene product, preferably enzymatic activity, carbon
XX CC compound catabolism, biosynthetic, transporter, transcriptional,
XX CC transnational, signal transduction, DNA replication and cell division
XX CC activity. The method is useful for identifying a compound having the
XX CC ability to inhibit growth or proliferation of C. albicans cells and for
XX CC treating infection by C. albicans. The present sequence is that of a PCR
XX CC primer used in the method of the invention. Note: The sequence data for
XX CC this patent is not represented in the printed specification but is based
XX CC on sequence information supplied to Derwent by the European Patent Office
XX SO Sequence 24 BP; 4 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 2.8%; Score 14; DB 6; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+04;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 334 TTTCTGCTGCTGCA 347
XX DB 11 TTTCTGCTGCTGCA 24
XX
XX RESULT 41
XX AAL42621
XX ID AAL42621 standard; DNA; 25 BP.
XX AC AAL42621;
XX XX
XX DT 11-JUL-2002 (first entry)
XX DE Mouse inhibitor of nitric oxide synthase (INOS) antisense PCR primer.
XX XX
XX KM Mouse; PCR; primer; ss; inhibitor of nitric oxide synthase; INOS;
XX KM tumour necrosis factor TNF;
XX KM peroxisome proliferator activated receptor-delta activator;
XX KM PPAR-delta activator; inflammatory condition; shock state; septic shock;
XX KM haemorrhagic shock; traumatic shock; immune disorder;
XX KM gastrointestinal motility; post-operative ileus;
XX KM central nervous system disease; migraine; CNS trauma; schizophrenia;
XX KM sleep disorders; acute pain; musculoskeletal pain; post operative pain;

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KM cancer pain; HIV.
XX
OS Mus sp.
XX WO200228433-A2.
PN
XX 11-APR-2002.
PD
XX 02-OCT-2001; 2001WO-GB004370.
PF
XX 05-OCT-2000; 2000GB-00024362.
PR
XX (GLAXO) GLAXO GROUP LTD.
PA
XX Buchan KM;
PI
XX WPI; 2002-394317/42.
DR
XX
PT Method, useful for the treatment of diseases for which an inhibitor of NO
PT synthase and/or TNF is indicated, e.g. inflammatory conditions, comprises
PT administration of a peroxisome proliferator activated receptor-delta
PT activator.
XX
XX Example 2b; Page 22; 30pp; English.
XX
CC The invention comprises a method for treating diseases for which an
CC inhibitor of nitric oxide synthase (iNOS) and/or tumour necrosis factor
CC (TNF) is indicated. The method of the invention involves administering a
CC peroxisome proliferator activated receptor-delta (PPAR-delta) activator.
CC The method of the invention is useful in the treatment of: inflammatory
CC conditions; shock states (e.g. septic shock, haemorrhagic shock or
CC traumatic shock); immune disorders; disorders of gastrointestinal
CC motility (e.g. post-operative ileus); diseases of the central nervous
CC system (e.g. migraine, CNS trauma, schizophrenia or sleep disorders);
CC acute pain (e.g. musculoskeletal, post operative, or cancer); and HIV
CC infection. The present DNA sequence, represents a mouse inhibitor of
CC nitric oxide synthase (iNOS) PCR primer
XX
SQ Sequence 25 BP; 2 A; 6 C; 10 G; 7 T; 0 U; 0 Other;
Query Match 2.8%; Score 14; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 305 AGAGCCTCGTGCT 318
DB 8 AGAGCCTCGTGCT 21
RESULT 42
ID AAK9746 standard; DNA; 25 BP.
XX
AC AAK9746;
XX
DT 11-JUL-2002 (first entry)
XX
DE Mouse iNOS anti-sense PCR primer.
XX
KM Mouse; PCR; murine; antiinflammatory; inflammatory disease;
KM peroxisome proliferator activated receptor-delta; PPAR delta activator;
KM joint; rheumatoid arthritis; osteoarthritis; prosthetic joint failure;
KM gastrointestinal tract; ulcerative colitis; Crohn's disease; burn injury;
KM inflammatory bowel disease; adult respiratory distress syndrome; eczema;
KM cystic fibrosis; chronic obstructive pulmonary disease; dermatitis;
KM multiple sclerosis; glomerulonephritis; psoriasis; urticaria; asthma;
KM glaucoma; systemic lupus erythematosus; sepsis; atherosclerosis; hypoxic;
KM ischaemic heart disease; nitric oxide synthase inhibitor; iNOS; ss.
XX
OS Mus sp.
XX WO200228434-A2.
XX

PD 11-APR-2002.
XX
XX 01-OCT-2001; 2001WO-GB004373.
PF
XX 05-OCT-2000; 2000GB-00024361.
PR
XX (GLAXO) GLAXO GROUP LTD.
PA
XX Buchan KM;
PI
XX WPI; 2002-394318/42.
DR
XX
PT Method, useful in the treatment of inflammatory diseases or conditions,
PT e.g. arthritis, asthma, multiple sclerosis or dermatitis, comprises
PT administration of a peroxisome proliferator activated receptor-delta
PT activator.
XX
XX Example 2; Page 21; 29pp; English.
XX
CC The invention relates to a method for treating inflammatory diseases, and
CC comprises the administration of a peroxisome proliferator activated
CC receptor-delta (PPAR delta) activator. The peroxisome proliferator
CC activated receptor-delta (PPAR delta) activator can be used in the
CC treatment of inflammatory diseases or conditions, e.g. of joints
CC (rheumatoid arthritis, osteoarthritis or prosthetic joint failure),
CC gastrointestinal tract (ulcerative colitis, Crohn's disease, inflammatory
CC bowel disease), lungs (adult respiratory distress syndrome, asthma,
CC cystic fibrosis or chronic obstructive pulmonary disease), nervous tissue
CC (multiple sclerosis), pancreas, kidneys (glomerulonephritis), skin
CC (dermatitis, psoriasis, eczema, urticaria or burn injury), eyes
CC (glaucoma), multi-organ diseases (systemic lupus erythematosus or
CC sepsis), inflammation of viral or bacterial infections atherosclerosis or
CC hypoxic or ischaemic heart disease. This polynucleotide sequence
CC represents a PCR primer used in reverse transcriptase amplification of
CC nitric oxide synthase inhibitor (iNOS) mRNA. The RT-PCR was used in
CC investigating the inhibition of iNOS activity by PPAR delta activators of
CC the invention
XX
SQ Sequence 25 BP; 2 A; 6 C; 10 G; 7 T; 0 U; 0 Other;
Query Match 2.8%; Score 14; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 305 AGAGCCTCGTGCT 318
DB 8 AGAGCCTCGTGCT 21
RESULT 43
ID ACK25054/C
XX
XX ACK25054 standard; DNA; 25 BP.
XX
AC ACK25054;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 125035.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; diallelic marker; polymorphism; human;
KM cross-species comparison.
OS Homo sapiens.
XX
XX US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX

PA (AFVY-) AFFYMETRIX INC.
XX
PI Miltmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 125035; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 2 A; 9 C; 8 G; 6 T; 0 U; 0 Other;
XX
Query Match 2.8%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 53 CCGACCGAGAGCG 66
DB 16 CCGACCGAGAGCG 3
XX
RESULT 44
ACH63234
ID ACH63234 standard; DNA; 25 BP.
XX
AC ACH63234;
XX
DT 17-OCT-2003 (first entry)
XX
DE DNA target sequence #12370 useful in array for genetic analyses.
XX
KW Gene expression analysis; array; hybridization; genetic variation;
KW tag-labelled compound; gene family; in situ hybridization;
KW library screening; Southern hybridization; Northern hybridization;
KW dot-blot hybridization; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
OS US2003082596-A1.
XX
PN 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
XX

PA (MITT/) MITTMANN M.
XX
PI Miltmann M;
XX
DR WPI; 2003-576608/54.
XX
PT New probe array useful e.g. for monitoring gene expression levels, for
PT analyzing genetic variations, or for hybridizing tag-labelled compounds,
PT comprises multiple nucleic acid probes.
XX
PS Claim 1; SEQ ID NO 12370; 9pp; English.
XX
CC The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridization to a DNA library, in analyzing genetic
CC variations, and in hybridizing tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in in situ hybridizations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced. In Southern, Northern,
CC or dot-blot hybridization of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/psidbEntry.html
XX
SQ Sequence 25 BP; 4 A; 9 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 2.8%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 126 CTGCCACCTGTACT 139
DB 5 CTGCCACCTGTACT 18
XX
RESULT 45
ABV74186
ID ABV74186 standard; DNA; 26 BP.
XX
AC ABV74186;
XX
DT 27-JAN-2003 (first entry)
XX
DE Murine FIZZ1 probe mFIZZ1.probe1.
XX
KW FIZZ1; mFIZZ1; mouse; found in inflammatory zone-1; metabolic disorder;
KW obesity; anorectic; gene therapy; probe; ss.
XX
OS Mus musculus.
XX
OS WO200279383-A2.
XX
PN 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US010136.
XX
PR 30-MAR-2001; 2001US-0280571P.
XX
PR 29-MAR-2002; 2002US-00112917.
XX
PA (GENTH) GENENTECH INC.
XX

PI Adams SH;
XX
DR WPI; 2003-040672/03.
XX
PT Increasing metabolic activity in a subject for treating or preventing
PT e.g., obesity comprises increasing activity of FIZZ1 gene.
XX
PS Example; Page 78; 107pp; English.
XX
CC The present sequence is that of a probe, designated mFIZZ1.probe1, which
CC was used in an example of the invention for quantitation of FIZZ1 (found
CC in inflammatory zone-1) mRNA in mice. Results showed that FIZZ1
CC expression is markedly depressed in the white adipose tissue of obese,
CC leptin-deficient ob/ob mice. The invention provides methods of using
CC human and murine FIZZ1 polynucleotides, polypeptides and antibodies to
CC increase metabolic activity in a subject, to measure the FIZZ1 agonist or
CC antagonist activity of a compound, to screen a subject for a FIZZ1
CC related metabolic disorder, to measure the obesity-reducing activity of a
CC modality, to reduce the metabolic activity of a subject, and to alter
CC expression of FIZZ1 in the WAT of a subject. The FIZZ1 nucleic acids and
CC proteins are useful in the treatment of metabolic disorders such as
CC obesity, cachexia and increased metabolic rate caused by severe burns
XX
SQ Sequence 26 BP; 3 A; 4 C; 11 G; 8 T; 0 U; 0 Other;
XX
Query Match 2.8%; Score 14; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 474 TGACTGCTACTGGG 487
DB 9 TGACTGCTACTGGG 22
XX
RESULT 46
ID AAC63911/C
ID AAC63911 standard; DNA; 30 BP.
XX
AC AAC63911;
XX
DT 06-AUG-2003 (revised)
DT 09-FEB-2001 (first entry)
XX
DE Chromobacterium SC-YM-1 esterase mutation/PCR primer, SEQ ID NO:10.
XX
XX
XX Bacterase; enantiomer resolution; racemic mixture;
XX 2-oxobicyclo(3.1.0)hexane-6-carboxylate ester;
XX pharmaceutical synthetic intermediate; plasmid construction;
XX mutagenic oligonucleotide; PCR primer; ss.
XX
XX Chromobacterium sp.
XX
XX EP1046712-A2.
XX
XX 25-OCT-2000.
XX
XX 17-APR-2000; 2000EP-00108383.
XX
XX 16-APR-1999; 99JP-00109645.
XX
XX (SUMO) SUMITOMO CHEM CO LTD.
XX
XX Kudo J, Takashima Y, Mine S;
XX WPI; 2001-000879/01.
XX
XX
XX Resolving 2-oxobicyclo(3.1.0)hexane-6-carboxylates into enantiomer esters
XX and enantiomer acids useful as pharmaceutical intermediates by contacting
XX enzyme with 2-oxobicyclo(3.1.0)hexane-6-carboxylate.
XX
XX Example; Page 29; 35pp; English.
XX
XX The invention relates to methods of resolving enantiomers of 2-

CC oxobicyclo(3.1.0)hexane-6-carboxylate esters such that one enantiomer is
CC in an ester form and the other enantiomer is in an acid form. The methods
CC involve contacting 2-oxobicyclo(3.1.0)hexane-6-carboxylate ester with an
CC enzyme which preferentially hydrolyses one enantiomer of the ester of 2-
CC oxobicyclo(3.1.0)hexane-6-carboxylate to obtain one enantiomer as an acid
CC and the other as an ester. The methods are used to resolve 2-
CC oxobicyclo(3.1.0)hexane-6-carboxylates, which are useful as intermediates
CC for pharmaceuticals. An example of an enzyme which may be used in the
CC methods of the invention is an esterase from Chromobacterium SC-YM-1
CC (FERM BP-6703 transferred from FERM P-14009). The present sequence
CC represents an oligonucleotide used to generate a mutant esterase and
CC which was also used as a PCR primer in plasmid construction. (Updated on
CC 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 30 BP; 4 A; 9 C; 11 G; 6 T; 0 U; 0 Other;
XX
Query Match 2.8%; Score 14; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 216 CGCGCTGCTGAACA 229
DB 30 CGCGCTGCTGAACA 17
XX
RESULT 47
ID AAT34531
ID AAT34531 standard; DNA; 15 BP.
XX
AC AAT34531;
XX
DT 10-OCT-1996 (first entry)
DT XX
XX
DE Human Fas antigen 5' PCR primer.
XX
XX Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;
XX angioimmunoblastic lymphadenopathy; ALD; PCR; primer;
XX polymerase chain reaction; ss.
XX
XX Synthetic.
XX
XX WO9620206-A1.
XX
XX 04-JUL-1996.
XX
XX 22-DEC-1995; 95WO-US017083.
XX
XX 23-DEC-1994; 94US-00371263.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Mountz JD, Liu C, Zhou T, Cheng J;
XX WPI; 1996-321796/32.
XX
XX
XX Natural, soluble form of Fas antigen secreted by human cells is result of
XX alternative mRNA processing - used to diagnose Fas-associated disease,
XX e.g. systemic lupus erythematosus.
XX
XX Example 1; Page 74; 152pp; English.
XX
XX A PCR primer (AAT34531) is based on nucleotides 1-22 of human Fas antigen
XX cDNA (see also AAT34526). It was used with a primer (AAT34532)
XX complementary to nucleotides 1316-1336 of the cDNA to amplify human fas
XX mRNA from nucleotides 170-1336. The template mRNA was obtained from the
XX peripheral blood mononuclear cells of healthy subjects and from systemic
XX lupus erythematosus (SLE) and angioimmunoblastic lymphadenopathy
XX patients. PCR products were cloned into a PCR vector, expressed in E.
XX coli, and sequenced (see also AAT34533-34). 4 Distinct mRNA variants (see
XX also AAT34527-30) were identified
SQ
XX
XX Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

PF 15-MAR-2000; 2000WO-US006851.
 XX
 XX 15-MAR-2000; 2000WO-US006851.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 PA (BLUM/) BLUMENFELD A.
 PI Blumenfeld A, Gueella JF, Slangenaupt S;
 XX WPI; 2001-590074/66.
 DR
 XX
 XX Identifying an individual carrying a gene associated with familial
 PT dysautonomia, comprises detecting a polymorphism located between D9s12
 PT and D9s105 inclusive on human chromosome 9, linked to the gene associated
 PT with dysautonomia.
 XX
 XX Claim 10, Page 21; 28pp; English.
 PS
 XX The invention relates to a method for identification of an individual
 CC carrying a gene associated with familial dysautonomia. This involves
 CC detecting the presence of a polymorphism located between D9s12 and D9s105
 CC inclusive on human chromosome 9, which is linked to the gene associated
 CC with familial dysautonomia. Hence the presence of the polymorphism is
 CC indicative of the presence of the disease-associated gene. A nucleic acid
 CC sequence comprising the familial dysautonomia gene, and PCR primers
 CC encoding sequences flanking markers of the gene are useful for carrying
 CC out genetic testing of the disorder. This sequence represents a PCR
 CC primer used to detect the 8882GA marker
 XX
 SQ Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 2.6%; Score 13; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.2e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 195 CCTGGGTGACAG 207
 |||||
 2 CCTGGGTGACAG 14
 DB

RESULT 51
 ABN07848/C
 ID ABN07848 standard; DNA; 17 BP.
 XX
 AC ABN07848;
 XX
 DT 29-MAY-2002 (first entry)
 DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7840.
 XX
 XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KM skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 DT 25-MAY-2001; 2001WO-US016981.
 PF
 XX 26-MAY-2000; 2000US-0207456P.
 XX 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 XX (AEOM-) AEOMICA INC.
 PA
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 DR
 XX
 XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption/ionization, comprises human myosin-like protein hGDMLP-1.
 XX
 PS Disclosure; SEQ ID NO 7840; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 2.6%; Score 13; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.2e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 30 CACCTGCTGCTTC 42
 |||||
 16 CACCTGCTGCTTC 4
 DB

RESULT 52
 ABN07850/C
 ID ABN07850 standard; DNA; 17 BP.
 XX
 AC ABN07850;
 XX
 DT 29-MAY-2002 (first entry)
 DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7842.
 XX
 XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KM skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 DT 25-MAY-2001; 2001WO-US016981.
 PF
 XX

PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234468P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0268660P.
XX
XX (ABOM-) AEOMICA INC.
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 7842; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognize hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionization, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 5 A; 2 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 2.64; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 CACCTGCTGCTTC 42
Db 14 CACCTGCTGCTTC 2

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
PN WO200192524-A2.
PD 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234468P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0268660P.
XX
XX (ABOM-) AEOMICA INC.
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 7843; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognize hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionization, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 6 A; 2 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 2.64; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 CACCTGCTGCTTC 42
Db 13 CACCTGCTGCTTC 1

RESULT 54
ABN07847/c
ID ABN07847 standard; DNA; 17 BP.
XX
AC ABN07847;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7839.
XX
KM Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KM skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEWICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 7839; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionization, as
XX therapeutic supplement in patients having specific deficiency in hGDMLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMLP-1, in particular heart
XX and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence

SO Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 30 CACCTGCTCTTC 42
DB 17 CACCTGCTCTTC 5
XX
RESULT 55
ABN07849/c
ID ABN07849 standard; DNA; 17 BP.
XX
AC ABN07849;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7841.
XX
KM Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KM skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEWICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 7841; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionization, as

CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 2.6%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 30 CACCTGCTGCTTC 42
Db 15 CACCTGCTGCTTC 3
RESULT 56
ABZ60565/c
ID ABZ60565 standard; RNA; 17 BP.
XX
AC ABZ60565;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human K-Ras DNAzyme substrate #677.
DE
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KM anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX
XX 06-JUN-2001; 2001US-0296249P.
XX
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX Claim 58; Page 98; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention

SQ Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;
Query Match 2.6%; Score 13; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 195 CCGGGGACACAG 207
Db 15 CCGGGGACACAG 3
RESULT 57
ADB45449/c
ID ADB45449 standard; DNA; 17 BP.
XX
XX ADB45449;
XX
XX 18-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #5772.
DE
XX Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
XX
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
XX
XX 17-SEP-2002; 2002WO-IB004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX Disclosure; Page 706; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.
XX
SQ Sequence 17 BP; 9 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 2.6%; Score 13; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 371 TTCTGTACTG 383
 |||||
 DB 16 TTCTGTACTG 4

RESULT 58
 AAQ26547/c
 ID AAQ26547 standard; DNA; 18 BP.

XX AC AAQ26547;

XX DT 08-JAN-1993 (first entry)

XX DE Control probe #2 for caucosoid RING11 gene.

XX KW Immunosuppressants; immunoenhancers; treatment; diagnosis; screening;
 KW immune disorders; transporter peptides; proteasome complex;
 KW MHC class I molecules; HLA; antigen processing; antigen presentation;
 KW autoimmune disease; ankylosing spondylitis; prenatal diagnosis;
 KW polymerase chain reaction; ss.

XX OS Synthetic.

XX PN WO9211289-A1.

XX PD 09-JUL-1992.

XX PF 19-DEC-1991; 91WO-GB002278.

XX PR 19-DEC-1990; 90GB-00027520.

XX PR 16-SEP-1991; 91GB-00019711.

XX PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.

XX PI Trowdale J, Kelly AP, Glynn R, Powis SH;

XX DR WPI; 1992-250030/30.

XX PT DNA encoding RING4, RING10, RING11 AND RING12 proteins - for treatment
 PT and diagnosis of immune disorders and screening of new immunosuppressants
 PT and immuno:enhancers.

XX PS Example 2; Page 40; 101pp; English.

XX CC This probe was used together with AAQ26546-51 to analyse caucosoid
 CC controls by oligonucleotide typing, whilst investigating RING 11
 CC polymorphisms - see AAQ26544,5

XX SQ Sequence 18 BP; 4 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.6%; Score 13; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.2e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 CTGCTGACGCT 123
 |||||
 DB 13 CTGCTGACGCT 1

RESULT 59
 AAV48442
 ID AAV48442 standard; DNA; 18 BP.

XX AC AAV48442;

XX DT 15-OCT-1998 (first entry)

XX DE Transforming growth factor beta-1 antisense oligonucleotide N30.

XX KW Transforming growth factor beta-1; TGF beta-1; antisense oligonucleotide;
 KW modulate; gene expression; ss.

XX OS Synthetic.
 OS Homo sapiens.
 XX EP856579-A1.

XX PD 05-AUG-1998.

XX PF 31-JAN-1997; 97EP-00101531.

XX PR 31-JAN-1997; 97EP-00101531.

XX PA (BIOG-) BIOGNOSTIK GBS BIOMOLEKULARE DIAGNOSTIK.

XX PI Schlengersiepen K, Brysch W;

XX DR WPI; 1998-400910/35.

XX PT Preparation of antisense oligonucleotide(s) which lack long runs of
 PT consecutive guanosine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.

XX PS Example 1; Fig 3a; 286pp; English.

XX CC AAV48412-84 represent antisense oligonucleotides directed against
 CC transforming growth factor beta-1 (TGF beta-1). The oligonucleotides
 CC exemplify the invention. The specification describes oligonucleotides
 CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
 CC can each form three hydrogen bonds to cytosine; do not contain four
 CC consecutive nucleotides able to form three H-bonds; do not contain four
 CC consecutive cytosines; do not contain two sequences of three consecutive
 CC nucleotides each able to form three H-bonds to three consecutive
 CC cytosines, and the ratio between residues able to form two H-bonds each
 CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
 CC oligonucleotides are used to modulate expression of genes, particularly
 CC the genes for p53, ErbB-2, JunB, JunD, TGF-beta 1 or beta 2 to control
 CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
 CC kidney cells, osteoblasts, osteoblasts and/or keratinocytes). The
 CC oligonucleotides can also be used to analyse function of proteins (by
 CC altering their expression or activity) and therapeutically, e.g. in cases
 CC of cancer or (targeting TGF) for stimulating the immune system

XX SQ Sequence 18 BP; 1 A; 7 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 2.6%; Score 13; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.2e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 317 CTCTCCACGGGG 329
 |||||
 DB 6 CTCTCCACGGGG 18

RESULT 60
 AA277396/c
 ID AA277396 standard; DNA; 18 BP.

XX AC AA277396;

XX DT 10-SEP-2001 (first entry)

XX DE Human biallelic marker downstream amplification primer SEQ ID NO:11752.

XX KW Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.

XX OS Homo sapiens.

PN WO954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB000822.
XX
XX 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
DR
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX
XX Claim 9; Page 2736; 2745pp; English.
XX
XX AA265654 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA265579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
XX Sequence 18 BP; 6 A; 1 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 2.6%; Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 412 ACCATCATGATC 424
DB 15 ACCTATCATGATC 3
RESULT 61
AA275225/c
ID AA275225 standard; DNA; 18 BP.
XX
XX AA275225;
AC
XX
XX 10-SEP-2001 (first entry)
DT
XX
XX Human biallelic marker downstream amplification primer SEQ ID NO:9581.
DE
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO954500-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 21-APR-1999; 99WO-IB000822.
PF
XX
XX 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
PR

XX
XX (GEST), GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
DR
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX
XX Claim 8; Page 2273; 2745pp; English.
XX
XX AA265654 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
XX Sequence 18 BP; 9 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 2.6%; Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 332 TGTTCGTGCTGC 344
DB 16 TGTTCGTGCTGC 4
RESULT 62
AAF83133/c
ID AAF83133 standard; DNA; 18 BP.
XX
XX AAF83133;
AC
XX
XX 29-JUN-2001 (first entry)
DT
XX
XX Sequence of primer 17697469 SS.
DE
XX
XX Osteoprotegerin; opg; human; transcriptional regulation; bone disease;
KW arterial disease; immune function; lymph node development; T-cell;
KW B-cell; antiarthritic; immunomodulatory; antirheumatic; antinflammatory;
KW cardiant; PCR primer; ss.
XX
XX
XX Synthetic.
OS
XX
XX WO200123562-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 26-SEP-2000; 2000WO-US026497.
PF
XX
XX 27-SEP-1999; 99US-0155803P.
PR
XX
XX (ELIL) LILLY & CO ELI.
PA (MILE) MILES R R.
PA (ONYT) ONYTA J E.
PA (THIR) THIRONAVOKKARASU K.
XX
XX Chandrasekhar S, Halladay DL, Martin TJ;
PI
XX WPI; 2001-261682/29.
DR
XX

PT Isolated nucleic acid fragment comprising the transcriptional regulatory
PT region of the human osteoprotegerin (opg) gene, useful for identifying
PT compounds which are useful in the treatment of bone disease, arthritis
PT and arterial disease.
XX
XX Disclosure, Page 89, 136pp, English.
XX
XX The invention provides the transcriptional regulatory region of the human
CC osteoprotegerin (opg) gene, and fragments exhibiting human opg gene
CC transcriptional regulatory activity. The isolated opg nucleic acid
CC fragments are useful in an assay to identify an agonist or antagonist of
CC opg expression. They are also useful for the manufacture of a composition
CC for the diagnosis of a human susceptible to, predisposed to, or at
CC increased risk for developing a symptom, condition, or disease caused by
CC over- or under-expression of opg. The agonist, antagonist and modulators
CC are useful in the treatment of a disease in a human caused by abnormal
CC expression of opg. The disease is bone disease, arthritis, arterial
CC disease, abnormal immune function, abnormal lymph node development, or
CC abnormal T- or B-cell function caused by abnormal expression of opg.
CC Sequences AAF83129-136 represent PCR primers which are not related to the
CC present invention. The specification has certain pages missing and the
CC above mentioned primers are a part of pages from other patent
CC specifications
XX
XX Sequence 18 BP, 3 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.6%; Score 13; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 207 GTGCTGACGCGC 219
DB 14 GTGCTGACGCGC 2
RESULT 63
AAF83134
ID AAF83134 standard; DNA; 18 BP.
XX
XX AAF83134;
AC
XX
XX 29-JUN-2001 (first entry)
DT
XX
XX Sequence of primer 17897469 S6.
DE
XX Osteoprotegerin; opg; human; transcriptional regulation; bone disease;
XX arterial disease; immune function; lymph node development; T-cell;
XX B-cell; antiarthritic; immunomodulatory; antirheumatic; antiinflammatory;
XX cardiant; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO200123562-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 26-SEP-2000; 2000WO-US026497.
PF
XX
XX 27-SEP-1999; 99US-0155803P.
PR
XX
XX (ELIL) LILLY & CO ELI.
PA
XX (MILE/) MILES R R.
PA (ONYI/) ONYIA J E.
PA (THIR/) THIRUNAVUKKARASU K.
XX
XX
XX Chandraseekar S, Halladay DL, Martin TJ;
PI
XX
XX WPI; 2001-281682/29.
DR
XX
XX Isolated nucleic acid fragment comprising the transcriptional regulatory
PT region of the human osteoprotegerin (opg) gene, useful for identifying
PT compounds which are useful in the treatment of bone disease, arthritis
PT and arterial disease.

XX
XX Disclosure, Page 89, 136pp, English.
PS
XX
XX The invention provides the transcriptional regulatory region of the human
CC osteoprotegerin (opg) gene, and fragments exhibiting human opg gene
CC transcriptional regulatory activity. The isolated opg nucleic acid
CC fragments are useful in an assay to identify an agonist or antagonist of
CC opg expression. They are also useful for the manufacture of a composition
CC for the diagnosis of a human susceptible to, predisposed to, or at
CC increased risk for developing a symptom, condition, or disease caused by
CC over- or under-expression of opg. The agonist, antagonist and modulators
CC are useful in the treatment of a disease in a human caused by abnormal
CC expression of opg. The disease is bone disease, arthritis, arterial
CC disease, abnormal immune function, abnormal lymph node development, or
CC abnormal T- or B-cell function caused by abnormal expression of opg.
CC Sequences AAF83129-136 represent PCR primers which are not related to the
CC present invention. The specification has certain pages missing and the
CC above mentioned primers are a part of pages from other patent
CC specifications
XX
XX Sequence 18 BP, 3 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.6%; Score 13; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 207 GTGCTGACGCGC 219
DB 5 GTGCTGACGCGC 17
RESULT 64
AAS02440/C
ID AAS02440 standard; DNA; 18 BP.
XX
XX AAS02440;
AC
XX
XX 18-JUL-2001 (first entry)
DT
XX
XX Human TSRI, sequencing primer 17897469 S5.
DE
XX
XX Human; Thrombospondin repeat domain; TSRI; cancer; breast cancer;
XX rheumatoid arthritis; ocular neovascularisation; wound healing;
XX angiogenesis; immune associated disorder; gestational disorder;
XX pre-eclampsia; neuronal development; immunogen; antibody; antisense;
XX agonist; TSRI; sequencing primer; 17897469 S5; ss.
XX
XX Homo sapiens.
XX
XX WO200123561-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 27-SEP-2000; 2000WO-US026432.
PF
XX
XX 27-SEP-1999; 99US-0156217P.
PR 27-JUN-2000; 2000US-0214759P.
PR 26-SEP-2000; 2000US-00669360.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Vernet C, Tchernev VT, Boldog FL, Herrmann JL;
PI
XX
XX WPI; 2001-266157/27.
DR
XX
XX TSRI PRO (PRO comprising thrombospondin-1 repeat) domain useful to
PT identify molecules modulating TSRI activity or function, for treating
PT cancer, rheumatoid arthritis and ocular neovascularization.
XX
XX Example 1, Page 89, 116pp, English.
PS
XX
XX The sequence represents a sequencing primer used to sequence the cDNA
CC clone encoding the Human thrombospondin-1 repeat (TSRI) domain containing

CC protein, TSR1. Members of the TSR superfamily, TSRX proteins, include
CC proteins responsible for cell attachment, spreading, motility,
CC proliferation, cytoskeletal organization, wound healing and angiogenesis.
CC TSRX, TSRX polynucleotides and anti-TSRX antibodies are useful for
CC diagnosing, treating or preventing cancer, rheumatoid arthritis, ocular
CC neovascularization, wound healing, immune associated disorders and
CC gestational diseases (e.g. pre-eclampsia). TSRX and TSRX polynucleotides
CC can be used to identify members of the TSR superfamily, to screen for
CC molecules which inhibit or enhance TSRX activity or function, as targets
CC for identification of small molecules that modulate or inhibit e.g.
CC angiogenesis or neuronal development. Also TSRX antisense molecules or
CC other agonists are useful for detecting and treating breast cancer. TSRX
CC proteins can be used to screen drugs or compounds that modulate TSRX
CC activity or expression as well as to treat disorders characterized by
CC insufficient or excessive production of TSRX or production of TSRX forms
CC that have decreased or aberrant activity compared to TSRX wild-type. Anti
CC -TSRX antibodies can be used to isolate TSRXs and modulate TSRX activity.
CC Portions or fragments of TSRX cDNAs are used as polynucleotide reagents
CC and are used for tissue typing and forensic identification
CC
CC
SQ Sequence 18 BP, 3 A, 6 C, 6 G, 3 T, 0 U, 0 Other;
Query Match 2.6%; Score 13; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 207 GTGCTGTGACGCGC 219
DB 14 GTGCTGTGACGCGC 2
RESULT 65
AAS02441
ID AAS02441 standard; DNA; 18 BP.
AC AAS02441;
XX
DT 18-JUL-2001 (first entry)
XX
DE Human TSR1, sequencing primer 17897469 S6.
XX
XX Human; Thrombospondin repeat domain; TSRX; cancer; breast cancer;
KW rheumatoid arthritis; ocular neovascularization; wound healing;
KW angiogenesis; immune associated disorder; gestational disorder;
KW pre-eclampsia; neuronal development; immunogen; antibody; antisense;
KW agonist; TSR1; sequencing primer; 17897469 S6; ss.
XX
XX Homo sapiens.
OS
XX
PN WO200123561-A2.
PD
XX 05-APR-2001.
PD
XX 27-SEP-2000; 2000MO-US026432.
PF
XX 27-SEP-1999; 99US-0156217P.
PR 27-JUN-2000; 2000US-0214759P.
PR 26-SEP-2000; 2000US-00669360.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
PI Shimketa RA, Vernet C, Tchervet VT, Boldog FL, Herrmann JL;
XX WPI; 2001-266157/27.
DR
XX
XX TSRX PRO (PRO comprising thrombospondin-I repeat) domain useful to
PT identify molecules modulating TSRX activity or function, for treating
PT cancer, rheumatoid arthritis and ocular neovascularization.
XX
XX Example 1; Page 89; 116pp; English.
PS
XX The sequence represents a sequencing primer used to sequence the cDNA
CC clone encoding the Human thrombospondin-1 repeat (TSR) domain containing

CC protein, TSR1. Members of the TSR superfamily, TSRX proteins, include
CC proteins responsible for cell attachment, spreading, motility,
CC proliferation, cytoskeletal organization, wound healing and angiogenesis.
CC TSRX, TSRX polynucleotides and anti-TSRX antibodies are useful for
CC diagnosing, treating or preventing cancer, rheumatoid arthritis, ocular
CC neovascularization, wound healing, immune associated disorders and
CC gestational diseases (e.g. pre-eclampsia). TSRX and TSRX polynucleotides
CC can be used to identify members of the TSR superfamily, to screen for
CC molecules which inhibit or enhance TSRX activity or function, as targets
CC for identification of small molecules that modulate or inhibit e.g.
CC angiogenesis or neuronal development. Also TSRX antisense molecules or
CC other agonists are useful for detecting and treating breast cancer. TSRX
CC proteins can be used to screen drugs or compounds that modulate TSRX
CC activity or expression as well as to treat disorders characterized by
CC insufficient or excessive production of TSRX or production of TSRX forms
CC that have decreased or aberrant activity compared to TSRX wild-type. Anti
CC -TSRX antibodies can be used to isolate TSRXs and modulate TSRX activity.
CC Portions or fragments of TSRX cDNAs are used as polynucleotide reagents
CC and are used for tissue typing and forensic identification
CC
CC
SQ Sequence 18 BP, 3 A, 6 C, 6 G, 3 T, 0 U, 0 Other;
Query Match 2.6%; Score 13; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 207 GTGCTGTGACGCGC 219
DB 5 GTGCTGTGACGCGC 17
RESULT 66
ABA82453
ID ABA82453 standard; DNA; 18 BP.
AC ABA82453;
XX
DT 25-JUN-2002 (first entry)
XX
DE Zmax1 gene region physical map preparation STS marker #412.
XX
XX Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
KW sequence tagged site; STS; osteoporosis; osteopathia; gene therapy;
KW antisense therapy; vaccine; bone disorder; Paget's disease; adapter;
KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX
PN WO200177327-A1.
PD
XX 18-OCT-2001.
PD
XX 21-JUN-2000; 2000MO-US016951.
PF
XX 05-APR-2000; 2000US-00543771.
PR 05-APR-2000; 2000US-00544398.
PR
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX WPI; 2001-657171/75.
DR
XX
XX New high bone mass (HBM) and Zmax1 genes and proteins useful for
PT modulating bone mass for the treatment of e.g. osteoporosis.
PT
XX Disclosure, Page 36; 443pp; English.
PS
XX The present invention describes the human Zmax1 gene and the high bone
CC mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM
CC genes have osteoblastic activities. The genes can be used in gene therapy,
CC antisense therapy and in the production of vaccines. They can be used in

CC the diagnosis and treatment of bone disorders including osteoporosis,
CC Paget's disease, sclerosteosis, osteomalacia and fibrous dysplasia.
CC ABA82018 to ABA82700 and AAG6158 to AAG6193 represent sequences used in
CC the exemplification of the present invention

XX Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.6%; Score 13; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 ACAAGTGTCTGGA 215
|||||

DB 2 ACAAGTGTCTGGA 14

RESULT 67

ABK23250
ID ABK23250 standard; DNA; 18 BP.

AC ABK23250;

XX 09-APR-2002 (first entry)

DE Human Zmax1 cDNA reverse PCR primer #206.

XX Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
XX lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
XX osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
XX neurovascular condition; wound healing; gene therapy; PCR primer; probe;
XX bone development disorder; arteriosclerotic; cardiovascular;
XX osteopathic; cerebroprotective.

OS Homo sapiens.

XX MO200192891-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016946.

XX 26-MAY-2000; 2000US-00578900.

PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.

PI Canull JF, Little RD, Recker RR, Johnson ML;

DR WPI; 2002-097784/13.

PT Identifying molecules involved in lipid regulation, useful for
PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
PT identifying a molecule that binds to high bone mass gene or its
PT corresponding wild type gene.

PS Disclosure; Page 41; 409pp; English.

CC The invention relates to a method for identifying a molecule involved in
CC lipid regulation comprising identifying a molecule that binds to or
CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
CC gene, Zmax1. Compounds identified by the method are useful for treating,
CC diagnosing, preventing or screening for normal and abnormal lipid-
CC associated conditions, including arteriosclerosis, cardiovascular
CC disease, stroke, and osteoporosis. The compounds may also be used in the
CC treatment or prevention of diabetic atherosclerosis, neurovascular
CC conditions caused by plaque build-up, poor circulation due to plaque
CC build-up and associated poor wound healing. The methods may be used in
CC gene therapy, pharmaceutical development, and diagnostic assays for bone
CC development disorders. Molecules identified by comparison of Zmax1 and
CC HBM systems can be used as surrogate markers in pharmaceutical
CC development. In diagnosis of human or animal bone disease, and in the
CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers

CC and adapters of the invention

XX Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.6%; Score 13; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 ACAAGTGTCTGGA 215
|||||

DB 2 ACAAGTGTCTGGA 14

RESULT 68

ACC45833
ID ACC45833 standard; DNA; 18 BP.

AC ACC45833;

XX 02-JUN-2003 (first entry)

DE Human HBM STS marker reverse primer #206.

XX Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
XX gene therapy; bone density modulation; bone strength; trabecular number;
XX bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
XX osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.

OS Homo sapiens.

XX WO200292764-A2.

XX 21-NOV-2002.

XX 13-MAY-2002; 2002WO-US014876.

XX 11-MAY-2001; 2001US-0290071P.

XX 17-MAY-2001; 2001US-0291311P.

XX 01-FEB-2002; 2002US-0353058P.

XX 04-MAR-2002; 2002US-0361293P.

PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.

PI Bablj P, Bex FJ, Yaworsky PJ, Bodine PV;

DR WPI; 2003-129278/12.

PT New transgenic animals (e.g. mice), useful as models for studying bone
PT density modulation, developing drugs for treating or preventing bone
PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
PT reduced bone density.

PS Disclosure; Page 57; 603pp; English.

CC The invention relates to novel transgenic animals expressing the high
CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
CC an LRP5 that is modulated by an altered gene control sequence introduced
CC by homologous or non-homologous recombination. The transgenic animals are
CC for the study of bone density modulation or bone mass modulation. The
CC invention has osteopathic and cytoskeletal activity. The polynucleotides of
CC the invention may have a use in gene therapy. The transgenic animals and
CC nucleic acids are for the study of bone density modulation, where the
CC bone mass is modulated relative to non-transgenic animals of the same
CC species in more than one parameter selected from bone density, bone
CC strength, trabecular number, bone size, or bone tissue connectivity. The
CC transgenic animals, nucleic acids and methods are useful for identifying
CC molecules involved in bone development, and for developing pharmaceutical
CC compositions, which may be employed for treating or preventing bone
CC diseases, e.g., osteoporosis, osteomalacia, rickets, Paget's disease, or
CC neoplasms of the bone. The transgenic animals and nucleic acids are also
CC useful in methods for diagnosing diseases involved in bone development.

CC or characterised by reduced bone density or mass. The present sequence is
CC used in the exemplification of the invention

SO Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.6%; Score 13; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.2e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 ACAAGTCTCTGA 215

Db 2 ACAAGTCTCTGA 14

RESULT 69

ADB98531 standard; DNA; 18 BP.

AC ADB98531;

DT 04-DEC-2003 (first entry)

DE Sequence tagged site #412 used to prepare Zmax1 (LRP5) gene region map.

XX Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;

XX bone mass modulation; osteoporosis; STS; sequence tagged site; ds.

OS Homo sapiens.

PN WO200292000-A2.

PD 21-NOV-2002.

PF 13-MAY-2002; 2002MO-US014877.

PR 11-MAY-2001; 2001US-0290071P.

PR 17-MAY-2001; 2001US-0291311P.

PR 01-FEB-2002; 2002US-0353058P.

PR 04-MAR-2002; 2002US-0361293P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PA (AMHP-) WYETH.

PI Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;

XX WPI; 2003-129214/12.

PT New nucleic acid comprising a mutation in LRP5 or LRP6, useful for

PT diagnosing a HBM-like phenotype in a subject and for preparing a

PT composition for modulating bone mass and/or lipid levels in a subject

PT suffering from e.g. osteoporosis.

XX Example 2; Page 64; 629pp; English.

XX The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and

XX LRP6 mutants, which results in a HBM-like phenotype when expressed in a

XX cell. The HBM-like phenotype results in bone mass modulation and/or lipid

XX level modulation. The invention is useful for diagnosing a HBM-like

XX phenotype in a subject and for preparing a composition for modulating

XX bone mass and/or lipid levels in a subject suffering from e.g.

XX osteoporosis. The present sequence is a Sequence Tagged Site (STS)

XX CC marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene

XX region.

CC Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

QY Query Match 2.6%; Score 13; DB 10; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.2e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 ACAAGTCTCTGA 215

Db 2 ACAAGTCTCTGA 14

RESULT 70

ABZ75622 standard; DNA; 19 BP.

AC ABZ75622;

DT 15-MAY-2003 (first entry)

DE STR marker 21-32S specific PCR primer 32S forward.

XX Aneuploidy; chromosome; multiplex assay; polymerase chain reaction; PCR;

XX short tandem repeat; STR; turner syndrome; cystic fibrosis; primer; ss.

OS Homo sapiens.

PN WO200268685-A2.

PD 06-SEP-2002.

PF 26-FEB-2002; 2002MO-GB000839.

PR 26-FEB-2001; 2001GB-00004690.

PA (CYTO-) CYTOGENETIC DNA SERVICES LTD.

PI Levett LJ, Liddle S;

DR WPI; 2002-707013/76.

PT Detecting aneuploidy of a chromosome in a fetus by using a multiplex

PT polymerase chain reaction assay comprising chromosome-specific short

PT tandem repeat markers.

XX Example 1; Page 16; 30pp; English.

XX The invention relates to detecting aneuploidy of a chromosome and

XX involves using a multiplex polymerase chain reaction assay having

XX chromosome-specific short tandem repeat (STR) markers. The STR marker 21-

XX 32S (informal designation) is useful as a marker for the diagnosis of

XX aneuploidy of a chromosome, particularly trisomy 21, 13, 18 or X, or

XX Turner Syndrome. The STR marker Y-40S (informal designation) is useful as

XX a marker for the diagnosis of the sex of an individual. Marker CF508 is

XX useful for detecting the presence or absence of a genetic disease.

XX CC particularly cystic fibrosis. Sequences ABZ75621-22 represent PCR primers

XX specific for the STR marker 21-32S

SO Sequence 19 BP; 4 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.6%; Score 13; DB 6; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.2e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 CTTGGGTGACAG 207

Db 7 CTTGGGTGACAG 19

RESULT 71

ABK1325 standard; DNA; 19 BP.

AC ABK1325;

DT 05-JUN-2002 (first entry)

DE Arabidopsis Acyl coenzyme A thioesterase 4 PCR primer ACH4-LBamHI.

XX ss; PCR; ACH4; Acyl coenzyme A thioesterase; plant; transgenic;

XX lipid oxidation; regulation of Coenzyme A; fatty acid metabolism; primer;

XX ACH4-LBamHI.

```

XX Arabidopsis thaliana.
OS
XX WO200208433-A2.
XX
XX PD
XX 31-JAN-2002.
XX
XX PF
XX 19-JUL-2001; 2001MO-US022907.
XX
XX PR
XX 21-JUL-2000; 2000US-0220028P.
XX
XX PR
XX 16-JUL-2001; 2001US-00906408.
XX
XX PA
XX (TILT/) TILTON G B.
XX (SHOC/) SHOCKEY J M.
XX (BROW/) BROWSE J A.
XX
XX P1
XX Tilton GB, Shockey JM, Browse JA;
XX
XX DR
XX WPI; 2002-241573/29.
XX
XX PT
XX Novel acyl coenzyme A thioesterase gene useful for altering a phenotype
XX of a plant, making a transgenic plant and for producing variants of acyl-
XX CoA thioesterases.
XX
XX PS
XX Example 1; Page 47; 78pp; English.
XX
XX CC
XX The invention relates to an isolated acyl coenzyme A thioesterase (ACH)
XX encoding nucleic acid, encoding one of ACH1, ACH2, ACH4 or ACH5. ACH
XX enzymes have a role in lipid oxidation, regulation of Coenzyme A pools
XX and in fatty acid metabolism. Also include are a host cell transfected
XX with the nucleic acid, a transgenic plant transfected with the nucleic
XX acid (including its seed or oil) and ACH antisense molecules. The ACH
XX nucleic acid is useful for altering a phenotype of a plant and for making
XX a transgenic plant, by transfecting the plant tissue with the ACH nucleic
XX acid under conditions such that a transgenic plant is generated. The ACH
XX nucleic acid is also useful for producing variants of acyl-CoA
XX thioesterases. The present sequence is a PCR primer used to amplify
XX Arabidopsis ACH4 encoding sequences
XX
XX SQ
XX Sequence 19 BP; 5 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX
XX Query Match 2.6%; Score 13; DB 6; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 4.2e+04;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX QY
XX 250 ATCCTGAAGAATT 262
XX |||||
XX 2 ATCCTGAAGAATT 14
XX
XX DB
XX
XX RESULT 72
XX ACH66467
XX ID ACH66467 standard; DNA; 19 BP.
XX
XX AC
XX ACH66467;
XX
XX DT
XX 16-OCT-2003 (first entry)
XX
XX DE
XX Sense PCR primer used to amplify CDC37.
XX
XX KW
XX PCR, primer; ss; genomic DNA; gDNA; untranslated region; UTR;
XX DNA high-density microarray; biosite; large scale production; gDNA probe;
XX microarray; Type II primer.
XX
XX KW
XX Homo sapiens.
XX
XX OS
XX US2003073085-A1.
XX
XX PN
XX 17-APR-2003.
XX
XX PD
XX
XX PF
XX 05-OCT-2001; 2001US-00972469.
XX
XX PR
XX 05-OCT-2001; 2001US-00972469.
XX
XX

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(LATF/) LAI F.
(ZHOU/) ZHOU D.
Lai F., Zhou D;
WPI, 2003-555942/52.

Amplifying expressed genetic sequences from genomic DNA of mammalian or higher order plant species for printing on DNA microarrays, involves using the 3' untranslated region of the gene sequence.

Disclosure; Page 7; 15pp; English.

The invention discloses a method for amplifying expressed genetic sequences from genomic DNA (gDNA) from mammalian or higher order plant species. The method involves identifying a 3' untranslated region (UTR) of a gDNA sequence, designing probe, performing PCR, separating the product by size differentiation and performing a second PCR to amplify the predetermined sequence. Also claimed is a biological analysis device, comprising a substrate and an array of a set of expressed genetic sequences, located on the substrate, which are generated by the method above and a DNA high-density microarray comprising a substrate upon which are deposited an array of biosites of genomic DNA fragments having the sequence of at least one exon, and absent polyadenine and vector sequences, where the genomic DNA fragments have a sequence length of from about 75-2000 nucleotides. The method is efficient for amplifying gene sequences, enables large-scale production of gDNA sequences, generates large quantities of gDNA probes, which enables greater efficiency for printing in microarray formats, fabricates high-density DNA arrays of enhanced, widely varying genetic content and aberrations from using RNA-derived sequences by simple PCR amplifications without cloning. The method produces amplified sequences that have greater specificity and size consistency than that observed with cDNA fragments, and allows for greater signal sensitivity than oligonucleotides. The sequence presented is a Type II gene specific primer

Sequence 19 BP; 2 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.6%; Score 13; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 CTGCTTCAGCCC 48
|||||||
Dd 1 CTGCTTCAGCCC 13

RESULT 73
AD01975/c
ID AD014975 standard; RNA; 19 BP.
AC AD014975;
XX
DT 01-JUL-2004 (first entry)
DE Human PDGFR-targeted siNA lower strand SEQ ID NO:406.
KW cytosolic; vasotropic; nephrotropic; cerebroprotective;
KW treating leukaemia; solid tumors; restenosis; polycystic kidney disease;
KW bronchitis; glomerulonephritis; stroke; RNA interference;
KW short interfering nucleic acid; siNA; short interfering RNA; siRNA;
KW double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
KW expression modulation; gene therapy; drug screening; diagnosis;
KW therapeutic target identification; pharmacogenomics;
KW gene function analysis; gene mapping; human;
KW plactet derived growth factor receptor; PDGFR; ss.
OS Homo sapiens.
XX
PN WO2003072704-A2.
XX
PD 04-SEP-2003.

```
PF 05-FEB-2003; 2003WO-US003473.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0353124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Mcswiggen J, Belgelman L, Chowrira B;
PI WPI; 2003-731605/69.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of tumors, downregulates expression of the platelet-derived
PT growth factor receptor gene.
XX
XX Example 3; SEQ ID NO 406; 148bp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human platelet-derived growth factor
CC receptor (PDGFR) gene by RNA interference. The siNAs may or may not
CC comprise ribonucleotides and may be double or single stranded. They
CC further comprise sense and antisense regions, or alternatively are
CC assembled from a sense oligonucleotide and an antisense oligonucleotide.
CC Specifically, the siNAs include short interfering RNA (siRNA, double-
CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
CC can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siRNA; conjugates and/or
CC complexes of siRNA; and vectors that express siNA. The siNAs are used to
CC modulate expression of the PDGFR gene in cells, tissue explants or
CC organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
CC for the treatment of a variety of conditions. They may be used for
CC treating leukaemia and solid tumours, restenosis, polycystic kidney
CC disease, bronchiolitis, glomerulonephritis and stroke. The siNAs are also
CC useful for drug screening, diagnosis, therapeutic target identification
CC and validation, genetic engineering, pharmacogenomics, studying gene
CC function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC The present sequence represents the lower strand of a human PDGFR-
CC targeted double-stranded siNA, which is identical to the PDGFR transcript
CC target sequence.
XX
XX Sequence 19 BP; 5 A; 6 C; 5 G; 0 T; 3 U; 0 Other;
SQ
Query Match 2.6%; Score 13; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 108 GGCTGCGCTGCAG 120
Db 15 GGCTGCGCTGCAG 3
RESULT 74
AD014664
ID AD014664 standard; RNA; 19 BP.
XX
XX AD014664;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human PDGFR-targeted siNA upper strand SEQ ID NO:95.
DB
XX
XX cytosstatic; vasotropic; nephroretropic; cerebroprotective;
KM treating leukaemia; solid tumors; restenosis; polycystic kidney disease;
KM bronchiolitis; glomerulonephritis; stroke; RNA interference;
KM short interfering nucleic acid; siNA; short interfering RNA; siRNA;
KM double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
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```
KM expression modulation; gene therapy; drug screening; diagnosis;
KM therapeutic target identification; pharmacogenomics;
KM gene function analysis; gene mapping; human;
KM platelet derived growth factor receptor; PDGFR; ss.
XX
XX Homo sapiens.
OS
XX W02003072704-A2.
PN
XX
XX 04-SEP-2003.
PD
XX
XX 05-FEB-2003; 2003WO-US003473.
PE
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0353124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Mcswiggen J, Belgelman L, Chowrira B;
PI WPI; 2003-731605/69.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of tumors, downregulates expression of the platelet-derived
PT growth factor receptor gene.
XX
XX Example 3; SEQ ID NO 95; 148bp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human platelet-derived growth factor
CC receptor (PDGFR) gene by RNA interference. The siNAs may or may not
CC comprise ribonucleotides and may be double or single stranded. They
CC further comprise sense and antisense regions, or alternatively are
CC assembled from a sense oligonucleotide and an antisense oligonucleotide.
CC Specifically, the siNAs include short interfering RNA (siRNA, double-
CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
CC can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siRNA; conjugates and/or
CC complexes of siRNA; and vectors that express siNA. The siNAs are used to
CC modulate expression of the PDGFR gene in cells, tissue explants or
CC organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
CC for the treatment of a variety of conditions. They may be used for
CC treating leukaemia and solid tumours, restenosis, polycystic kidney
CC disease, bronchiolitis, glomerulonephritis and stroke. The siNAs are also
CC useful for drug screening, diagnosis, therapeutic target identification
CC and validation, genetic engineering, pharmacogenomics, studying gene
CC function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC The present sequence represents the upper strand of a human PDGFR-
CC targeted double-stranded siNA, which is identical to the PDGFR transcript
CC target sequence.
XX
XX Sequence 19 BP; 3 A; 5 C; 6 G; 0 T; 5 U; 0 Other;
SQ
Query Match 2.6%; Score 13; DB 11; Length 19;
Best Local Similarity 76.9%; Pred. No. 4.2e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 108 GGCTGCGCTGCAG 120
Db 5 GGCTGCGCTGCAG 17
RESULT 75
ADM82819/c
ID ADM82819 standard; DNA; 19 BP.
XX
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AC ADM82819;
 XX 03-JUN-2004 (first entry)-
 XX
 XX
 DE PKG RT-PCR primer, SEQ ID NO:17.
 XX
 XX Schizophrenia; attention-deficit-hyperactivity disorder; ADHD;
 KW bipolar disorder; frontal lobe; hypothalamus; differential expression;
 KW stress response; hypothalamo-pituitary-adrenal axis; HPA axis disruption;
 KW screening; diagnosis; monitoring; prevention; drug screening;
 KW transgenic mouse; animal model; nootropic; tranquiliser; neuroleptic;
 KW expression analysis; PK; real-time PCR; reverse transcription-PCR;
 KW RT-PCR; primer; ss.
 XX
 XX Unidentified.
 XX
 XX NO2004007762-A2.
 XX
 XX 22-JAN-2004.
 XX
 XX 10-JUL-2003; 2003WO-EP007491.
 XX
 XX 11-JUL-2002; 2002US-0395088P.
 XX 22-MAY-2003; 2003US-0472489P.
 XX
 XX (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS PHARMA GMBH.
 XX (UYMA-) UNIV MARYLAND BALTIMORE.
 XX
 XX Bilbe G, Kinnunen A, Koenig JI;
 XX WPI; 2004-122979/12.
 DR
 XX
 XX Use of known genes associated with schizophrenia, attention-deficit-
 PT hyperactivity disorder and bipolar disorder for screening, monitoring
 PT progression or treating schizophrenia, attention-deficit-hyperactivity
 PT disorder or bipolar disorder.
 PT
 XX
 XX Example 3; SEQ ID NO 17; 72bp; English.
 PS
 XX
 XX The invention relates to the identification of genes that are
 CC differentially expressed in the frontal lobe and/or hypothalamus of a
 CC patient with schizophrenia, attention-deficit-hyperactivity disorder
 CC (ADHD) and bipolar disorder, and to the identification of genes
 CC associated with a normal or abnormal stress response related to
 CC disruption of the hypothalamo-pituitary-adrenal (HPA) axis. These genes,
 CC although known, have not previously been associated with schizophrenia,
 CC attention-deficit-hyperactivity disorder (ADHD), bipolar disorder and
 CC stress responses (which can precipitate exacerbate the above conditions).
 CC The genes can be used for screening an individual with schizophrenia,
 CC ADHD and/or bipolar disorder, for monitoring the progression or treatment
 CC of these conditions, for identifying agents useful in the treatment of
 CC schizophrenia, ADHD and/or bipolar disorder, and for treating or
 CC preventing schizophrenia, ADHD and/or bipolar disorder. The invention
 CC also relates to a transgenic mouse model of schizophrenia, ADHD and/or
 CC bipolar disorder in which an endogenous orthologue of a human gene
 CC associated with schizophrenia, ADHD and/or bipolar disorder is disrupted.
 CC 7 genes known to be associated with schizophrenia, ADHD and/or bipolar
 CC disorder are excluded from many aspects of the invention; these are Vamp2
 CC (synaptobrevin II), glutamic acid decarboxylase (GAD65), GTP-binding
 CC protein (G-alpha-0), acidic calcium-independent phospholipase A2
 CC (aiPLA2), synaptotagmin (syn11), NCAM and synapsin 2. The methods and
 CC agents of the invention are useful in diagnosing, screening, treating,
 CC monitoring and/or preventing schizophrenia, ADHD and/or bipolar disorder.
 CC Sequences ADM82803-ADM82829 represent reverse transcription-PCR (RT-PCR)
 CC primers and TaqMan probes used in real-time PCR of the following
 CC schizophrenia, ADHD and/or bipolar disorder-associated genes: acidic
 CC calcium-independent phospholipase A2 (aiPLA2; GenBank AF014009), aldolase
 CC A (GenBank U20643), densin 180 (GenBank U66707), GABA-B receptor 1c
 CC (GenBank AB016160), grina; PK; rbln (GenBank U77931); synapsin 2
 CC (GenBank A1145494); and Vamp2 (synaptobrevin II; GenBank A1101103).
 XX
 XX Sequence 19 BP; 2 A; 4 C; 8 G; 5 T; 0 U; 0 Other;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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5	15	3.0	25 15 US-10-261-517-12	Sequence 12, Appl
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ALIGNMENTS

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Sequence 21, Application US/10422523

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; Publication No. US20040002103A1
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; TITLE OF INVENTION: SYNTHETIC LIGATION REASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIV-146-15A US
; CURRENT APPLICATION NUMBER: 2003-04-24
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
US-10-422-523-21
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QY 296 TGTTCACCGAGGCC 310
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RESULT 2
US-10-116-949-37
Sequence 37, Application US/10116949
Publication No. US20030044911A1

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; GENERAL INFORMATION:
; APPLICANT: Letman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Bojing
; APPLICANT: Duh, Fun-Wel
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/10/116,949
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/470,443
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/114,359
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-116-949-37
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DB 6 GTTACTGCTGTGACC 20

RESULT 3
US-10-215-112-6487
Sequence 6487, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:


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; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215.112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6487
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-6487

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DB 8 CGGCTGCTACGGCTG 22

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; Sequence 20798, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098.263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 20798
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-20798

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DB 4 TGATTACGAGTCAC 18

RESULT 5
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; Sequence 12, Application US/10261517
; Publication No. US20030143583A1
; GENERAL INFORMATION:
; APPLICANT: Climent-Johneson, Isabel
; APPLICANT: Dahlman-Wright, Karin
; APPLICANT: Lake, Stefan
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: NOVEL RESPONSE ELEMENT
; FILE REFERENCE: 13425-032001
; CURRENT APPLICATION NUMBER: US/10/261.517
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/09/645,629
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/151,867
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: SE 9903009-0
; PRIOR FILING DATE: 1999-08-26
```

```

; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-261-517-12

Query Match
Best Local Similarity 100.0%; Score 15; DB 15; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 AAAACATGTGACCG 304
DB 21 AAAACATGTGACCG 7

RESULT 6
US-10-440-850-367
; Sequence 367, Application US/10440850
; Publication No. US20030207837A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Reve
; TITLE OF INVENTION: Immune Responses
; FILE REFERENCE: 250/130 (MBH00-900-A)
; CURRENT APPLICATION NUMBER: US/10/440,850
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/650,012
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 08/585,684
; PRIOR FILING DATE: 1996-01-12
; PRIOR APPLICATION NUMBER: US 60/000,951
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: US 09/038,073
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 2285
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 367
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-440-850-367

Query Match
Best Local Similarity 78.6%; Score 14; DB 15; Length 15;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 257 AGAATACCTGGCA 270
DB 2 AGAATACCTGGCA 15

RESULT 7
US-10-712-672-1858/c
; Sequence 1858, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowitra, Bharat
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
```

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; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1858
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-1858
```

```

Query Match          2.8%; Score 14; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      386 GTGGCCTGGCGCAGC 359
      |||||
DB      14 GTGGCCTGGCGCAGC 1
```

RESULT 8

```

US-09-891-517-99/c
; Sequence 99, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: TORIMURA, MASAKI
; APPLICANT: KURATA, SHINYA
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOXOZU
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
; FILE OF INVENTION: METHOD
; FILE REFERENCE: 210352US-1994-163-0-X
; CURRENT APPLICATION NUMBER: US/09/891,517
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: JP2000-193133
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: JP2000-226115
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP2000-292483
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-891-517-99
```

```

Query Match          2.8%; Score 14; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      304 GAGAGCCTGCTGGC 317
      |||||
DB      18 GAGAGCCTGCTGGC 5
```

RESULT 9

```

US-10-751-736-36439/c
; Sequence 36439, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
```

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36439
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-751-736-36439
```

```

Query Match          2.8%; Score 14; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      128 GCCACCTGACTGG 141
      |||||
DB      18 GCCACCTGACTGG 5
```

```

RESULT 10
US-10-751-736-36440/c
; Sequence 36440, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36440
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-36440
```

```

Query Match          2.8%; Score 14; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      128 GCCACCTGACTGG 141
      |||||
DB      16 GCCACCTGACTGG 3
```

```

RESULT 11
US-10-751-736-36640/c
; Sequence 36640, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
```

NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36640
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-751-736-36640

Query Match 2.8%; Score 14; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 GCCACCTGTACTGG 141
|||||
Db 19 GCCACCTGTACTGG 6

RESULT 12
US-10-751-736-36641/c
Sequence 36641, Application US/10751736
Publication No. US20040265230A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36641
LENGTH: 21
TYPE: RNA
ORGANISM: RNA1
US-10-751-736-36641

Query Match 2.8%; Score 14; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 GCCACCTGTACTGG 141
|||||
Db 17 GCCACCTGTACTGG 4

RESULT 13
US-10-751-736-47110
Sequence 47110, Application US/10751736
Publication No. US20040265230A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 47110
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-751-736-47110

Query Match 2.8%; Score 14; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 GCAGCTTCGGTAG 408
|||||
Db 6 GCAGCTTCGGTAG 19

RESULT 14
US-10-751-736-47111
Sequence 47111, Application US/10751736
Publication No. US20040265230A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 47111
LENGTH: 21
TYPE: RNA
ORGANISM: RNA1
US-10-751-736-47111

Query Match 2.8%; Score 14; DB 18; Length 21;
Best Local Similarity 78.6%; Pred. No. 6.1e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 395 GCAGCTTCGGTAG 408
|||||
Db 4 GCAGCTTCGGTAG 17

RESULT 15
US-10-751-736-47113
Sequence 47113, Application US/10751736
Publication No. US20040265230A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 47113
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-751-736-47113

Query Match 2.8%; Score 14; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 GCAGCTTCGGTAG 408
|||||

Db 3 GCAGCTTCGCTGAG 16

RESULT 16

US-10-751-736-47114
; Sequence 47114, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeich
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47114
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNA1
US-10-751-736-47114

Query Match 2.8%; Score 14; DB 18; Length 21;
Best Local Similarity 78.6%; Pred. No. 6.1e+03;

Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 395 GCAGCTTCGCTGAG 408
|||||:|||||

Db 1 GCAGCTTCGCTGAG 14

RESULT 17

US-10-142-662-1
; Sequence 1, Application US/10142662
; Publication No. US20030211462A1
; GENERAL INFORMATION:
; APPLICANT: Payan, Donald
; APPLICANT: Wu, Xian
; APPLICANT: Shen, Mary
; APPLICANT: Yu, Simon
; TITLE OF INVENTION: DIRECTIONALLY CLONED RANDOM CDNA EXPRESSION VECTOR LIBRARIES,
; FILE REFERENCE: A-71241/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/142,662
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-142-662-1

Query Match 2.8%; Score 14; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 GCCAGTGGCCGTAA 463
|||||:|||||

Db 9 GCCAGTGGCCGTAA 22

RESULT 18

US-10-142-662-3
; Sequence 3, Application US/10142662
; Publication No. US20030211462A1

; GENERAL INFORMATION:
; APPLICANT: Payan, Donald
; APPLICANT: Wu, Xian
; APPLICANT: Shen, Mary
; APPLICANT: Yu, Simon
; TITLE OF INVENTION: DIRECTIONALLY CLONED RANDOM CDNA EXPRESSION VECTOR LIBRARIES,
; FILE REFERENCE: A-71241/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/142,662
; CURRENT FILING DATE: 2002-12-10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-142-662-3

Query Match 2.8%; Score 14; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 GCCAGTGGCCGTAA 463
|||||:|||||

Db 9 GCCAGTGGCCGTAA 22

RESULT 19

US-10-325-694-19/C
; Sequence 19, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KOPER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 24
; TYPE: DNA
; ORGANISM: HUMAN
US-10-325-694-19

Query Match 2.8%; Score 14; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 GTGAGCTCAACCTG 198
|||||:|||||

Db 14 GTGAGCTCAACCTG 1

RESULT 20

US-10-032-585-4828
; Sequence 4828, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4828
LENGTH: 24
TYPE: DNA
ORGANISM: Candida albicans
US-10-032-585-4828

Query Match 2.8%; Score 14; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 TTTCGTCTGTCTGA 347
|||||
Db 11 TTTCGTCTGTCTGA 24

RESULT 21
US-10-215-112-12370
Sequence 12370, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
FILE REFERENCE: Test3
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12370
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12370

Query Match 2.8%; Score 14; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 CTGCACCTGTACT 139
|||||
Db 5 CTGCACCTGTACT 18

RESULT 22
US-10-098-263B-125035/C
Sequence 125035, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 125035
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-125035

Query Match 2.8%; Score 14; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 CCGACCGAGAGCG 66
|||||

Db 16 CCGACCGAGAGCG 3

RESULT 23
US-10-775-169-1155
Sequence 1155, Application US/10775169
Publication No. US20040175743A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Butczynski, Michael
APPLICANT: Twine, Natalie
APPLICANT: Dorne, Andrew
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AM101080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1155
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-10-775-169-1155

Query Match 2.8%; Score 14; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 CCTCAGCAGTGTGC 107
|||||
Db 9 CCTCAGCAGTGTGC 22

RESULT 24
US-10-775-169-1156
Sequence 1156, Application US/10775169
Publication No. US20040175743A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Butczynski, Michael
APPLICANT: Twine, Natalie
APPLICANT: Dorne, Andrew
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AM101080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1156
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-10-775-169-1156

Query Match 2.8%; Score 14; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 CCTCAGCAGTGTGC 107
|||||
Db 3 CCTCAGCAGTGTGC 16

RESULT 25
US-10-112-917-6
Sequence 6, Application US/10112917
Publication No. US20030104351A1
GENERAL INFORMATION:
APPLICANT: Adams, Sean H
TITLE OF INVENTION: RIZZI FOR METABOLISM REGULATION
FILE REFERENCE: 9800080-0002

;; CURRENT APPLICATION NUMBER: US/10/112,917
;; CURRENT FILING DATE: 2002-08-28
;; PRIOR APPLICATION NUMBER: 60/280,571
;; PRIOR FILING DATE: 2001-03-30
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 6
;; LENGTH: 26
;; TYPE: DNA
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: oligonucleotide probe
US-10-112-917-6

Query Match 2.8%; Score 14; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 TGAAGTCTACTGG 487
Db 9 TGAAGTCTACTGG 22

RESULT 26
US-10-142-662-5/c
; Sequence 5, Application US/10142662
; Publication No. US20030211462A1
; GENERAL INFORMATION:
; APPLICANT: Payan, Donald
; APPLICANT: Wu, Xian
; APPLICANT: Shen, Mary
; APPLICANT: Yu, Simon
; TITLE OF INVENTION: DIRECTIONALLY CLONED RANDOM CDNA EXPRESSION VECTOR LIBRARIES,
; FILE REFERENCE: A-71241/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/142,662
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-142-662-5

Query Match 2.8%; Score 14; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 GCCAGTGGCCGTAA 463
Db 19 GCCAGTGGCCGTAA 6

RESULT 27
US-09-866-108-7839/c
; Sequence 7839, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456

;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 60/266,860
;; PRIOR FILING DATE: 2001-02-05
;; NUMBER OF SEQ ID NOS: 15752
;; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7839
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7839

Query Match 2.6%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCTTC 42
Db 17 CACCTGCTGCTTC 5

RESULT 28
US-09-866-108-7840/c
; Sequence 7840, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7840
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7840
```

```
Query Match 2.6%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 30 CACCTGCTGCTTC 42
Db 16 CACCTGCTGCTTC 4
```

RESULT 29

```
US-09-866-108-7841/c
; Sequence 7841, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7841
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7841
```

```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7841
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7841
```

```
Query Match 2.6%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 30 CACCTGCTGCTTC 42
Db 15 CACCTGCTGCTTC 3
```

RESULT 30

```
US-09-866-108-7842/c
; Sequence 7842, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7842
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7842
```

```

; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 7842
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7842

Query Match      2.6%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      30 CACCTGCTGCTTC 42
Db      14 CACCTGCTGCTTC 2

RESULT 31
US-09-866-108-7843/C
; Sequence 7843, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: UT, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 7843
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7843

Query Match      2.6%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      30 CACCTGCTGCTTC 42
Db      13 CACCTGCTGCTTC 1

RESULT 32
US-10-238-700-677/C
; Sequence 677, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSwigen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MHE01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 677
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-677

Query Match      2.6%; Score 13; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      195 CCTGGGTGACAAG 207
Db      15 CCTGGGTGACAAG 3

RESULT 33
US-10-723-361-7839/C
; Sequence 7839, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: UT, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
```


D_b 16 CACCTGCTGCTTC 4

PRIOR FILING DATE: 2001-05-25

```
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7842
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7842
```

```
Query Match      2.6%; Score 13; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      30 CACCTGCTGCTTC 42
          |||||
Db       14 CACCTGCTGCTTC 2
```

```
RESULT 37
US-10-723-361-7843/c
; Sequence 7843, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: UT, Yongsang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MTOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
```

```
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7843
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7843
```

```
Query Match      2.6%; Score 13; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      30 CACCTGCTGCTTC 42
          |||||
Db       13 CACCTGCTGCTTC 1
```

```
RESULT 38
US-10-349-143-9581/c
; Sequence 9581, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9581
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-5860 for SEQ 1716, in complem
US-10-349-143-9581
```

```
Query Match      2.6%; Score 13; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      332 TGTTCCTGCTGCTC 344
          |||||
Db       16 TGTTCCTGCTGCTC 4
```

```
RESULT 39
US-10-349-143-11752/c
; Sequence 11752, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
```

```
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO: 11752
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-5075 for SEQ 3887, in compleme
US-10-349-143-11752

Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 412 ACCTATCAGTATC 424
DB 15 ACCTATCAGTATC 3

RESULT 40
US-10-731-739-478
; Sequence 478, Application US/10731739
; Publication No. US20040176582A1
; GENERAL INFORMATION:
; APPLICANT: Canull, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/10/731,739
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/09/544,398B
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-731-739-478

Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 203 ACAAGTGTCTGGA 215
DB 2 ACAAGTGTCTGGA 14

RESULT 41
US-10-477-238A-478
; Sequence 478, Application US/10477238A
; Publication No. US20040221326A1
; GENERAL INFORMATION:
; APPLICANT: Babij, Philip
; APPLICANT: Yaworsky, Paul
; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-212
; CURRENT APPLICATION NUMBER: US/10/477,238A
```

```
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-238A-478

Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 203 ACAAGTGTCTGGA 215
DB 2 ACAAGTGTCTGGA 14

RESULT 42
US-10-680-287A-478
; Sequence 478, Application US/10680287A
; Publication No. US20040244069A1
; GENERAL INFORMATION:
; APPLICANT: Babij, Philip
; APPLICANT: Yaworsky, Paul
; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-179
; CURRENT APPLICATION NUMBER: US/10/680,287A
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: PCT/US02/14876
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-680-287A-478

Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 203 ACAAGTGTCTGGA 215
DB 2 ACAAGTGTCTGGA 14

RESULT 43
US-09-906-408A-37
; Sequence 37, Application US/09906408A
; Publication No. US20030028915A1
; GENERAL INFORMATION:
; APPLICANT: Tilton, Gregory
; APPLICANT: Shockey, Jay
```

APPLICANT: Browne, John
TITLE OF INVENTION: ACYL Coenzyme A Thioesterases
FILE REFERENCE: DOW-04678
CURRENT APPLICATION NUMBER: US/09/906,408A
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/220,028
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
SEQ ID NO 37
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-906-408A-37

Query Match 2.6%; Score 13; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 ATCTGAAGATT 262
DB 2 ATCTGAAGATT 14

RESULT 44
US-09-972-469-61
Sequence 61, Application US/09972469
Publication No. US2003007085A1
GENERAL INFORMATION:
APPLICANT: Lai, Fang
APPLICANT: Zhou, Daxing
TITLE OF INVENTION: AMPLIFYING EXPRESSED SEQUENCES FROM GENOMIC DNA OF HIGHER-ORDER
FILE REFERENCE: SF01-290
CURRENT APPLICATION NUMBER: US/09/972,469
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn version 3.1
SEQ ID NO 61
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-09-972-469-61

Query Match 2.6%; Score 13; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 CTGCTTCAGCCC 48
DB 1 CTGCTTCAGCCC 13

RESULT 45
US-10-224-005-101/c
Sequence 101, Application US/10224005
Publication No. US20030143732A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwigen, James
APPLICANT: Fosnaugh, Kathy
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Adenosine A1 Receptor (A1
FILE REFERENCE: 900/041 (MEHB01-1110-A)
CURRENT APPLICATION NUMBER: US/10/224,005
CURRENT FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: US 60/315,315
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 347
SOFTWARE: PatentIn version 3.0
SEQ ID NO 101

LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-224-005-101

Query Match 2.6%; Score 13; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 CTGGGGCTGCACC 150
DB 17 CTGGGGCTGCACC 5

RESULT 46
US-10-224-005-262
Sequence 262, Application US/10224005
Publication No. US20030143732A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwigen, James
APPLICANT: Fosnaugh, Kathy
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Adenosine A1 Receptor (A1
FILE REFERENCE: 900/041 (MEHB01-1110-A)
CURRENT APPLICATION NUMBER: US/10/224,005
CURRENT FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: US 60/315,315
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 347
SOFTWARE: PatentIn version 3.0
SEQ ID NO 262
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-224-005-262

Query Match 2.6%; Score 13; DB 15; Length 19;
Best Local Similarity 84.6%; Pred. No. 2.2e+04;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 138 CTGGGGCTGCACC 150
DB 3 CTGGGGCTGCACC 15

RESULT 47
US-10-356-625-100
Sequence 100, Application US/10356625
Publication No. US20030186290A1
GENERAL INFORMATION:
APPLICANT: Tournier-Lasserre, Elisabeth
APPLICANT: Joutel, Anne
APPLICANT: Bousset, Marie-Germaine
APPLICANT: Bach, Jean-Francois
TITLE OF INVENTION: GENE INVOLVED IN CADASIL, METHOD OF DIAGNOSIS AND
FILE REFERENCE: 03715, 0048-00000
CURRENT APPLICATION NUMBER: US/10/356,625
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: US/09/230,652
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: FR 96 09733
PRIOR FILING DATE: 1996-08-01
PRIOR APPLICATION NUMBER: FR 97 04680
PRIOR FILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: PCT/FR97/01433
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 163

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 100
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-356-625-100

Query Match 2.6%; Score 13; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 TGCTTCGACCCA 49
|||
DB 8 TGCTTCGACCCA 20

RESULT 48

US-10-160-787-20/c
Sequence 20, Application US/10160787
Publication No. US20030225256A1
GENERAL INFORMATION:
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 2 EXPRESSION
FILE REFERENCE: PRTS-0204
CURRENT APPLICATION NUMBER: US/10/160,787
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 20
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-160-787-20

Query Match 2.6%; Score 13; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 294 CATGTTGACCGAG 306
|||
DB 18 CATGTTGACCGAG 6

RESULT 49

US-10-160-787-97
Sequence 97, Application US/10160787
Publication No. US20030225256A1
GENERAL INFORMATION:
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 2 EXPRESSION
FILE REFERENCE: PRTS-0204
CURRENT APPLICATION NUMBER: US/10/160,787
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 97
LENGTH: 20
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
US-10-160-787-97

Query Match 2.6%; Score 13; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 294 CATGTTGACCGAG 306
|||
DB 3 CATGTTGACCGAG 15

RESULT 50

US-10-159-856-37/c
Sequence 37, Application US/10159856
Publication No. US20030228689A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freiler
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRESSION
FILE REFERENCE: PRTS-0365
CURRENT APPLICATION NUMBER: US/10/159,856
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 37
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-159-856-37

Query Match 2.6%; Score 13; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 381 CTGCTGTGCGCTG 393
|||
DB 18 CTGCTGTGCGCTG 6

RESULT 51

US-10-318-389-23
Sequence 23, Application US/10318389
Publication No. US20040121328A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF PHOSPHODIESTERASE 8A EXPRESSION
FILE REFERENCE: PRTS-0062
CURRENT APPLICATION NUMBER: US/10/318,389
CURRENT FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 23
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-318-389-23

Query Match 2.6%; Score 13; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 313 GTGGCTCTCCAGC 325
|||
DB 7 GTGGCTCTCCAGC 19

RESULT 52

US-10-318-389-94/c
Sequence 94, Application US/10318389
Publication No. US20040121328A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF PHOSPHODIESTERASE 8A EXPRESSION
FILE REFERENCE: PRTS-0062
CURRENT APPLICATION NUMBER: US/10/318,389
CURRENT FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 94
LENGTH: 20
TYPE: DNA

ORGANISM: H. sapiens
FEATURE:
US-10-318-389-94

Query Match 2.6%; Score 13; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 GTGGCTCTCCAGC 325
DB 14 GTGGCTCTCCAGC 2

RESULT 53
US-10-184-085A-763/c
; Sequence 763, Application US/10184085A
; Publication No. US20030155950A1
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Minna, John D.
; APPLICANT: Luebke, Kevin, J.
; APPLICANT: Balog, Robert P.
; TITLE OF INVENTION: Identification of Chemically Modified Polymers
; FILE REFERENCE: 11929-1035
; CURRENT APPLICATION NUMBER: US/10/184,085A
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/301,370
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 1291
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 763
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-184-085A-763

Query Match 2.6%; Score 13; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 GCTTCCTGAGCT 410
DB 15 GCTTCCTGAGCT 3

RESULT 54
US-10-751-736-3929
; Sequence 3929, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3929
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI
US-10-751-736-3929

Query Match 2.6%; Score 13; DB 18; Length 21;
Best Local Similarity 69.2%; Pred. No. 2.2e+04;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 380 ACTGCTGTGACCT 392
DB 8 ACUGCUGGACCT 20

RESULT 55
US-10-751-736-11683
; Sequence 11683, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11683
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-11683

Query Match 2.6%; Score 13; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCTTC 42
DB 7 CACCTGCTGCTTC 19

RESULT 56
US-10-751-736-11684
; Sequence 11684, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11684
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI
US-10-751-736-11684

Query Match 2.6%; Score 13; DB 18; Length 21;
Best Local Similarity 69.2%; Pred. No. 2.2e+04;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCTTC 42
DB 5 CACCTGCTGCTTC 17

RESULT 57
US-10-751-736-11686

```
; Sequence 11686, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11686
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-11686

Query Match      2.6%; Score 13; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      30 CACCTGCTGCTTC 42
Db      4 CACCTGCTGCTTC 16

RESULT 58
US-10-751-736-11687
; Sequence 11687, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11687
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNA1
US-10-751-736-11687

Query Match      2.6%; Score 13; DB 18; Length 21;
Best Local Similarity 69.2%; Pred. No. 2.2e+04;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy      30 CACCTGCTGCTTC 42
Db      2 CACCTGCTGCTTC 14

RESULT 59
US-10-751-736-36637/c
; Sequence 36637, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
```

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36637
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-36637

Query Match      2.6%; Score 13; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      129 CCACCTGACTGG 141
Db      21 CCACCTGACTGG 9

RESULT 60
US-10-751-736-36638/c
; Sequence 36638, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36638
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNA1
US-10-751-736-36638

Query Match      2.6%; Score 13; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      129 CCACCTGACTGG 141
Db      19 CCACCTGACTGG 7

RESULT 61
US-10-751-736-36643/c
; Sequence 36643, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
```

NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36643
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-751-736-36643

Query Match 2.6%; Score 13; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 GCCACCTGTACTG 140
DB 13 GCCACCTGTACTG 1

RESULT 62
US-10-751-736-49746
Sequence 49746, Application US/10751736
Publication No. US20040265230A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 49746
LENGTH: 21
TYPE: RNA
ORGANISM: RNA1
US-10-751-736-49746

Query Match 2.6%; Score 13; DB 18; Length 21;
Best Local Similarity 61.5%; Pred. No. 2.2e+04;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 437 CTGCTCCGAGTT 449
DB 8 CUGCUCCGAGU 20

RESULT 63
US-10-751-736-49795/C
Sequence 49795, Application US/10751736
Publication No. US20040265230A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 49795
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-751-736-49795

Query Match 2.6%; Score 13; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 TGCACCTGTGCT 40
DB 18 TGCACCTGTGCT 6

RESULT 64
US-10-751-736-49796/C
Sequence 49796, Application US/10751736
Publication No. US20040265230A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 49796
LENGTH: 21
TYPE: RNA
ORGANISM: RNA1
US-10-751-736-49796

Query Match 2.6%; Score 13; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 TGCACCTGTGCT 40
DB 16 TGCACCTGTGCT 4

RESULT 65
US-10-751-736-49798/C
Sequence 49798, Application US/10751736
Publication No. US20040265230A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 49798
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-751-736-49798

Query Match 2.6%; Score 13; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 TGCACCTGTGCT 40
DB 16 TGCACCTGTGCT 4

Db 14 TGCACTGTCTGCT 2

RESULT 66

US-10-203-939-46
; Sequence 46, Application US/10203939
; Publication No. US20030172396A1
; GENERAL INFORMATION:
; APPLICANT: Bar Ilan University
; TITLE OF INVENTION: Nucleic Acid Sequences and Different Uses Thereof
; FILE REFERENCE: BAR ILAN UNIV. (Chem)
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 134580
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Melon P1124111F
US-10-203-939-46

Query Match 2.6%; Score 13; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 225 GACACACACAGC 237

Db 5 GACACACACAGC 17

RESULT 67

US-10-236-392-297
; Sequence 297, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Scacie J
; APPLICANT: Caterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Larochele, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Miller, Teabelle
; APPLICANT: Padigarau, Muralihara
; APPLICANT: Paturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Raetelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 2102-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30

; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 297
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-236-392-297

Query Match 2.6%; Score 13; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 413 CCTATCATGTCG 425

Db 6 CCTATCATGTCG 18

RESULT 68

US-10-806-782-5
; Sequence 5, Application US/10806782
; Publication No. US20040166061A1
; GENERAL INFORMATION:
; APPLICANT: Enerback, Sven
; APPLICANT: Carlsson, Peter
; TITLE OF INVENTION: Animal Model
; FILE REFERENCE: 10806-117A
; CURRENT APPLICATION NUMBER: US/10/806,782
; PRIOR APPLICATION NUMBER: US/03-23,782
; PRIOR FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/587,945
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 60/190,692
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/085,380
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: SE 9701963-2
; PRIOR FILING DATE: 1997-05-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 5' primer
US-10-806-782-5

Query Match 2.6%; Score 13; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 CTGAGCCTTCT 127

Db 9 CTGCAGCCTTCT 21

RESULT 69
ME-10-438

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US-10-438-657-12
Sequence 12, Application US/10438657
Publication No. US2003026194A1
GENERAL INFORMATION:
APPLICANT: EISHINGDRELO, Haifeng
APPLICANT: CAI, Jidong
APPLICANT: ARDATT, Mohamad Ali
APPLICANT: SANDRASAGRA, Anthony
TITLE OF INVENTION: A NOVEL G PROTEIN-COUPLED RECEPTOR, GAVE 2
FILE REFERENCE: USAV001/0051 USNP
CURRENT APPLICATION NUMBER: US/10/438,657
CURRENT FILING DATE: 2003-05-15
PRIORITY APPLICATION NUMBER: US 60/382,375
PRIORITY FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Probe
US-10-438-657-12

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Query Match	2.6%	Score 13	DB 15	Length 23
Best Local Similarity	100.0%	Pred. No.	2.2e+04	
Matches 13	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	1	TGCCCTCTGCAAG	13
Db	8	TGCCCTCTGCAAG	20

RESULT 70

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US-10-296-665-2
Sequence 2, Application US/10296665
Publication No. US20040093630A1
GENERAL INFORMATION:
APPLICANT: TG BIOTECH, INC.; Tae-Lin HUH
APPLICANT: HUH, Tae-Lin
APPLICANT: PARK, Hae-Chul
APPLICANT: KIM, Chul-Hee
APPLICANT: KIM, Hyung-seok
TITLE OF INVENTION: ZEBRAFISH HUC PROMOTER CAPABLE OF DIRECTING NEURON-SPECIFIC EXPRESSION OF A FOREIGN GENE IN TRANSGENIC ANIMAL HAVING HUC PROMOTER AND ITS USE IN SCREENING NEURONAL MUTANT ANIMALS USING THE TRANSGENIC ANIMAL
FILE REFERENCE: 58049-00011
CURRENT APPLICATION NUMBER: US/10/296,665
CURRENT FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: primer
FEATURE:
NAME/KEY: primer blind
LOCATION: (1)..(24)
OTHER INFORMATION:
US-10-296-665-2

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Query Match	2.6%	Score 13;	DB 16;	Length 24;
Best Local Similarity	100.0%;	Pred. No. 2.2e+04;		
Matches 13; Conservative	0;	Mismatches	0;	Gaps 0

94 CCTCAGCAGTGTG 106

Db 1 CCTCAGCAGTGTG 13

RESULT 71
THE-10-300

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US-10-300-263-7/c
/ Sequence 7, Application US/10300263
/ Publication No. US20040096634M1
/ GENERAL INFORMATION:
/ APPLICANT: Kenneth W. Dobie
/ TITLE OF INVENTION: MODULATION OF HIP-1 PROTEIN INTERACTOR EXPRESSION
/ FILE REFERENCE: RTS-0431
/ CURRENT APPLICATION NUMBER: US/10/300,263
/ CURRENT FILING DATE: 2002-11-19
/ NUMBER OF SEQ ID NOS: 154
/ SEQ ID NO 7
/ LENGTH: 24
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: PCR Probe
/ US-10-300-263-7

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Query Match	2.6%	Score 13	DB 16	Length 24
Best Local Similarity	100.0%	Pred. No. 2.2e+04		
Matches 13, Conservative 0		Mismatches 0	Indels 0	Gaps 0

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QY      206 AGTGTCTGGACGG 218
          |||||
Db      13  AGTGTCTGGACGG 1

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RESULT 72

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US-09-866-108-12731/c
/ Sequence 12731, Application US/09866108
/ Patent No. US20020048800A1
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: UI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wenheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMIC-7
/ CURRENT APPLICATION NUMBER: US/09/866,108
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263, 6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30

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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 12731
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-12731

Query Match 2.6%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 CACCTGCTGCTTC 42
|||||
Db 25 CACCTGCTGCTTC 13

RESULT 73
US-09-866-108-12732/c
Sequence 12732, Application US/09866108
Patent No. US2002004800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 12732
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens

US-09-866-108-12732

Query Match 2.6%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 CACCTGCTGCTTC 42
|||||
Db 24 CACCTGCTGCTTC 12

RESULT 74
US-09-866-108-12733/c
Sequence 12733, Application US/09866108
Patent No. US2002004800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 12733
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens

US-09-866-108-12733

Query Match 2.6%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 CACCTGCTGCTTC 42
|||||
Db 23 CACCTGCTGCTTC 11

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RESULT 75
US-09-866-108-12734/c
; Sequence 12734, Application US/09866.108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wenheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aemica Sequence Listing Engine
; SEQ ID NO 12734
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-12734

Query Match 2.6%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
30 CACCTGCTGCTTC 42
22 CACCTGCTGCTTC 10

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Search completed: February 3, 2005, 00:11:26
Job time : 276.669 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 15:25:00 : Search time 47.7685 Seconds
(without alignments)
7410.178 Million cell updates/sec

Title: US-10-048-046-1_COPY_1516_2013

Perfect score: 498

Sequence: 1 tggccctcgtgaaggaagcca.....gtcactggggtcgctactgc 498

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 0

Total number of hits satisfying chosen parameters: 682300

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Listing first 150 summaries

Database :

Issued Patents NA:*

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- 2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCRUS.COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	3.0	20	4	US-09-657-453A-51
2	15	3.0	22	4	US-09-470-443-37
3	15	3.0	25	4	US-09-645-629-12
4	14	2.8	15	2	US-08-585-684B-790
5	14	2.8	15	2	US-08-585-684B-791
6	14	2.8	15	2	US-08-585-684B-792
7	14	2.8	15	3	US-09-038-073-790
8	14	2.8	15	3	US-09-038-073-791
9	14	2.8	15	3	US-09-038-073-792
10	14	2.8	30	4	US-09-549-564-10
11	13	2.6	17	4	US-09-866-108A-7839
12	13	2.6	17	4	US-09-866-108A-7840
13	13	2.6	17	4	US-09-866-108A-7841
14	13	2.6	17	4	US-09-866-108A-7842
15	13	2.6	17	4	US-09-866-108A-7843
16	13	2.6	18	4	US-09-422-978-9581
17	13	2.6	18	4	US-09-422-978-9581
18	13	2.6	18	4	US-09-544-398B-478
19	13	2.6	20	1	US-08-480-784-4
20	13	2.6	20	1	US-08-480-784-4
21	13	2.6	20	1	US-08-487-002-4
22	13	2.6	20	1	US-08-483-554B-4
23	13	2.6	20	1	US-08-488-011B-4
24	13	2.6	20	3	US-08-850-727-4
25	13	2.6	20	4	US-09-230-652-100
26	13	2.6	20	4	US-09-445-174B-2
27	13	2.6	20	5	PCT-US95-10202-4

28	13	2.6	20	5	PCT-US95-10203-4	Sequence 4, Appl1
29	13	2.6	20	5	PCT-US95-10220-4	Sequence 4, Appl1
30	13	2.6	22	4	US-09-617-548-2	Sequence 2, Appl1
31	13	2.6	22	4	US-09-587-945-5	Sequence 5, Appl1
32	13	2.6	24	2	US-08-808-550-8	Sequence 8, Appl1
33	13	2.6	24	2	US-08-691-814B-53	Sequence 53, Appl1
34	13	2.6	24	2	US-08-859-998-767	Sequence 767, Appl1
35	13	2.6	24	2	US-09-325-928-767	Sequence 767, Appl1
36	13	2.6	24	4	US-09-225-201B-767	Sequence 767, Appl1
37	13	2.6	25	3	US-08-343-998-12	Sequence 12, Appl1
38	13	2.6	25	3	US-09-667-135-17	Sequence 17, Appl1
39	13	2.6	25	4	US-09-866-108A-12731	Sequence 12731, A
40	13	2.6	25	4	US-09-866-108A-12732	Sequence 12732, A
41	13	2.6	25	4	US-09-866-108A-12733	Sequence 12733, A
42	13	2.6	25	4	US-09-866-108A-12734	Sequence 12734, A
43	13	2.6	25	4	US-09-866-108A-12735	Sequence 12735, A
44	13	2.6	25	4	US-09-866-108A-12736	Sequence 12736, A
45	13	2.6	25	4	US-09-866-108A-12737	Sequence 12737, A
46	13	2.6	25	4	US-09-866-108A-12738	Sequence 12738, A
47	13	2.6	25	4	US-09-866-108A-12739	Sequence 12739, A
48	13	2.6	25	4	US-09-866-108A-12740	Sequence 12740, A
49	13	2.6	25	4	US-09-866-108A-12741	Sequence 12741, A
50	13	2.6	25	4	US-09-866-108A-12742	Sequence 12742, A
51	13	2.6	28	1	US-09-866-108A-12743	Sequence 12743, A
52	13	2.6	28	1	US-08-330-790A-4	Sequence 4, Appl1
53	13	2.6	28	1	US-08-468-658-4	Sequence 4, Appl1
54	13	2.6	28	5	PCT-US95-13345-4	Sequence 4, Appl1
55	13	2.6	30	3	US-08-297-395-44	Sequence 44, Appl1
56	12	2.4	14	3	US-08-765-340-104	Sequence 104, Appl1
57	12	2.4	17	1	US-08-758-306-141	Sequence 141, Appl1
58	12	2.4	17	1	US-08-758-306-145	Sequence 145, Appl1
59	12	2.4	17	1	US-08-758-306-143	Sequence 143, Appl1
60	12	2.4	17	1	US-08-758-306-411	Sequence 411, Appl1
61	12	2.4	17	1	US-08-758-306-413	Sequence 413, Appl1
62	12	2.4	17	3	US-08-584-040-4138	Sequence 4138, Appl1
63	12	2.4	17	4	US-09-673-809-95	Sequence 95, Appl1
64	12	2.4	17	4	US-09-371-772B-1905	Sequence 1905, Appl1
65	12	2.4	17	4	US-09-371-772B-5231	Sequence 5231, Appl1
66	12	2.4	17	4	US-09-371-772B-5232	Sequence 5232, Appl1
67	12	2.4	17	4	US-09-371-772B-5233	Sequence 5233, Appl1
68	12	2.4	17	4	US-09-371-772B-6628	Sequence 6628, Appl1
69	12	2.4	17	4	US-09-854-140-12	Sequence 12, Appl1
70	12	2.4	17	4	US-09-866-108A-7838	Sequence 7838, Appl1
71	12	2.4	17	4	US-09-866-108A-7844	Sequence 7844, Appl1
72	12	2.4	17	4	US-09-866-108A-10378	Sequence 10378, Appl1
73	12	2.4	17	4	US-09-866-108A-10379	Sequence 10379, Appl1
74	12	2.4	17	4	US-09-866-108A-10380	Sequence 10380, Appl1
75	12	2.4	17	4	US-09-866-108A-10381	Sequence 10381, Appl1
76	12	2.4	17	4	US-09-866-108A-10382	Sequence 10382, Appl1
77	12	2.4	17	4	US-09-866-108A-10383	Sequence 10383, Appl1
78	12	2.4	17	4	US-09-820-296-6	Sequence 6, Appl1
79	12	2.4	17	4	US-09-820-296B-6	Sequence 6, Appl1
80	12	2.4	18	1	US-08-050-232-13	Sequence 13, Appl1
81	12	2.4	18	1	US-08-569-926-12	Sequence 12, Appl1
82	12	2.4	18	1	US-08-373-124A-35	Sequence 35, Appl1
83	12	2.4	18	1	US-08-363-240A-1097	Sequence 1097, Appl1
84	12	2.4	18	1	US-08-435-628-35	Sequence 35, Appl1
85	12	2.4	18	1	US-08-661-767-13	Sequence 13, Appl1
86	12	2.4	18	3	US-08-155-005A-12	Sequence 12, Appl1
87	12	2.4	18	3	US-09-363-783-12	Sequence 12, Appl1
88	12	2.4	18	3	US-08-761-708-12	Sequence 12, Appl1
89	12	2.4	18	3	US-09-117-860-60	Sequence 60, Appl1
90	12	2.4	18	3	US-09-117-860-61	Sequence 61, Appl1
91	12	2.4	18	3	US-09-320-911-12	Sequence 12, Appl1
92	12	2.4	18	4	US-09-077-619-3	Sequence 3, Appl1
93	12	2.4	18	4	US-09-124-304-12	Sequence 12, Appl1
94	12	2.4	18	4	US-09-661-758A-12	Sequence 12, Appl1
95	12	2.4	18	4	US-09-666-791-4209	Sequence 4209, Appl1
96	12	2.4	18	4	US-09-696-791-4210	Sequence 4210, Appl1
97	12	2.4	18	6	5176995-14	Patent No. 5176995
98	12	2.4	19	1	US-08-127-954-25	Sequence 25, Appl1
99	12	2.4	19	1	US-08-502-185-6	Sequence 6, Appl1
100	12	2.4	19	1	US-08-398-945-6	Sequence 6, Appl1

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c 101 12 2.4 19 1 US-08-569-926-1 Sequence 1, Appl1
c 102 12 2.4 19 1 US-08-569-926-21 Sequence 21, Appl1
c 103 12 2.4 19 1 US-08-501-779-6 Sequence 6, Appl1
c 104 12 2.4 19 1 US-08-701-380-8 Sequence 8, Appl1
c 105 12 2.4 19 1 US-08-501-713-6 Sequence 6, Appl1
c 106 12 2.4 19 1 US-08-378-860-6 Sequence 6, Appl1
c 107 12 2.4 19 1 US-08-501-626-6 Sequence 6, Appl1
c 108 12 2.4 19 1 US-08-501-356-6 Sequence 6, Appl1
c 109 12 2.4 19 3 US-08-577-081A-73 Sequence 73, Appl1
c 110 12 2.4 19 3 US-09-032-365A-42 Sequence 42, Appl1
c 111 12 2.4 19 3 US-09-179-558-25 Sequence 25, Appl1
c 112 12 2.4 19 3 US-08-761-708-1 Sequence 1, Appl1
c 113 12 2.4 19 3 US-08-761-708-21 Sequence 21, Appl1
c 114 12 2.4 19 3 US-08-761-708-22 Sequence 22, Appl1
c 115 12 2.4 19 3 US-08-761-708-23 Sequence 23, Appl1
c 116 12 2.4 19 3 US-09-150-999-7 Sequence 7, Appl1
c 117 12 2.4 19 3 US-09-320-911-1 Sequence 21, Appl1
c 118 12 2.4 19 3 US-09-320-911-21 Sequence 21, Appl1
c 119 12 2.4 19 3 US-09-320-911-22 Sequence 22, Appl1
c 120 12 2.4 19 3 US-09-320-911-23 Sequence 23, Appl1
c 121 12 2.4 19 4 US-09-722-825-25 Sequence 25, Appl1
c 122 12 2.4 19 4 US-09-722-825-25 Sequence 25, Appl1
c 123 12 2.4 19 4 US-09-722-87-25 Sequence 25, Appl1
c 124 12 2.4 19 4 US-09-382-465-7 Sequence 7, Appl1
c 125 12 2.4 19 4 US-09-124-304-1 Sequence 1, Appl1
c 126 12 2.4 19 4 US-09-124-304-21 Sequence 21, Appl1
c 127 12 2.4 19 4 US-09-124-304-22 Sequence 22, Appl1
c 128 12 2.4 19 4 US-09-124-304-23 Sequence 23, Appl1
c 129 12 2.4 20 1 US-08-502-185-5 Sequence 5, Appl1
c 130 12 2.4 20 1 US-08-502-185-29 Sequence 29, Appl1
c 131 12 2.4 20 1 US-08-398-945-5 Sequence 5, Appl1
c 132 12 2.4 20 1 US-08-398-945-29 Sequence 29, Appl1
c 133 12 2.4 20 1 US-08-569-926-2 Sequence 2, Appl1
c 134 12 2.4 20 1 US-08-260-515-18 Sequence 18, Appl1
c 135 12 2.4 20 1 US-08-501-779-5 Sequence 5, Appl1
c 136 12 2.4 20 1 US-08-501-779-29 Sequence 29, Appl1
c 137 12 2.4 20 1 US-08-501-713-5 Sequence 5, Appl1
c 138 12 2.4 20 1 US-08-501-713-29 Sequence 29, Appl1
c 139 12 2.4 20 1 US-08-378-860-5 Sequence 5, Appl1
c 140 12 2.4 20 1 US-08-378-860-29 Sequence 29, Appl1
c 141 12 2.4 20 1 US-08-501-626-5 Sequence 5, Appl1
c 142 12 2.4 20 1 US-08-501-626-29 Sequence 29, Appl1
c 143 12 2.4 20 1 US-08-501-356-5 Sequence 5, Appl1
c 144 12 2.4 20 1 US-08-501-356-29 Sequence 29, Appl1
c 145 12 2.4 20 3 US-09-366-257-21 Sequence 21, Appl1
c 146 12 2.4 20 3 US-09-249-730-207 Sequence 207, Appl1
c 147 12 2.4 20 3 US-08-765-340-16 Sequence 16, Appl1
c 148 12 2.4 20 3 US-08-765-340-17 Sequence 17, Appl1
c 149 12 2.4 20 3 US-08-765-340-92 Sequence 92, Appl1
c 150 12 2.4 20 3 US-09-433-694-14 Sequence 14, Appl1
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ALIGNMENTS

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RESULT 1
US-09-657-453A-51/c
; Sequence 51, Application US/09657453A
; Patent No. 6458591
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHORYLASE KINASE ALPHA 2 EXPRESS
; FILE REFERENCE: RUS-0136
; CURRENT APPLICATION NUMBER: US/09/657, 453A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 105
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
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US-09-657-453A-51
Query Match 3.0%; Score 15; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CCTGTCGACCTGCTG 38
Db 20 CCTGTCGACCTGCTG 6

RESULT 2
US-09-470-443-37
; Sequence 37, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-470-443-37

Query Match 3.0%; Score 15; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 GTTACTGCTGNGGCC 391
Db 6 GTTACTGCTGNGGCC 20

RESULT 3
US-09-645-629-12/c
; Sequence 12, Application US/09645629
; Patent No. 6472515
; GENERAL INFORMATION:
; APPLICANT: Clement-Johansson, Isabel
; APPLICANT: Dahlman-Wright, Karin
; APPLICANT: Lake, Staffan
; APPLICANT: Waseerman, Wyeth
; TITLE OF INVENTION: NOVEL RESPONSE ELEMENT
; FILE REFERENCE: 13425-032001
; CURRENT APPLICATION NUMBER: US/09/645,629
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: SE 9904269-9
; PRIOR FILING DATE: 1999-11-25
; PRIOR APPLICATION NUMBER: US 60/151,867
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: SE 9903009-0
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
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FEATURE:
OTHER INFORMATION: synthetically generated oligonucleotide
US-09-645-629-12

Query Match 3.0%; Score 15; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 AAAACATGTCGACCG 304
|||||
DB 21 AAAACATGTCGACCG 7

RESULT 4
US-08-585-684B-790
Sequence 790, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 790:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-790
Query Match 2.8%; Score 14; DB 2; Length 15;
Best Local Similarity 78.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 257 AGAATTACTGCGCA 270
|||||
DB 2 AGAATUACCGGCA 15

RESULT 5
US-08-585-684B-791
Sequence 791, Application US/08585684B

Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 791:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-791
Query Match 2.8%; Score 14; DB 2; Length 15;
Best Local Similarity 78.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 257 AGAATTACTGCGCA 270
|||||
DB 2 AGAATUACCGGCA 15

RESULT 6
US-08-585-684B-792
Sequence 792, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 792:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-792

Query Match 2.8%; Score 14; DB 2; Length 15;
Best Local Similarity 78.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 257 AGAATTACCTGGCA 270
||||:||||:||||
DB 2 AGAATUACCTGGCA 15

RESULT 7
US-09-038-073-790
Sequence 790, Application US/09038073
Patent No. 6194150
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 790:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-038-073-790

Query Match 2.8%; Score 14; DB 3; Length 15;
Best Local Similarity 78.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 257 AGAATTACCTGGCA 270
||||:||||:||||
DB 2 AGAATUACCTGGCA 15

RESULT 8
US-09-038-073-791
Sequence 791, Application US/09038073
Patent No. 6194150
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 791:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-038-073-791

Query Match 2.8%; Score 14; DB 3; Length 15;
Best Local Similarity 78.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 257 AGAATACCTGGCA 270
 ||||:||||
 Db 2 AGAAUUAUCCUGGCA 15

RESULT 9
 US-09-038-073-792

Sequence 792, Application US/09038073
 Patent No. 6194150
 GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Daniel T.
 APPLICANT: Jarvis, Thale
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
 NUMBER OF SEQUENCES: 2751
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/038, 073
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/585,684
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Matbuz, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 218/078
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 488-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 792:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-038-073-792

Query Match 2.8%; Score 14; DB 3; Length 15;
 Best Local Similarity 78.6%; Pred. No. 1.5e+03;

Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 257 AGAATACCTGGCA 270
 ||||:||||
 Db 2 AGAAUUAUCCUGGCA 15

RESULT 10
 US-09-549-564-10/c

Sequence 10, Application US/09549564
 Patent No. 6407284
 GENERAL INFORMATION:
 APPLICANT: KUDO, Junko et al.
 TITLE OF INVENTION: METHOD OF RESOLVING 2-OXOBICYCLO[3.1.0]HEXANE-6-CARBOXYLIC ACID
 FILE REFERENCE: 2185-0425P
 CURRENT APPLICATION NUMBER: US/09/549,564

CURRENT FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.0

SEQ ID NO 10

LENGTH: 30

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Designed oligonucleotide primer to introduce the site-

OTHER INFORMATION: directed mutagenesis Gly160Ser, Gly189Tyr or Gly189Phe into

US-09-549-564-10

Query Match 2.8%; Score 14; DB 4; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 216 CGGCGTGTGACCA 229
 ||||:||||
 Db 30 CGGCGTGTGACCA 17

RESULT 11
 US-09-866-108A-7839/c

Sequence 7839, Application US/09866108A
 Patent No. 6686188
 GENERAL INFORMATION:
 APPLICANT: GU, Yizhong
 APPLICANT: JI, Yonggang
 APPLICANT: PENN, Sharon G.
 APPLICANT: HANZEL, David K.
 APPLICANT: RANK, David R.
 APPLICANT: CHEN, Wensheng
 TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 FILE REFERENCE: AEOMICA-7
 CURRENT APPLICATION NUMBER: US/09/866,108A
 FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 15755
 SOFTWARE: Aeomica Sequence Listing Engine
 Patent No. 6686188
 SEQ ID NO 7839
 LENGTH: 17
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-866-108A-7839

Query Match 2.8%; Score 13; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 30 CACCTGTCTTTC 42
 ||||:||||
 Db 30 CACCTGTCTTTC 42

Db 17 CACCTGCTCTTC 5

```
RESULT 12
US-09-866-108A-7840/C
; Sequence 7840, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7840
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7840

Query Match 2.6%; Score 13; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTCTTC 42
Db 16 CACCTGCTCTTC 4

RESULT 13
US-09-866-108A-7841/C
; Sequence 7841, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
```

```
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7841
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7841
```

```
Query Match 2.6%; Score 13; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTCTTC 42
Db 15 CACCTGCTCTTC 3
```

```
RESULT 14
US-09-866-108A-7842/C
; Sequence 7842, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
```

```

; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acemica Sequence Listing Engine
; Patent NO. 6686188
; SEQ ID NO 7842
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7842

```

Query Match	2.6%	Score 13	DB 4	Length 17
Best Local Similarity	100.0%	Pred. No. 4.9e+03		
Matches 13	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	30	CACCTGCTGCTTC	42
Db	14	CACCTGCTGCTTC	2

RESULT 15
US-09-866-108A-7843/c
Sequence 7843, Application US/09866108A

```

1 GENERAL INFORMATION:
2 APPLICANT: GU, Yizhong
3 APPLICANT: JI, Yonggang
4 APPLICANT: PENN, Sharon G.
5 APPLICANT: HANZEL, David K.
6 APPLICANT: RANK, David R.
7 APPLICANT: CHEN, Wensheng
8 APPLICANT: SHANNON, Mark
9 TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
10 FILE REFERENCE: ABOVICA-7
11 CURRENT APPLICATION NUMBER: US/09/866,108A

```

```

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263. 6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Neomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7843
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7843
```

Query Match	2.6%;	Score 13;	DB 4;	Length 17;
Best Local Similarity	100.0%;	Pred. No. 4.9e+03;		
Matches 13;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	30	CACCTGCTGCTTC	42
Db	13	CACCTGCTGCTTC	1

RESULT 16
US-09-422-978-9581/c
; Sequence 9581, Application US/09422978

```

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; PTE REFERENCE: GENSEQ 000001

```

1 CURRENT APPLICATION NUMBER: US 09/442,978
 2 CURRENT FILING DATE: 1999-10-20
 3 EARLIER APPLICATION NUMBER: US 09/298,850
 4 EARLIER FILING DATE: 1999-04-21
 5 EARLIER APPLICATION NUMBER: US 60/109,733
 6 EARLIER FILING DATE: 1998-11-23
 7 EARLIER APPLICATION NUMBER: US 60/082,614
 8 EARLIER FILING DATE: 1998-04-21
 9 NUMBER OF SEQ ID NOS: 11796

```

; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/key: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-5860 for SEQ 1716, in complem
; OS-09-422-978-5861

```

Query Match	2.6%	Score 13;	DB 4;	Length 18;
Best Local Similarity	100.0%	Pred. No. 4.9e+03;		
Matches 13; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	332	TGTTTCTGCTGTC	344
Db	16	TGTTTCTGCTGTC	4

RESULT 17
US-09-422-978-11752/c
; Sequence 11752, Application US/09422978

```

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Ballester markers for use in constructing a high density...
; PTE REFERENCE: CENSEC 000001

```

```

1 CURRENT APPLICATION NUMBER: US 09/442,918
2 CURRENT FILING DATE: 1999-10-20
3 EARLIER APPLICATION NUMBER: US 09/298,850
4 EARLIER FILING DATE: 1999-04-21
5 EARLIER APPLICATION NUMBER: US 60/109,732
6 EARLIER FILING DATE: 1998-11-23
7 EARLIER APPLICATION NUMBER: US 60/083,614
8 EARLIER FILING DATE: 1998-04-21
9 NUMBER OF SEQ ID NOS: 11756
10 SEQ ID NO 11752

```

```

; ORGANISM: Homo Sapiens
;
; FEATURES:
;   NAME/KEY: primer_bind
;   LOCATION: 1..18
;   OTHER INFORMATION: downstream amplification primer 99-5075 for SRQ 3887, in complem
US-09-422-978-11752

```

Query Match 2.6%; Score 13; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 412 ACCTATCATATC 424
|||||
15 ACCTATCATATC 3

Db 15 ACCTATCATATC 3

RESULT 18

US-09-544-398B-478
Sequence 478, Application US/09544398B
Patent No. 6770461
GENERAL INFORMATION:
APPLICANT: Carulli, John P.
APPLICANT: Recker, Robert R.
APPLICANT: Johnson, Mark L.
TITLE OF INVENTION: High bone mass gene of 11q13.3
FILE REFERENCE: 032796-013
CURRENT APPLICATION NUMBER: US/09/544,398B
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 09/229,319
PRIOR FILING DATE: 1999-01-13
PRIOR APPLICATION NUMBER: US 60/071,449
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: US 60/105,511
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 641
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 478
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-544-398B-478

Query Match 2.6%; Score 13; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 ACAAGTCTCGGA 215
|||||
2 ACAAGTCTCGGA 14

Db 2 ACAAGTCTCGGA 14

RESULT 19

US-08-480-784-4/C
Sequence 4, Application US/08480784
Patent No. 5693473
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Hershman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,784
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: 8754 B
US-08-480-784-4

Query Match 2.6%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCCTGCTCC 444
|||||
16 CATTCCTGCTCC 4

Db 16 CATTCCTGCTCC 4

RESULT 20

US-08-483-553-4/C
Sequence 4, Application US/08483553
Patent No. 5709999
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Hershman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/483,553
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/409,305
: FILING DATE: 24-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/348,824
: FILING DATE: 29-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/308,104
: FILING DATE: 16-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/300,266
: FILING DATE: 02-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/289,221
: FILING DATE: 12-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Ihnen, Jeffrey L.
: REGISTRATION NUMBER: 28,957
: REFERENCE/DOCKET NUMBER: 24884-109347
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-962-4810
: TELEFAX: 202-962-8300
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 20 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: CLONE: 8754 B
: US-08-483-553-4

Query Match      2.6%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      432 CATTCCTGCTTCC 444
Db      16 CATTCCTGCTTCC 4

RESULT 21
US-08-487-002-4/c
: Sequence 4, Application US/08487002
: Patent No. 5710001
: GENERAL INFORMATION:
: APPLICANT: Shattuck-Bidens, Donna M.
: APPLICANT: Simard, Jacques
: APPLICANT: Eml, Mitsuru
: APPLICANT: Nakamura, Yusuke
: APPLICANT: Durocher, Francine
: TITLE OF INVENTION: 17q-linked Breast and Ovarian Cancer
: TITLE OF INVENTION: Susceptibility Gene
: NUMBER OF SEQUENCES: 85
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
: STREET: 1201 New York Avenue, N.W., Suite 1000
: CITY: Washington
```

```

: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,002
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/409,305
: FILING DATE: 24-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/348,824
: FILING DATE: 29-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/308,104
: FILING DATE: 16-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/300,266
: FILING DATE: 02-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/289,221
: FILING DATE: 12-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Ihnen, Jeffrey L.
: REGISTRATION NUMBER: 28,957
: REFERENCE/DOCKET NUMBER: 24884-109347
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-962-4810
: TELEFAX: 202-962-8300
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 20 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: CLONE: 8754 B
: US-08-487-002-4

Query Match      2.6%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      432 CATTCCTGCTTCC 444
Db      16 CATTCCTGCTTCC 4

RESULT 22
US-08-483-554B-4/c
: Sequence 4, Application US/08483554B
: Patent No. 5747282
: GENERAL INFORMATION:
: APPLICANT: Skolnick, Mark H.
: APPLICANT: Goldgar, David E.
: APPLICANT: Miki, Yoshio
: APPLICANT: Swenson, Jeff
: APPLICANT: Kamb, Alexander
: APPLICANT: Hershman, Keith D.
: APPLICANT: Shattuck-Bidens, Donna M.
: APPLICANT: Tavliagian, Sean V.
: APPLICANT: Wiseman, Roger W.
: APPLICANT: Futreal, P. Andrew
: TITLE OF INVENTION: 17q-linked Breast and Ovarian Cancer
```

TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,554B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: 8754 B
US-08-483-554B-4

Query Match 2.6%; Score 13; DB 1; Length 20;
Best local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCCTGCTTC 444
DB 16 CATTCCTGCTTC 4

RESULT 23
US-08-488-011B-4/c
Sequence 4, Application US/08488011B
Patent No. 5753441
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldger, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kanb, Alexander

APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,011B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347-09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: 8754 B
US-08-488-011B-4

Query Match 2.6%; Score 13; DB 1; Length 20;
Best local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCCTGCTTC 444
DB 16 CATTCCTGCTTC 4

RESULT 24
US-08-850-727-4/c
Sequence 4, Application US/08850727
Patent No. 6162897

```

GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,727
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,554
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-8100
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: 8754 B
US-08-850-727-4

Query Match 2.6%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCTGCTTCC 444
|||||
16 CATTCTGCTTCC 4
Db
```

```

RESULT 25:
US-09-230-652-100
Sequence 100, Application US/09230652A
Patent No. 653775
GENERAL INFORMATION:
APPLICANT: Tournier-Lasserre, Elisabeth
APPLICANT: Joutel, Anne
APPLICANT: Bousser, Marie-Germaine
APPLICANT: Bach, Jean-Francois
TITLE OF INVENTION: GENE INVOLVED IN CADASIL, METHOD OF DIAGNOSIS AND
TITLE OF INVENTION: THERAPEUTIC APPLICATION
FILE REFERENCE: 03715.0048-00000
CURRENT APPLICATION NUMBER: US/09/230,652A
CURRENT FILING DATE: 1999-05-17
EARLIER APPLICATION NUMBER: FR 96 09733
EARLIER FILING DATE: 1996-08-01
EARLIER APPLICATION NUMBER: FR 97 04680
EARLIER FILING DATE: 1997-04-16
EARLIER APPLICATION NUMBER: PCT/FR97/01433
EARLIER FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 163
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 100
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-230-652-100
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```

Query Match 2.6%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TGCTTCAGCCCA 49
|||||
8 TGCTTCAGCCCA 20
Db
```

```

RESULT 26
US-09-445-174B-2/C
Sequence 2, Application US/09445174B
Patent No. 673396
GENERAL INFORMATION:
APPLICANT: van Ommen, Garrit J.B.
APPLICANT: Petrij-Bosch, Anne
APPLICANT: Bakker, Egbert
APPLICANT: Devilee, Peter
TITLE OF INVENTION: A diagnostic test kit for determining a predisposition
TITLE OF INVENTION: for breast and ovarian cancer, materials and methods
FILE REFERENCE: 294-78
CURRENT APPLICATION NUMBER: US/09/445,174B
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: PCT/NL98/00325
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: EP 97201700.8
PRIOR FILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer reverse
US-09-445-174B-2
```

```

Query Match 2.6%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCTGCTTCC 444
|||||
16 CATTCTGCTTCC 4
Db
```

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCTGCTTCC 444

Db 16 CATTCTGCTTCC 4

RESULT 27

PCT-US95-10202-4/c

; Sequence 4, Application PC/TUS9510202

; GENERAL INFORMATION:

; APPLICANT: Shattuck-Eidens, Donna M.

; APPLICANT: Eml, Mitsuru

; APPLICANT: Nakamura, Yunaake

; APPLICANT: Dutocher, Francine

; TITLE OF INVENTION: In Vivo Mutations and Polymorphisms

; TITLE OF INVENTION: In the 17q-Linked Breast and Ovarian Cancer

; NUMBER OF SEQUENCES: 85

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

; STREET: 1201 New York Avenue, N.W., Suite 1000

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/10202

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/409,305

; FILING DATE: 24-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/348,824

; FILING DATE: 29-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08-308,104

; FILING DATE: 16-SEP-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/300,266

; FILING DATE: 02-SEP-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/289,221

; FILING DATE: 12-AUG-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Ihnen, Jeffrey L.

; REGISTRATION NUMBER: 28,957

; REFERENCE/DOCKET NUMBER: 24884-109347

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-962-4810

; TELEFAX: 202-962-8300

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs

; TYPE: nucleic acid

PCT-US95-10202-4

Query Match

Best Local Similarity 100.0%; Pred. No. 4.9e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CATTCTGCTTCC 444

Db 16 CATTCTGCTTCC 4

RESULT 28

PCT-US95-10203-4/c

; Sequence 4, Application PC/TUS9510203

; GENERAL INFORMATION:

; APPLICANT: Skolnick, Mark H.

; APPLICANT: Goldgar, David E.

; APPLICANT: Miki, Yoshio

; APPLICANT: Swenson, Jeff

; APPLICANT: Kamb, Alexander

; APPLICANT: Harshman, Keith D.

; APPLICANT: Shattuck-Eidens, Donna M.

; APPLICANT: Tavligian, Sean V.

; APPLICANT: Wiseman, Roger W.

; APPLICANT: Futreal, P. Andrew

; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer

; TITLE OF INVENTION: Susceptibility Gene

; NUMBER OF SEQUENCES: 85

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

; STREET: 1201 New York Avenue, N.W., Suite 1000

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/10203

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/409,305

; FILING DATE: 24-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08-348,824

; FILING DATE: 29-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08-308,104

; FILING DATE: 16-SEP-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/289,221

; FILING DATE: 12-AUG-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Ihnen, Jeffrey L.

; REGISTRATION NUMBER: 28,957

; REFERENCE/DOCKET NUMBER: 24884-109347


```
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: 8754 B
PCT-US95-10203-4

Query Match
Best Local Similarity 100.0%; Score 13; DB 5; Length 20;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 432 CATTCCTGCTTCC 444
Db 16 CATTCCTGCTTCC 4

RESULT 29
PCT-US95-10220-4/c
Sequence 4, Application PC/TUS9510220
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David B.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseeman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: Method for Diagnosing a
TITLE OF INVENTION: Predisposition for Breast and Ovarian Cancer
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10220
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08-308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
```

```
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: 8754 B
PCT-US95-10220-4

Query Match
Best Local Similarity 100.0%; Score 13; DB 5; Length 20;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 432 CATTCCTGCTTCC 444
Db 16 CATTCCTGCTTCC 4

RESULT 30
US-09-617-548-2
Sequence 2, Application US/09617548
Patent No. 6476214
GENERAL INFORMATION:
APPLICANT: EAGLES, Peter Anthony Winter
APPLICANT: ZHENG, Richard Qihao
TITLE OF INVENTION: INHIBITION OF CYTOKINE PRODUCTION
FILE REFERENCE: N & V 604-557 BTG 137 766
CURRENT APPLICATION NUMBER: US/09/617,548
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: GB 9801391.5
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: GB 9824794.3
PRIOR FILING DATE: 1998-11-11
PRIOR APPLICATION NUMBER: PCT/GB99/00179
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 22
TYPE: DNA
ORGANISM: Human interleukin-4 promoter
US-09-617-548-2

Query Match
Best Local Similarity 100.0%; Score 13; DB 4; Length 22;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 TGGCACCCTGACT 139
Db 7 TGGCACCCTGACT 19

RESULT 31
US-09-587-945-5
Sequence 5, Application US/09587945
Patent No. 6709860
GENERAL INFORMATION:
APPLICANT: Enerback, Sven
APPLICANT: Carlsson, Peter
TITLE OF INVENTION: Animal Model
FILE REFERENCE: 10806-117A
CURRENT APPLICATION NUMBER: US/09/587,945
CURRENT FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: US 60/190,692
```

PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/085,380
PRIOR FILING DATE: 1998-05-26
PRIOR APPLICATION NUMBER: SE 9701963-2
PRIOR FILING DATE: 1997-05-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 5' primer
US-09-587-945-5

Query Match 2.6%; Score 13; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 CTGCAGCCTTCT 127
DB 9 CTGCAGCCTTCT 21

RESULT 32
US-08-808-550-8/C
Sequence 8, Application US/0808550
Patent No. 5871992
GENERAL INFORMATION:
APPLICANT: Teebor, George W.
APPLICANT: Hilbert, Timothy P.
TITLE OF INVENTION: MAMMALIAN ENDONUCLEASE III AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,550
FILING DATE: 26-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-001 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer P3"
HYPOTHETICAL: NO
US-08-808-550-8

Query Match 2.6%; Score 13; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AGGAGCCAGCC 24
DB 18 AGGAGCCAGCC 6

RESULT 33
US-08-691-814B-53/C
Sequence 53, Application US/08691814B
Patent No. 5981218
GENERAL INFORMATION:
APPLICANT: Rio, Marie-Christine
APPLICANT: Tomasetto, Catherine
APPLICANT: Basset, Paul
APPLICANT: Byrne, Jennifer
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,814B
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,183
FILING DATE: 09-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1383.0090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-691-814B-53

Query Match 2.6%; Score 13; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 CTGGGGCTGCACC 150
DB 18 CTGGGGCTGCACC 6

RESULT 34
US-08-859-998-767
Sequence 767, Application US/0885998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Ukhadeze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 767:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-767

Query Match 2.6%; Score 13; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AGCCAGCCCTGT 28
Db 6 AGCCAGCCCTGT 18

RESULT 35
US-09-225-928-767
Sequence 767, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilaashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 767:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 767:
US-09-225-928-767

Query Match 2.6%; Score 13; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AGCCAGCCCTGT 28
Db 6 AGCCAGCCCTGT 18

RESULT 36
US-09-225-201B-767
Sequence 767, Application US/09225201B
Patent No. 6489455
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilaashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,201B
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 767:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

```

; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 767:
US-09-225-201B-767

Query Match          2.6%; Score 13; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 AGCCAGCGCCTGT 28
      |||
      6 AGCCAGCGCCTGT 18

RESULT 37
US-08-343-998-12
; Sequence 12, Application US/08343998A
; Patent No. 6020123
; GENERAL INFORMATION:
; APPLICANT: Sotgiu, Pierre
; APPLICANT: Brechot, Christian
; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES FOR THE AMPLIFICATION OF THE
; TITLE OF INVENTION: GENOME OF THE RETROVIRUSES OF THE HIV-2 AND SIV TYPE,
; TITLE OF INVENTION: AND THEIR USES FOR IN VITRO DIAGNOSIS OF THE INFECTIONS
; TITLE OF INVENTION: DUE TO THESE VIRUSES
; FILE REFERENCE: 2356.0065-01
; CURRENT APPLICATION NUMBER: US/08/343.998A
; CURRENT FILING DATE: 1994-11-18
; EARLIER APPLICATION NUMBER: 07/820.600
; EARLIER FILING DATE: 1992-01-22
; EARLIER APPLICATION NUMBER: PCT/FR90/00394
; EARLIER FILING DATE: 1990-06-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 2
; FEATURE:
US-08-343-998-12

Query Match          2.6%; Score 13; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      124 TTCTGCCACCTGT 136
      |||
      3 TTCTGCCACCTGT 15

Db

RESULT 38
US-09-667-135-17
; Sequence 17, Application US/09667135
; Patent No. 6521749
; GENERAL INFORMATION:
; APPLICANT: Vincent Ling
; APPLICANT: Kyriaki Dunussi-Joannopoulos
; TITLE OF INVENTION: NOVEL GL50 MOLECULES AND USES THEREFOR
; FILE REFERENCE: GNN-007
; CURRENT APPLICATION NUMBER: US/09/667.135
; CURRENT FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-667-135-17
```

```

Query Match          2.6%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 ACCTGCTGCTTC 43
      |||
      13 ACCTGCTGCTTC 25

Db

RESULT 39
US-09-866-108A-12731/c
; Sequence 12731, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 12731
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-866-108A-12731

Query Match          2.6%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      30 CACCTGCTGCTTC 42
      |||
      25 CACCTGCTGCTTC 13

Db

RESULT 40
US-09-866-108A-12732/c
; Sequence 12732, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
US-09-866-108A-12732
```

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/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: A60MCA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: A60MCA Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 12732
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-12732
```

```
Query Match 2.6%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 30 CACCTGCTGCTTC 42
Db 24 CACCTGCTGCTTC 12
```

```
RESULT 41
US-09-866-108A-12733/C
/ Sequence 12733, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: A60MCA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
```

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/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: A60MCA Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 12733
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-12733
```

```
Query Match 2.6%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 30 CACCTGCTGCTTC 42
Db 23 CACCTGCTGCTTC 11
```

```
RESULT 42
US-09-866-108A-12734/C
/ Sequence 12734, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: A60MCA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: A60MCA Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 12734
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-12734
```

```
Query Match      2.6%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      30 CACCTGCTGCTTC 42
Db      22 CACCTGCTGCTTC 10

RESULT 43
US-09-866-108A-12735/c
; Sequence 12735, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 12735
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-12735

Query Match      2.6%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      30 CACCTGCTGCTTC 42
Db      21 CACCTGCTGCTTC 9

RESULT 44
US-09-866-108A-12736/c
; Sequence 12736, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 12736
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-12736

Query Match      2.6%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      30 CACCTGCTGCTTC 42
Db      20 CACCTGCTGCTTC 8

RESULT 45
US-09-866-108A-12737/c
; Sequence 12737, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 12737
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-12737
```

```
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ SOFTWARE: Aecomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 12737
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-12737

Query Match          2.6%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      30 CACCTGCTGCTTC 42
Db      19 CACCTGCTGCTTC 7

RESULT 46
US-09-866-108A-12738/c
/ Sequence 12738, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEWICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aecomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 12738
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
```

```
US-09-866-108A-12738

Query Match          2.6%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      30 CACCTGCTGCTTC 42
Db      18 CACCTGCTGCTTC 6

RESULT 47
US-09-866-108A-12739/c
/ Sequence 12739, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEWICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aecomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 12739
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-12739

Query Match          2.6%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      30 CACCTGCTGCTTC 42
Db      17 CACCTGCTGCTTC 5

RESULT 48
US-09-866-108A-12740/c
/ Sequence 12740, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
```

```
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aeomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 12740
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-866-108A-12740

Query Match      2.6%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      30 CACCTGCTGCTTC 42
Db      16 CACCTGCTGCTTC 4

RESULT 49
/ US-09-866-108A-12741/c
/ Sequence 12741, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aeomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 12742
/ LENGTH: 25
/ TYPE: DNA
```

```
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aeomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 12741
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-866-108A-12741

Query Match      2.6%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      30 CACCTGCTGCTTC 42
Db      15 CACCTGCTGCTTC 3

RESULT 50
/ US-09-866-108A-12742/c
/ Sequence 12742, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aeomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 12742
/ LENGTH: 25
/ TYPE: DNA
```


ORGANISM: Homo sapiens
US-09-866-108A-12742

Query Match
Best Local Similarity 100.0%; Score 13; DB 4; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCTTC 42
DB 14 CACCTGCTGCTTC 2

RESULT 51
US-09-866-108A-12743/C
Sequence 12743, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AROMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 12743
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-12743

Query Match
Best Local Similarity 100.0%; Score 13; DB 4; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCTTC 42
DB 14 CACCTGCTGCTTC 1

RESULT 52
US-08-330-790A-4/C
Sequence 4, Application US/08330790A
Patent No. 5629178
GENERAL INFORMATION:
APPLICANT: Demers, Daniel B

TITLE OF INVENTION: A Method for Enhancing Amplification
TITLE OF INVENTION: in the Polymerase Chain Reaction
TITLE OF INVENTION: Employing Peptide Nucleic Acids (PNA)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,790A
FILING DATE: 28-OCTOBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul Devineky
REGISTRATION NUMBER: 28,553
REFERENCE/DOCKET NUMBER: 7513-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-330-790A-4

Query Match
Best Local Similarity 100.0%; Score 13; DB 1; Length 28;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 GCGGGAGAGTGT 336
DB 26 GCGGGAGAGTGT 14

RESULT 53
US-08-468-658-4/C
Sequence 4, Application US/08468658
Patent No. 5656461
GENERAL INFORMATION:
APPLICANT: Demers, Daniel B
TITLE OF INVENTION: A Method for Enhancing Amplification
TITLE OF INVENTION: in the Polymerase Chain Reaction
TITLE OF INVENTION: Employing Peptide Nucleic Acids (PNA)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCDERMOTT, WILL & EMERY
STREET: 1850 K St., N.W., Suite 450
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,658
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul Devinsky
REGISTRATION NUMBER: 28,553
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-658-4

Query Match 2.6%; Score 13; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 GCGGGAGTGT 336
|||||
DB 26 GCGGGAGTGT 14

RESULT 54
PCT-US95-13345-4/c
Sequence 4, Application PC/TUS9513345
GENERAL INFORMATION:
APPLICANT: Genetics & IVF Institute, Inc.
TITLE OF INVENTION: A Method for Enhancing Amplification
TITLE OF INVENTION: In the Polymerase Chain Reaction
TITLE OF INVENTION: Employing Peptide Nucleic Acids (PNA)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOPER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13345
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,790
FILING DATE: 28-OCTOBER-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Paul Devinsky
REGISTRATION NUMBER: 28,553
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-13345-4

Query Match 2.6%; Score 13; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 GCGGGAGTGT 336
|||||

DB 26 GCGGGAGTGT 14

RESULT 55
US-08-297-395-44/c
Sequence 44, Application US/08297395A
Patent No. 6039947
GENERAL INFORMATION:
APPLICANT: Howard L. Weiner
TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
TITLE OF INVENTION: EPITOPES OF MYELIN BASIC PROTEIN
FILE REFERENCE: 1010/05723US3
CURRENT APPLICATION NUMBER: US/08/297,395A
CURRENT FILING DATE: 1994-08-11
EARLIER APPLICATION NUMBER: 08/059,189
EARLIER FILING DATE: 1993-05-06
EARLIER APPLICATION NUMBER: 07/502,559
EARLIER FILING DATE: 1990-03-30
EARLIER APPLICATION NUMBER: PCT/US88/02139
EARLIER FILING DATE: 1988-06-24
EARLIER APPLICATION NUMBER: 07/065,734
EARLIER FILING DATE: 1987-06-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 30
TYPE: DNA
ORGANISM: Homo sapiens
US-08-297-395-44

Query Match 2.6%; Score 13; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 CTGCTGAGCCT 123
|||||
DB 19 CTGCTGAGCCT 7

RESULT 56
US-08-765-340-104/c
Sequence 104, Application US/08765340
Patent No. 6150092
GENERAL INFORMATION:
APPLICANT: UCHIDA, K.,
APPLICANT: UCHIDA, T.,
APPLICANT: TANAKA, Y.,
APPLICANT: MATSUDA, Y.,
APPLICANT: KONDO, S.,
TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
TITLE OF INVENTION: COMPOUND
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,340
FILING DATE: 23-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 145146/94
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 31130/94
FILING DATE: 21-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: SERUNIAN, LESLIE
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 1452-4005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-765-340-104

Query Match 2.4%; Score 12; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 334 TTCTGCTGCT 345
Db 12 TTCTGCTGCT 1

RESULT 57
US-08-758-306-141/C
Sequence 141, Application US/08758306
Patent No. 5807743
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: McSwiggen, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-758-306-141

Query Match 2.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 GCTGAACAA 233
Db 16 GCTGAACAA 5

RESULT 58
US-08-758-306-143/C
Sequence 143, Application US/08758306
Patent No. 5807743
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: McSwiggen, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-758-306-143

Query Match 2.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 GCTGAACAA 233
Db 13 GCTGAACAA 2

RESULT 59
US-08-758-306-145/C
; Sequence 145, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-145

Query Match 2.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 GCTGAACACAA 233
Db 12 GCTGAACACAA 1

RESULT 60
US-08-758-306-411/C
; Sequence 411, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 411:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-758-306-411

Query Match 2.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 GAAAAACATGTT 299
Db 13 GAAAAACATGTT 2

RESULT 61
US-08-758-306-413/C
; Sequence 413, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:

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: APPLICATION NUMBER: US/08/758,306
: FILING DATE: December 3, 1996
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Warburg, Richard J.
: REGISTRATION NUMBER: 32,327
: REFERENCE/DOCKET NUMBER: 212/132
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 413:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 17 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-08-758-306-413
:
Query Match          2.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
QY      288 GAAAAACTGTT 299
Db      12 GAAAAACTGTT 1
:
RESULT 62
US-08-584-040-4138/c
: Sequence 4138, Application US/08584040
: Patent No. 6346398
: GENERAL INFORMATION:
: APPLICANT: Pavco, Pamela
: APPLICANT: McSwiggen, James
: APPLICANT: Scinchcomb, Dan T.,
: APPLICANT: Escobedo, Jaime
: TITLE OF INVENTION: METHOD AND REAGENT FOR THE
: TITLE OF INVENTION: TREATMENT OF DISEASES OR
: TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
: TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
: GROWTH FACTOR
: NUMBER OF SEQUENCES: 8502
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071-2066
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Word Perfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/584,040
: FILING DATE: January 11, 1996
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/005,974
: FILING DATE: October 26, 1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Warburg, Richard J.
: REGISTRATION NUMBER: 32,327
: REFERENCE/DOCKET NUMBER: 218/064
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600

```

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: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 4138:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 17 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-08-584-040-4138
:
Query Match          2.4%; Score 12; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
QY      474 TGACTGCTACTG 485
Db      16 TGACTGCTACTG 5
:
RESULT 63
US-09-673-809-95/c
: Sequence 95, Application US/09673809
: Patent No. 6528261
: GENERAL INFORMATION:
: APPLICANT: INNOGENETICS N.V.
: TITLE OF INVENTION: Method for typing of HLA alleles.
: FILE REFERENCE: PCT99.86.HLA
: CURRENT APPLICATION NUMBER: US/09/673,809
: CURRENT FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 98870088.6
: PRIOR FILING DATE: 1998-04-20
: NUMBER OF SEQ ID NOS: 107
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 95
: LENGTH: 17
: TYPE: DNA
: ORGANISM: Homo sapiens
:
: US-09-673-809-95
:
Query Match          2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
QY      63 AGCGAGCGCGA 74
Db      16 AGCGAGCGCGA 5
:
RESULT 64
US-09-371-772B-1905/c
: Sequence 1905, Application US/09371772B
: Patent No. 6566127
: GENERAL INFORMATION:
: APPLICANT: Ribozyne Pharmaceuticals, Inc.
: APPLICANT: Pavco, Pam
: APPLICANT: McSwiggen, Jim
: APPLICANT: Scinchcomb, Dan
: APPLICANT: Escobedo, Jaime
: TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
: TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
: FILE REFERENCE: MBH00,876-C (237/198)
: CURRENT APPLICATION NUMBER: US/09/371,772B
: CURRENT FILING DATE: 1999-08-10
: PRIOR APPLICATION NUMBER: 1995-10-26
: PRIOR FILING DATE: 1995-10-26
: PRIOR APPLICATION NUMBER: US 08/584,040
: PRIOR FILING DATE: 1996-01-08
: NUMBER OF SEQ ID NOS: 14225
: SOFTWARE: Patentln version 3.0
: SEQ ID NO 1905
: LENGTH: 17
: TYPE: RNA
: ORGANISM: Homo sapiens

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US-09-371-772B-1905

Query Match 2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 TGAAGTCTGACG 485
|||||
Db 16 TGAAGTCTGACG 5

RESULT 65

US-09-371-772B-5231/c
; Sequence 5231, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005, 974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584, 040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5231
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5231

Query Match 2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 AAGTGTCTGAC 216
|||||
Db 17 AAGTGTCTGAC 6

RESULT 66

US-09-371-772B-5232/c
; Sequence 5232, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005, 974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584, 040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5232
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5232

Query Match 2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 AAGTGTCTGAC 216
|||||
Db 16 AAGTGTCTGAC 5

RESULT 67

US-09-371-772B-5233/c
; Sequence 5233, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005, 974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584, 040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5233
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5233

Query Match 2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 AAGTGTCTGAC 216
|||||
Db 12 AAGTGTCTGAC 1

RESULT 68

US-09-371-772B-6628/c
; Sequence 6628, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005, 974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584, 040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6628
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6628

Query Match 2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 474 TGACTGCTACTG 485
Db 13 TGACTGCTACTG 2

RESULT 69
US-09-854-140-12/C
Sequence 12, Application US/09854140
Patent No. 6664055
GENERAL INFORMATION:
APPLICANT: SCHIEFER, HANS H.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: KAINATE RECEPTOR SUBUNIT GLUR7 POLYMORPHISMS FOR
TITLE OF INVENTION: DIAGNOSING PREDISPOSITION AND FOR THERAPY OF MOOD
FILE REFERENCE: 088802-8051
CURRENT APPLICATION NUMBER: US/09/854,140
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-854-140-12

Query Match 2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 CTGCTGCGAGCC 122
Db 12 CTGCTGCGAGCC 1

RESULT 70
US-09-866-108A-7838/C
Sequence 7838, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: A60MCA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: A60MCA Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 7838
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-7838

Query Match 2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACCGCTGCTTC 42
Db 17 ACCGCTGCTTC 6

RESULT 71
US-09-866-108A-7844/C
Sequence 7844, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: A60MCA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: A60MCA Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 7844
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-7844

Query Match 2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CACCTGCTGCT 41
Db 12 CACCTGCTGCT 1

RESULT 72

US-09-866-108A-10378/C
Sequence 10378, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 10378
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-10378

Query Match 2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 239 ACGAGTCAGACA 250
Db 17 ACGAGTCAGACA 6

RESULT 73

US-09-866-108A-10379/C
Sequence 10379, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 10379
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-10379

Query Match 2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 239 ACGAGTCAGACA 250
Db 16 ACGAGTCAGACA 5

RESULT 74

US-09-866-108A-10380/C
Sequence 10380, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 10380
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-10380

Query Match 2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 ACGAGTCAGACA 250
DB 15 ACGAGTCAGACA 4

RESULT 75
US-09-866-108A-10381/C
Sequence 10381, Application US/09866108A
Patent No. 6686188

GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 10381
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-10381

Query Match 2.4%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 ACGAGTCAGACA 250
DB 14 ACGAGTCAGACA 3

Search completed: February 2, 2005, 23:37:51
Job time : 48.7685 secs

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